Structural Variation as a Catalyst of Adaptation and Speciation: From Populations to Kingdoms

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In sexual species, gene flow is considered to be the greatest impediment to speciation. The main problem with gene flow is that although divergent selection facilitates the buildup of associations between alleles favoured in local environments and those causing reproductive isolation, gene flow and recombination break the associations apart. However, examples of speciation in the face of gene flow began accumulating in the late 20th century, with accelerating evidence over the past two decades. How can this happen? In my talk, I will attempt to answer this question, drawing on a series of investigations of wild sunflower species, ranging from genome-wide association studies of phenotypic variation to field-based analyses of reproductive barrier strength, to functional characterization of candidate genes underlying reproductive isolation. I will show that most of the traits and genes that contribute to local adaptation and reproductive isolation in wild sunflowers are associated with recombination suppressors, mainly chromosomal inversions and other structural variants, thereby resolving the antagonism between selection and gene flow. Lastly, I will present a survey of more than 1000 animal, fungal, and plant genomes showing that chromosomal inversions are abundant across the three kingdoms. I will conclude by arguing that this genetic architecture offers a general solution for how speciation can occur in the presence of gene flow.

Key Words: adaptation, speciation, structural variation, inversions, sunflowers

China-Africa Cooperation for Plant Diversity Conservation and Sustainable Use

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Eastern Africa hosts exceptionally rich biodiversity across unique ecosystems including rainforests, savannas, and montane forests, supporting over 33,000 plant species with striking floristic endemism in hotspots like the Eastern Afromontane, Madagascar and the Horn of Africa. However, our assessments of African biodiversity datasets reveal severe shortages across species inventories, genetic sequences, and functional trait records alike. To address these deficits, we implemented a series of field surveys and floristic evaluations to identify priority protected areas, discover and name hidden new species, and advance targeted biodiversity conservation. A number of newly discovered plant species highlight the importance of continued research and exploration. The floristic patterns in these regions are influenced by factors such as altitude, climate, and geographical isolation, with key endemism centers identified in places like the Simen Mountains in Ethiopia. But biodiversity conservation in these areas faces challenges from threats like climate change, habitat destruction, and human activities. The evolving role of technology in conservation, such as the genomic evolution on representative lineages, such as baobabs and Welwitschia, as well as the development of application in field investigations, is facilitating biodiversity conservation. Additionally, collaborative efforts are pivotal in advancing conservation research and implementing sustainable practices. Flora of Kenya, is a flagship project launched from 2015, aiming to document the total of ca. 7,000 species of vascular plants in Kenya, with a total of 31 planned volumes. And only two volumes (Rubiaceae and Orchidaceae) have been completed, and the rest require accelerated progress. These combined efforts faciliated the preservation of Africa's rich biodiversity, which is essential for ecological balance and the well-being and livihoods of African communities.

Nuclear Phylogenomics, Evolutionary Analyses of Floral and Fruit Traits and Impact of WGD on Regulatory Genes

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Whole-genome duplications (WGDs) have been detected throughout angiosperm history, including at the origins of large families and are thought to have contributed to angiosperm diversity. Flowers and fruits are two important characteristics of angiosperms and are crucial for their reproductive success, with great impact on crop yield and ecosystem health. Floral zygomorphy (bilateral symmetry) can facilitate interactions with pollinators and have originated from the ancestral actinomorphy (radial symmetry) over 200 types. Zygomorphy is found in the three largest families (Asteraceae, Orchidaceae, and Fabaceae) and also the order Lamiaceae and represent one of the most impactful floral morphological transition. The fruit both protects developing seeds and facilitates seed dispersal; specifically, fleshy fruits provide nutritious food for a variety of animals and are important for human nutrition and are thought to have evolved from ancestral dry fruits. The distribution of both dry and fleshy fruits in the same order and sometimes in the same family support the idea that fleshy fruits have originated numerous times, as also supported by structurally different types of fleshy fruits. We have used nuclear genes to clarify relationships among members of Asteraceae and Orchidaceae, examined the history of their zygomorphic flowers, and analyzed the molecular evolution of genes, such as MADS-box genes, that play important roles in regulating development of zygomorphic flowers. We have further used floral organ specific transcriptomes to identify putative novel regulators of floral organ development with an emphasis on zygomorphy. Furthermore, we have reconstructed nuclear phylogenies across angiosperms, and for Rosaceae, Cucurbitaceae, and Solanaceae, and use these phylogenetic relationships to trace the patterns of fleshy fruit evolution and related fruit-developmental genes. These analyses provide new insights into the evolution of floral zygomorphy and dry and fleshy fruits and support crucial roles of WGDs in providing new genetic materials that allow the molecular and morphological innovations.

Key Words: WGD, zygomorphy, fleshy fruit, MADS-box

Parallel evolution of CoQ forms in flowering plants

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Coenzyme Q (CoQ), or ubiquinone, consists of a benzoquinone head group attached to a polyisoprenoid side chain of varying length, is the electron transporter in the mitochondrial respiratory chain that generates ATP, and essential to human health. Humans make Coq10 (10 isoprene units), but most staple food crops and some vegetables and fruits produce CoQ9. The side chain is synthesized by Coq1. Through extensive examination of the distributions of CoQ9 and CoQ10 in land plants and the Coq1 sequence variations of By extensive investigation of over 1000 plant species, we identified key amino acid changes, including one at position 240, that occurred independently in multiple angiosperm lineages, generally paralleling the shifts of flowering plants from trees to herbs. Guided by natural variations, we edited the native Coq1 gene in rice and wheat to produce CoQ10, paving the way to CoQ10 biofortification. Our results highlight that knowledge from plant macroevolution can be highly valuable in designing beneficial crop traits.

Sunscreening of Chloroplasts with Protein Condensates Confers High-Light Tolerance to Plants

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Sunlight fuels life but generates singlet oxygen (1O2), which causes photodamage and triggers signaling and antioxidative defense pathways in chloroplasts where photosynthesis takes place. How cells sense 1O2 and instantaneously mount photoprotection remains elusive. We show that a key mediator of 1O2 responses, METHYLENE BLUE SENSITIVITY1 (MBS1), is conserved from plants to animals and comprises a zinc-finger (ZnF) domain flanked by intrinsically disordered regions. MBS1 plays a critical role in 1O2 sensing through ZnF conformational change and phase transition from liquid-like droplets to lower-dynamic condensates. These chloroplast-associated condensates under high light attenuate light penetration to shield chloroplasts from photodamage. In rice, MBS1-overexpressing lines exhibit enhanced high-light tolerance and yield in 4-year field trials. This work uncovers an elegant condensate-based “sunscreen” that protects photosynthesis, and offers a promising target for climate-resilient crop improvement.

The evolution of kiwifruit driven by two pulses of hybridyzations

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Kiwifruit has undergone a remarkably rapid transition from a wild liana to a global multi-billion-dollar commodity within a single century. However, its complex polyploid history and reticulate evolutionary origins have remained elusive. By integrating a newly assembled haplotype-resolved pan-genome and extensively sampled genomic sequences, we demonstrated that the commercially dominant green-fleshed hexaploid *var.* deliciosa and yellow-fleshed tetraploid *var.* chinensis were sequentially originated in two successive hybridization pulses, and tetraploid *var.* chinensis has been still evolving rapidly. Our analysis reveals that the ancient introgression was pivotal for high-altitude adaptation and the selection of key agronomic traits, including cold resistance and fruit flesh color. We characterized the *Kiwifruit Flesh Color Segregation* (*KFCS*) gene as a master regulator of chlorophyll degradation and cold responses. Our findings clarify the evolutionary history of kiwifruit, showing how hybridization can enhance and retain genetic diversity, while also establishing a foundation for future research on trait development, crop improvement, and genetic conservation.

Key Words: kiwifruit, hybridization, origin, adaptation

Toward a Genus-Level Plant Tree of Life: Integrating High-Throughput Sequencing and Taxonomic Expertise

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In the Sanger sequencing era, the use of single genes (e.g., rbcL, matK) or a small number of loci led to the establishment of phylogeny-based classification systems for land plants (e.g., APG). More recently, high-throughput sequencing approaches—including genome skimming, target enrichment, and whole-genome sequencing—have been widely applied to generate genomic resources across the plant tree of life, and plastid and nuclear phylogenomics have greatly strengthened the resolution at the family level and above. Over the past five years, de novo genomes have been produced at an unprecedented pace. However, major biases remain in genomic sampling at the genus and species levels: fewer than a quarter of the estimated 450,000 land plant species are represented by at least one DNA barcode (rbcL, matK, or ITS). The Earth BioGenome Project advocated for generating reference genomes for all of Earth's extant eukaryotic species (~1.8 million), and its revised second-phase target now seeks to cover at least 50% of all accepted genera, underscoring the pressing need for better taxaonomic representation at the genus level. We advocate for integrating genome-based initiatives with herbarium-based taxonomy, as a vouchered genome inventory is indispensable for ensuring traceability and repeatability, which in turn can better inform both the plant tree of life and conservation strategies.

Key Words: land plants, genome-scale sequencing, genus-level coverage, voucher specimens

Modulating plant growth-metabolic coordination for a sustainable green revolution

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The Green Revolution of the 1960s doubled global grain production but at the heavy cost of high nitrogen fertilizer input, posing a major sustainability challenge today. To solve this problem, we performed a serious of works to enhance nitrogen use efficiency (NUE) through fine tuning nitrogen responsive carbon nitrogen metabolism. We first identified a natural SNP in 8.7 kb upstream of RCN2 as the first plant functional insulator element (INS) and its binding protein OsYY1. Under low nitrogen conditions, OsYY1 binds flanking insulators to promote chromatin loop formation that represses RCN2 transcription. Gene editing at the INS region fine tunes chromatin conformation to confer high expression of RNC2, which relieves DELLA OsSPL14 inhibition, thereby enhancing the expression of genes involved in nitrogen assimilation and carbon nitrogen partitioning without pleiotropic trade offs, which boosts both yield and NUE. In parallel, we resolved the structural basis of GA triggered DELLA degradation using cryo EM and crystallography. GA GID1 binding induces a cooperative conformational change between DELLA's N terminal domain and C terminal α12 helix, creating a high affinity interface for recruiting the F box protein GID2/SLY1. Guided by this, we engineered dominant slr1 mutants (Y94A, Y580A) in rice, which showed moderately reduced height but maintained higher biomass and yield, with markedly improved nitrogen uptake and remobilization efficiency over the classic sd1 varieties, achieving 12–19% yield increases along with better harvest index. Collectively, these studies provide both a chromatin based epigenetic strategy and a structural blueprint for designing high NUE dwarf alleles, establishing a new paradigm for breeding “green super rice” with lower nitrogen input and higher output for sustainable agriculture.

Decoding Thermal Tolerance: From Arabidopsis to Maize

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Climate change is increasing temperature extremes, threatening crop productivity and food security. Understanding how plants perceive thermal signals and translating this knowledge into crop improvement are therefore critical. In this presentation, I will highlight our recent studies on thermal adaptation from Arabidopsis to maize. We identified the receptor kinase FERONIA (FER) as a plasma membrane thermosensor. Heat-induced sterol remodeling drives FER nanoclustering, which coordinates membrane organization and activates thermotolerance, revealing a biophysical mechanism of heat sensing. To accelerate crop improvement, we integrated genetics, multi-omics, AI-assisted structural design and genome editing. Using this approach, we identified COOL1, a key regulator underlying maize chilling tolerance and climatic adaptation. We further demonstrated that the SPX-RING E3 ligase NLA coordinates cold tolerance and phosphate homeostasis. Guided by AlphaFold-based structural modeling, we engineered an NLAΔ12 allele that overcomes the trade-off between cold tolerance and phosphate uptake, resulting in improved field performance under cold stress. Together, these studies demonstrate how fundamental discoveries can be translated into climate-resilient crop germplasm through AI-guided precision breeding.

Molecular Mechanisms of the plant wound response

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Crop breeding faces two key bottlenecks. Widespread adaptive compensation causes an inherent growth-defense trade-off in plants, making it challenging to simultaneously improve crop yield and stress resistance. Meanwhile, plant regeneration capacity is highly genotype-dependent, which severely restricts the application of genome-editing and transgenic technologies in breeding. Solving these bottlenecks requires major advances in the fundamental mechanisms of plant immunity and organ regeneration.To address these challenges, we use the tomato wound response as a model system to explore the regulatory mechanisms of plant immune homeostasis and organ regeneration. A critical conceptual innovation from the lab is the division of plant wound responses into two interconnected physiological processes: immunity and regeneration. Through systematic investigations, the lab deciphered a novel mechanism wherein plants employ functionally antagonistic systemin receptors (SYR1 and SYR2) as sensors of wound severity to fine-tune immune homeostasis. Additionally, the lab identified the peptide REF1 (Regeneration Factor 1) as the primary wound signal that triggers tissue repair and organ regeneration.These findings not only provide theoretical foundations and molecular targets for the synergistic improvement of crop yield and resistance, but also offer a convenient and universal technical approach for establishing high-efficiency genetic transformation systems independent of genotype constraints.

Key Words: tomato, wound response, systemin, REF1, regeneration

Remodeling Microbial Metabolism for Phytochemicals

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High-value phytochemicals such as artemisinin and taxol are indispensable for human health, yet current sourcing strategies face pressing challenges. The *first*—plant extraction—relies on indiscriminate harvesting that damages ecosystems or on cultivated sources that consume farmland. The *second*—chemical synthesis—suffers from costly or hazardous reagents, harsh conditions, poor stereoselectivity, long synthetic routes, low overall yields, and limited scalability. The *third*—heterologous expression of native plant genes—is hindered by cross-kingdom cellular differences that impede or even preclude the coordinated expression of multi-step phytochemical pathways in non-native hosts. What strategies can we adopt to meet these challenges? This talk will outline the fundamental obstacles underlying current phytochemical sourcing challenges, and then introduce the conceptualization and realization of microbial remodeling (MR) as a *fourth* approach. MR enables access to intact druggable phytochemicals (e.g., emodin, skyrin, protohypericin, hypericin) and the construction of pharmacophores for phytochemical-based drugs such as morphine, camptothecin, reserpine, vinblastine, and vincristine. Critically, MR does not require the characterization or use of any genes from native plants. Instead, it relies on the direct, few-step modification of microbial metabolic pathways—which are inherently more scalable and thus better suited for the biomanufacturing of valuable phytochemicals.

Key Words: phytochemical, biomanufacture, microbial remodeling

Mate selection in Brassicaceae stigmas

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Mate selection in Brassicaceae stigmas relies on a sophisticated molecular dialogue that distinguishes between self, conspecific, and interspecific pollen to optimize reproductive outcomes. In self-incompatible (SI) plants, the stigma performs dual mate selection: the SRK receptor recognizes self-pollen via the haplotype-specific SCR ligand and simultaneously detects interspecific pollen signal SIPS. Both unsuitable mates are decisively rejected through downstream activation of the FERONIA receptor kinase, which elevates reactive oxygen species (ROS). In self-compatible (SC) species, which lack SRK, the stigma shifts its selection strategy: FERONIA recognizes species-specific PCP-B signals from conspecific pollen, preferentially attenuating ROS to accelerate self-pollen germination while excluding interspecific competitors. Crucially, we identified SIPS as a widely exist interspecific pollen signal in Brassicaceae, which binds SRK regardless of species origin, enabling broad-spectrum rejection of undesirable mates. Thus, the integration of SRK and FERONIA at the stigma surface serves as the central decision-making hub for mate selection, coordinating the rejection of both self and interspecific pollen while favoring compatible conspecific partners. These insights open new possibilities for manipulating mate selection checkpoints to achieve distant hybridization in Brassicaceae crops.

十字花科柱头中的配偶选择依赖于精密的分子对话，以区分自身花粉、同种花粉和异种花粉，从而优化繁殖结果。在自交不亲和（SI）植物中，柱头执行双重配偶选择功能：SRK受体一方面通过单倍型特异性配体SCR识别自身花粉，另一方面通过SIPS信号识别远缘花粉，两者均通过下游FERONIA受体激酶升高活性氧（ROS）途径，排斥不适宜的"配偶"。在自交亲和（SC）植物中，由于缺乏SRK，柱头转换选择策略：FERONIA识别同种花粉携带的物种特异性PCP-B信号，优先降低ROS水平，比远缘花粉更快萌发生长。尤为重要的是，我们鉴定出SIPS是十字花科中广泛存在的远缘花粉信号，它不论物种来源均可与SRK发生跨种互作，从而实现广谱性排斥。综上，柱头表面的SRK与FERONIA信号整合构成了配偶选择的核心决策中枢，协调对自身花粉和远缘花粉的排斥，同时支持同种异花花粉生长。这些发现为操控配偶选择检查点、实现十字花科作物远缘杂交提供了新途径。

DNA-based species characterisation: from barcodes to genomes

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DNA-based approaches have provided scalable methods for species identification, discovery, monitoring and authentication. Plant DNA barcoding, based on standard markers such as rbcL, matK, trnH-psbA, trnL and ITS, has generated insights into natural history while also supporting applications including detection of invasive species, wildlife trade regulation and product authentication. Despite these successes, discrimination among closely related plant species remains challenging because standard barcodes sample only a tiny fraction of the genome, whereas species differences are often distributed across many genomic regions and shaped by complex evolutionary processes including hybridisation, recent radiations and incomplete lineage sorting.

This presentation reviews progress towards higher-resolution genomic approaches to plant species characterisation. Large-scale analyses demonstrate that genome skimming can substantially improve species discrimination via complete plastid genomes, with further gains from kmer-based analyses of the available partial coverage of the nuclear genome. Complementary studies of nuclear genomic datasets have provided quantitative insights into the proportion of plant species that form monophyletic groups and the amount of genomic information required to maximise discrimination among species.

The presentation then explores how resources generated by the Darwin Tree of Life Project and the wider Earth BioGenome Project are creating new opportunities to investigate species boundaries using whole-genome data across diverse plant lineages. Traditionally, efforts to improve species discrimination have relied on incrementally adding data to existing barcode systems and attempting to infer optimal approaches from incomplete views of genomic variation. By contrast, comprehensive genome sequencing allows the problem to be approached from the opposite direction: starting with a near-complete understanding of genomic differences among species and then identifying the subset of information that delivers the greatest discriminatory power. This approach offers a route to more informative and efficient DNA-based identification systems, while offering the potential for general insights into the genomic nature of plant species differences.

Key Words: DNA barcoding, whole genome sequencing, species identification, species differentiation

A large phylo-floristic study reveals evolutionary constraints on the past, present, and future assembly of a unique regional flora in North America

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With 1.4 million specimens the Wisconsin State Herbarium (WIS) is one of the largest in the Americas and Wisconsin offers botanists a unique opportunity to study species representing a confluence of global biomes: boreal conifer forests, eastern deciduous forest, savannas, and grasslands. The state harbors at least 2,640 species of vascular plants, of which 1,873 are native and 767 are introduced. We have sequenced the two-gene plant DNA barcode (*rbcL+matK*) and reconstructed a complete community phylogeny for the Wisconsin flora with genomic DNA extracted almost exclusively from herbarium specimens. At the same time >300,000 georeferenced specimens from the state were used together with bioclimatic and soil data to produce species distribution models for the flora, which were subsequently aggregated in order to determine patterns of species richness and phylogenetic diversity across the state. In order to predicted future phylofloristic change, a supermatrix of all Eastern North American vascular plants (ca. 2,300 spp) was studied under models that account for climate change. Among the many surprising results we uncovered are predictions that whereas species richness will increase as ca. 850 southern taxa move northward into the state, ca. 242 species will become extirpated by 2070. Unfortunately, these are not random, but instead represent 15% of monocots, 28% of ferns/ lycopods, and 30% of orchids. Furthermore, our models suggest that Wisconsin's projected climate will be unsuitable for most species to be able to retain their present distributions; only 65% will be able to retain more than half of their current distributions.

Key Words: climate change, DNA barcoding, flora, herbarium

Genetic mechanisms of homoploid hybrid speciation and their potential applications

同倍杂交物种起源的遗传机制及其可能的应用

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物种始终在分化路上。大多数姊妹或近缘物种之间物种都没有演化出完全的生殖隔离，就开始新的物种分化周期。因此，种间杂交在近缘物种之间十分广泛，但种间F1代杂种是否独立演化也受到亲本种种群数量影响。通过对同倍杂交物种的历史演化结果发现，杂交后代迭代演化中通过交替继承双亲合子前生殖隔离的高分化基因和关键性状，从而与两个亲本物种同时发生生殖隔离。这一简洁分子遗传模式，即亲本物种AABBCCDD与aabbccdd杂交迭代产生AAbbCCdd杂交物种，为鉴定关键杂交物种形成基因提供了基础。利用这一新机制和新开发的研究方法，阐明了动植物类群中若干类群的同倍杂交物种过程和鉴定了关键的同倍杂交物种形成基因。这一分子机制，类似于种内孟德尔定律的性状分离与组合；但种间杂交时，由于生殖隔离的复杂影响，不会形成孟德尔定律的群体统计比例，但导致更多更复杂的变异个体，成为自然选择演化为杂交物种的源泉。模型模拟和实验验证发现种间杂交后代迭代演化时，不仅交替继承合子前生殖隔离相关基因，形成新的合子前生殖隔离；也通过迭代进化消除合子后生殖隔离导致的杂交后代不育等杂交后代，保留能存活的后代；只需要迭代2-3代就能完成合子前生殖隔离性状的重新组合或通过分化基因的互作，产生新的合子前生殖隔离性状，同时也能恢复有性生殖、与亲本物种形成新的合子后生殖隔离，形成新的独立演化谱系（物种）。这一发现对于远缘人工杂交创制具有理想的新性状组合或创新性性状的动植物新种质（物种）具有重要的潜在利用价值。

Using phylogenomic and genomic approachs to understand mycoheterotroph diversity and evolution

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Phylogenomic and genomic tools are revolutionizing the study of plant diversity and evolution. Here we present several case studies across the plant Tree of Life, documenting the impact of these approaches for studying the diversity and evolution of fully mycoheterotrophic (FM) plants. Members of this fascinating plant guild obtain carbon from soil-fungal partnerships, and completely lack functional photosynthesis. The FM plants provide excellent opportunities for studying both convergent origins of heterotrophy from fully autotrophic ancestors, and their divergent evolution. Elevated rates of substitution and gene loss in FM lineages might be expected to hamper accurate phylogenetic inference. However, we demonstrate that nuclear, plastid and mitochondrial phylogenomic inferences are in general well supported and highly congruent with each other, across different mycoheterotrophic taxa. Ancestral-state reconstructions on trees inferred from nuclear phylogenomic data point to possible cryptic photosynthesis losses in uniformly FM clades, and careful study of nuclear-encoded plastid-related genes compared to other nuclear genes may aid in distinguishing partial mycoheterotrophs from other autotrophs, in addition to recent origins of full mycoheterotrophy. We also document recent insights on nuclear and organellar genome and molecular evolution, and the use of target-capture methods to study phylogeographic and microbiome variation in a mycoheterotrophic bryophyte.

Key Words: Full and partial mycoheterotrophy; gene ontology; molecular evolution; microbiomes; museomics; mycoheterotrophy; photosynthesis loss; phylogeography; target sequence capture.

Origin, Diversification, and Adaptive Evolution of the Grape Family (Vitaceae)

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Faced with environmental changes, plants may either “move” to track their ancestral habitats or “evolve” and adapt to new habitats. Vitaceae, the grape family, has evolved diverse adaptive traits facilitating a global expansion in wide-ranging habitats. This evolutionary history makes Vitaceae ideal for investigating for any preference between “move” or “evolve” strategies and their underlying mechanisms. We inferred patterns of biogeographic diversification and trait evolution in Vitaceae based on a robust phylogeny with dense sampling including 495 species (~52% of Vitaceae species). Vitaceae most likely originated from Asia, the diversity center of extant genera and the major source of dispersals. India and Australasia are recognized as the biggest sinks and dispersals to the two regions might be largely facilitated by land connection. At least four shifts in diversification rates have been detected respectively in Ampelocissus, Cyphostemma, Tetrastigma, and Vitis, which have either evolved key innovations or showed adaptation to specific habitats. In particular, we find that the Oligocene-Miocene boundary is a turning point in shifting strategies, before which Vitaceae lineages preferred to “move”, and after which, to “evolve”. The increase of niche opportunities mainly contributed to the frequent employment of the “evolve” strategy after the Oligocene-Miocene boundary, while putative key trait innovations also played a role.

Key Words: adaptation, diversification, key innovations, niche opportunities, Vitaceae

From Variation to Diversification: A Multiscale Framework of Evolution

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How the small genetic changes measured within populations scale up to the abrupt origins of biodiversity across the fossil record and the tree of life remains unresolved. Standard theory is gradualist and struggles with stasis broken by rapid bursts, multiple modes of heritable variation, and adaptation in lineages with little genetic variation. We recast a trait as the attractor of a gene-regulatory network, so genetic change is buffered as cryptic variation and released when the environment changes fast. Read as informational nonequilibrium, the framework recovers population genetics as a limit, makes stasis an equilibrium, and yields an evolutionary speed limit set by accessible variance. From a single mechanism, it reproduces stasis, punctuation, survival, and radiation; fits to public fossil and phylogenetic data reproduce known patterns; and makes discriminating, falsifiable predictions.

Multidimensional Diversity Patterns and Conservation Strategies of *Rhododendron* in China

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Rhododendron is the largest genus of woody plants in the Northern Hemisphere, comprising over 1,000 species worldwide with more than 600 species in China. Under anthropogenic global change, mountain plants are among the most threatened flora, making it essential to address conservation gaps to achieve the "30 × 30" target outlined in the Convention on Biological Diversity. Focusing on the emblematic genus of montane ecosystems in Asia, we compiled an updated checklist of 603 wild *Rhododendron* species in China and integrated high-resolution distribution, phylogenetic, functional trait, and environmental data to examine spatial diversity patterns, driving factors, and priority conservation areas. Our results indicated that the taxonomic, phylogenetic, and functional dimensions of Rhododendron diversity were highly consistent. The Three-Parallel-Rivers-Region in the Hengduan Mountains emerged as the overarching hotspot for richness, endemism, and uniqueness. These diversity patterns were collectively influenced by temperature seasonality and elevation range, with temperature-related energy factors further contributing to the overall phylogenetic and functional structures. The mechanisms underlying uniqueness exhibited regional divergence: In southwestern China, high uniqueness was attributed to the accumulation of intermediate-aged and younger distinctive lineages, coupled with rapid community differentiation; in southern China, it was mainly associated with strong spatial compositional differentiation among communities; whereas in northeastern China, it largely resulted from the preservation of relict lineages. Under the 10% conservation target, we delineated nine priority conservation units across the southwestern, southern, and northeastern mountainous regions of China. However, when the conservation target was increased to 30%, these priority areas expanded to encompass broader mountain regions, highlighting a greater conservation gap. This study provides innovative insights for incorporating multidimensional diversity into effective conservation efforts for *Rhododendron* species in China.

From Parasitism to Rapid Post-fire Resprouting: Native Medicinal Herbs (Thesium, Santalales) Underpin Carbon Sinks and Biodiversity Conservation in Forest-grassland Ecotones

从寄生到火后快速萌蘖：本土药草（檀香目百蕊草属）支撑林草交错带碳汇与生物多样性保护

Jun Chen

Demographic factors are intrinsically crucial to evaluate species' extinction risk. However, measuring them remains difficult and time-consuming and the use of genomic summary statistics has been advocated to assess the conservation status of a species. In the present study, we estimated (i) the census number (N_c), (ii) effective population size (N_e) over three different time periods, recent, historical and ancient, (iii) neutral genetic diversity (π_4), and (iv) a measure of the efficacy of purifying selection (π_0⁄π_4) for 101 plant species using population genomic sequencing data. Twenty-one species are from the Plant Species with Extremely Small Populations (PSESP) program of SW China. Threatened species exhibited significantly lower N_e, N_c, π_4, and weaker purifying selection, but had a higher N_e/N_c ratio than non-threatened ones. N_c was the main determinant in identifying conservation status, and contemporary neutral genetic diversity was predominantly influenced by historical N_e. In the absence of demographic information, genetic parameters are a good proxy of conservation status, likely because currently threatened species also had a low historical population size. In summary, our findings suggest that direct estimates of N_c are more useful than π_4, although the latter remains a valuable conservation indicator. Hence, efforts such as the PSESP should be extended.

Key Words: demographic history, census size, genetic diversity, IUCN threatened, PSESP

Genome of Alpine *Thesium ramosoides* (Santalales): Advancing the Plant Tree of Life 2.0 and Deciphering Evolution of Parasitism and Post-fire Rapid Regeneration

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Santalales host diverse parasitic lineages and represent a pivotal clade for investigating life-form innovation and adaptive evolution across the land plant Tree of Life. However, high-quality genomic resources remain scarce for most parasitic species, limiting phylogenomic reconstruction and exploration on the origin of key traits within the framework of "PLANeT" and Plant Tree of Life 2.0. As an alpine hemiparasite endemic to Mountains of the Southwest China, *Thesium ramosoides* has evolved hemiparasitic nutrition, tolerance to high-altitude stresses, and prominent post-fire regeneration simultaneously. The convergence of these distinct adaptive characteristics makes it an outstanding system to investigate the co-evolution of multiple complex traits. In this study, we assembled a chromosome-level reference genome of *T. ramosoides* using PacBio HiFi long reads combined with Hi-C scaffolding, filling the genomic gap of species-rich *Thesium*, contributing valuable datasets to Plant Tree of Life 2.0. Phylogenomic analyses

resolved the phylogenetic placement of *Thesium* in Santalales and explored the origin of parasitic lifestyles in this order. Comparative genomic analyses revealed pronounced contraction of photosynthesis-related gene families in *T. ramosoides* relative to autotrophic relatives, indicating functional genomic remodeling accompanying the transition to hemiparasitism. The absence of key root hair development genes correlates with the degenerate root hair phenotype observed in this species. Genomic signatures associated with responses to alpine stresses were detected, facilitating the persistence of this species under hypoxia and reduced pathogen pressure at high altitudes. Notably, expansion of gene families associated with meristem development is consistent with the presence of below-ground crown buds that enable rapid regeneration after mountain fires, underpinning its adaptive strategy under fire-prone environments. By integrating time-series transcriptomic data, we propose a post-fire "defense first, repair later, recovery last" model, in which resources are reallocated from immediate defense to rapid repair and ultimately to long-term recovery, to explain the adaptation of *T. ramosoides* to fire-prone habitats. Collectively, the genome of *T. ramosoides* preserves evolutionary footprints for three major adaptive traits: hemiparasitism, alpine tolerance, and post-fire regeneration, illustrating how multiple co-occurring selection pressures jointly shape genomic features. This study improves the phylogenetic framework of parasitic Santalales, offers novel insights into the evolutionary connections between the origin of plant parasitism and extremophilic adaptation, and advances our ecological and evolutionary understanding of how wildfires shape plant genomes and key functional traits.

Key Words: Thesium, Santalales, parasitic evolution, alpine adaptation, post-fire rapid regeneration

Artificial intelligence and the future of plant taxonomy

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Plant taxonomy is entering a computational era. Large-scale herbarium digitisation, citizen-science observations, genomic and phylogenomic datasets, ecological records, georeferenced occurrence data, and digitised taxonomic literature are generating unprecedented quantities of evidence for describing, identifying, delimiting, and classifying plant diversity. However, more data do not automatically lead to more stable or reproducible taxonomy. In many plant groups, especially those affected by hybridisation, introgression, polyploidy, incomplete lineage sorting, phenotypic plasticity, and cryptic divergence, different sources of evidence may support different taxonomic interpretations. Species boundaries may be blurred, named taxa may be non-monophyletic, and higher-level classifications may be difficult to reconcile with complex phylogenomic histories. These challenges raise a central question for modern plant systematics: how can heterogeneous evidence be assembled, compared, interpreted, and translated into defensible taxonomic decisions? In this review, we propose All-Evidence, AI-Assisted Taxonomy as a conceptual and operational framework for addressing this problem. We argue that artificial intelligence (AI), especially machine learning and deep learning, should not be understood as a replacement for taxonomists, species concepts, phylogenetic reasoning, or nomenclatural judgement. Rather, AI is most useful as an analytical and connective layer within phylogenetically anchored, lineage-based taxonomy. In this role, AI can help extract features from images, specimens, sequences, ecological data, and taxonomic texts; standardise heterogeneous evidence; detect hidden patterns and inconsistencies; quantify some aspects of uncertainty; and compare alternative taxonomic hypotheses in a more explicit and reproducible manner. We review current and emerging applications of AI in four major domains of plant taxonomy. First, in species identification, convolutional neural networks and related computer-vision approaches can assist in identifying field photographs and herbarium specimens, detecting potential misidentifications, and supporting large-scale curation of digital collections. These tools

are already useful for common and well-sampled taxa, but their reliability decreases for rare species, hybrid complexes, morphologically cryptic taxa, and lineages whose diagnostic characters are not visible in standard images. Second, in species delimitation, machine-learning methods can help explore genomic clusters, morphological variation, ecological differentiation, and alternative species hypotheses. However, algorithmic clusters should not be equated directly with species, because they may reflect population structure, sampling artefacts, local adaptation, introgression, or data-filtering choices rather than independently evolving lineages. Third, for higher-level classification and phylogenomic synthesis, AI can assist in model choice, tree search, gene-tree conflict analysis, network inference, orthology assessment, and the identification of genomic regions that support alternative backbone hypotheses. Nevertheless, formal classification remains a taxonomic act that must consider diagnosability, stability, nomenclatural practice, and communication needs. Fourth, in taxonomic knowledge mining, natural language processing and knowledge-graph approaches can extract scientific names, morphological characters, type information, distributions, ecological attributes, and synonymy relationships from floras, monographs, protologues, specimen labels, and online databases. These tools can transform fragmented taxonomic knowledge into more reusable, machine-readable systems, but they remain vulnerable to OCR errors, historical terminology, multilingual variation, unstable names, and inherited database errors. The central contribution of this review is to integrate these scattered AI applications into a single taxonomic framework. In All-Evidence, AI-Assisted Taxonomy, candidate taxonomic hypotheses are evaluated through convergent and conflicting evidence from morphology, phylogenomics, ecology, geography, images, text, specimens, and nomenclature. AI supports evidence assembly, feature extraction, conflict diagnosis, uncertainty assessment, and hypothesis comparison, while final decisions remain grounded in expert judgement, explicit species concepts, phylogenetic interpretation, field knowledge, and the rules of botanical nomenclature. This framework is particularly relevant for reticulate and morphologically difficult plant groups, where no single data type is sufficient and where subjective weighting of evidence has long limited reproducibility. We conclude that the future of AI in plant taxonomy lies not in automated classification, but in making the evidential basis of taxonomy more transparent, scalable, auditable, and updateable. Properly constrained and critically evaluated, AI can help taxonomists move from isolated evidence streams toward integrated, lineage-based, and reproducible classifications, while preserving the central role of taxonomic expertise in interpreting plant diversity.

Key Words: artificial intelligence; plant taxonomy; integrative taxonomy; species delimitation; phylogenomics; machine learning; all-evidence taxonomy; reticulate evolution.

The key roles of chromosomal inversions in adaptation and speciation

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Chromosomal inversions play key roles in adaptation and speciation in the presence of gene flow by suppressing recombination between locally adapted alleles. Population genomic analyses identified multiple large genomic regions consistent with inversions that differentiate ecotypes in wild sunflowers. The inversions are enriched in the ecotypes, show elevated linkage disequilibrium, and associate with key environmental variables, indicating their contribution to adaptive divergence. At the same time, although recombination suppression is expected to promote the accumulation of deleterious mutations, genome-wide analyses across sunflower species show limited evidence for such accumulation within inversions, likely due to low heterozygosity driven by divergent selection. Furthermore, inversions disproportionately contribute to parallel evolution by capturing co-adapted alleles of large phenotypic effect. In independent dune ecotypes, adaptive traits, shared quantitative trait loci, and signatures of selective sweeps are enriched within inversions, often involving the same alleles across populations. Together, these findings highlight inversions as key re-combination modifiers that promote adaptive divergence and parallel evolution while largely avoiding deleterious genetic load.

Key Words: chromosomal inversion, speciation, local adaptation, sunflower

Computer-controlled acoustic AI for dormancy and germination profiling in seeds: a tool for conservation science

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Seed dormancy and germination are fundamental to plant establishment, yet conventional assessment methods remain largely destructive, slow, and subjective, relying on counting radicle emergence over days or weeks. In conservation science, this is a particular limitation for rare, endangered, or seed-banked species, where each seed is a valuable genetic resource. Recent advances in AI-based acoustic detection of respiratory diseases, such as COVID-19 from cough recordings, demonstrate that subtle, biologically produced sound signatures can be converted into robust classifiers using machine-learning models. This work adapts the same conceptual logic to seeds, proposing a bench-top, computer-controlled acoustic AI system for the non-destructive detection of dormancy status and early germination in a controlled laboratory environment. The tool we have developed has a small seed chamber in which individual seeds or seed batches are placed under controlled temperature and humidity. Instead of using ambient microphones, the system employs air-coupled ultrasound or piezoelectric transducers to generate and receive mechanical waves that pass through or around the seed; the transducers are mounted on a scanning stage that allows sequential interrogation of multiple seeds. The acquired time-series signals are digitised and fed to a desktop computer, which extracts spectro-temporal features such as attenuation profiles, time-of-flight delays, resonance frequencies, micro-transient events, and spectrogram-based descriptors analogous to Mel-frequency cepstral coefficients. These features are labelled according to parallel germination assays, classifying seeds as dormant, non-dormant but not yet germinated, or actively germinating, and used to train convolutional neural networks, recurrent (LSTM) networks, and lightweight transformer-based classifiers that can run in real time on standard lab hardware. The application of this acoustic AI platform is versatile, spanning general use in seed laboratories, germplasm banks, and conservation-oriented restoration programmes. It can reduce the number of seeds consumed in destructive tests, guide dormancy-breaking treatments such as stratification or scarification, and support decisions on seed-lot prioritisation, sowing timing, and long-term seed-bank management. In

addition, it holds particular value for conservation-dependent species with limited seed numbers. By translating biologically relevant acoustic signatures into probabilistic dormancy and germination states, the system provides a non-invasive, repeatable decision-support tool for both experimental seed science and practical conservation work.

Key Words: acoustic AI; germination; non-destructive; seed dormancy; spectro-temporal.

A decade of floral ecology: meta-analytic insights from Shaw-Nature Reserve

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Plant-pollinator interactions have been known to vary over time, however, long-term data sets to show this variance are rare. In this study, Shaw Nature Reserve, a Missouri Botanical Garden site, is used to observe plant-pollinator interactions from 2012-2025. This site is located in Gray Summit, Missouri and includes four habitat types (prairie, glade, wetland, and forest). At this site, 18 plant species will be compared. For each species, main pollinator, visitation rate, morphological differences, phenology, weather, habitat type, and pollen limitation will be analyzed. Overall, the main goal of this study is to examine pollen limitation presence in species and examine patterns between each of the variables listed. Specifically, one of the major questions being if pollen limitation is associated with a pollinator, habitat, or if it is correlated more with environmental conditions. Initial findings showed that there are pattern differences across species for both visitation rate and main pollinator. However, the reasoning for these differences over time is still being examined. The current analyses will integrate pollen tube data to see how the pollinator activity is influencing the overall reproductive success of each species. Each of these species can be combined to provide insight for the cause of the variability seen in plant-pollinator networks.

Key Words: plant-pollinator networks, pollen limitation, pollination

Assessment of population and threats to *Cycas pectinata* in Nepal

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Cycas pectinata Buch.-Ham., an evergreen tree commonly referred to as a "living fossil," is primarily distributed in the tropical regions of the eastern Himalayan Indo-China zone. It is the only species of Cycas found in Nepal. There is a dearth of research specifically focusing on the population and ecology of this species in the country. The species is currently listed as Vulnerable (VU) on the IUCN Red List and in CITES Appendix II.This study aims to assess the current population status, distribution, and existing threats in eastern Nepal. Purposive sampling method was employed, with 32 concentric circular sample plots established to survey the population. A 15-m radius plot was used to count and assess adult trees, while a smaller 4-m radius concentric plot recorded seedlings and other forms of regeneration. Furthermore, three focus group discussions and interviews with 10 key informants were conducted to identify potential threats and conservation needs for C. pectinata.A total of 193 individuals were recorded across the sample plots in the study area. The regeneration status appears moderately healthy at the initial stage, with 112 young seedlings (originating from both seeds and vegetative bulbils) observed in the field. However, sapling counts were low, with only 18 individuals recorded. The area of occupancy is approximately 28 km², identified as the primary habitat. Based on the plot data, the extent of occurrence is about 671.47 km².Field data confirmed that the species prefers steep terrain near gullies and water sources, within forests dominated by *Shorea robusta*. It faces numerous threats, including biological invasions, forest fires, and a variety of traditional uses for food, medicine, and horticulture. The outcomes may hold significant value for policymakers, conservationists, and regulatory bodies in developing environmentally sound conservation programs.

Key Words: conservation, gymnosperm, habitat loss, threat

Alleles of Vegetable *Brassica oleracea* Improves Production Traits of Oilseed *B. napus*

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The narrow genetic base of the C subgenome of *B. napus* (AACC, 2*n* = 38) canola is one of the impediments for continued improvement of agronomic and seed traits of this crop, including heterosis in hybrid cultivars. The C genome of vegetable *B. oleracea* (CC, 2*n* = 18) is genetically distinct from the C subgenome of *B. napus*. To broaden the genetic base of the C subgenome of canola, we developed more than a thousand re-constituted *B. napus* canola lines from several *B. napus* × *B. oleracea* interspecific crosses using different variants of *B. oleracea* such as kale, cabbage, cauliflower and broccoli. Theoretically, self-pollinated generations of the F_1's (ACC) were expected to generate *B. oleracea* plants; however, all progeny stabilized into *B. napus*. To identify the alleles of *B. oleracea* beneficial for use in canola breeding, we phenotyped the populations in field trials and growth chambers, and genotyped using molecular markers. Based on this, we have demonstrated that an allele of Chinese kale (*B. oleracea* var. *alboglabra*) located at about 41 Mb region of C01 chromosome and an allele of cabbage cv. Bindsachsener (*B. oleracea* var. *capitata*) located at about 26.1–31.8 Mb region of C05 contributes to earliness of flowering in *B. napus* under both long- (16-18 h photoperiod) and short-day (10 h photoperiod) conditions. Through expression analysis of genes, we also identified several putative genes from the QTL regions which might have played a role in the earliness of flowering under the short-day condition. We also identified an allele of Chinese kale from 40-42 Mb region of C05 increases seed oil content in *B. napus*. Several canola lines derived from these interspecific crosses also exhibited significant heterosis in F_1 hybrids and contributed to hybrid seed yield in canola. Thus, a knowledge-based use of the *B. oleracea* gene pool in the breeding of the *B. napus* canola expected to take this crop to the next level of improvement.

Key Words: Canola, genetic diversity, earliness, oil, hybrid breedin

Unveiling the Economic and Pharmacological Importance of Bamboo in Perspective of its Species Diversity in Central Siwalik Churiya) Region, Nepal

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Bamboo are the fastest growing perennial woody grasses having versatile applications. Among these various applications, young bamboo culm have been found to be exceptionally useful in reducing body weight, and control diabetes. In accordance to this, most of the local people inhabiting the rural areas of Siwalik region of Nepal are basically relying on bamboo products for economic benefits as well as medicinal purpose. This demands the need to enlist the availability of bamboo species, to recognize local traditional practices in healing the ailments, and to further explore its pharmaceutical potential. Hence, the aim of this study was to identify the species diversity of bamboo, their ethno-pharmacological practices and economic importance. Data was collected by direct observation, key informant interviews, inventory technique, and household survey by using semi-structured and structured questionnaires. Ethnobotanical survey revealed that *Bambusa balcooa,* B. tulda, and *B. nutans* subsp. *cupulata* were found to be the most utilized in traditional medicine, and thus were the prioritized bamboo species for the study. With the objective of ascertaining their medicinal value, spectrophotometer was used to quantify the total phenolic and flavonoid contents of their leaves, and in-vitro 2,2-diphenyl-1-picrylhydrazyl (DPPH) free radical scavenging assay was measured. The agar well diffusion method was also employed to analyze their antibacterial properties. This study recorded three genera and nine species of bamboo *Ampelocalamus pattelaris* (Gamble) Stapleton, *Bambusa balcooa* Roxb., *B. bambos* (L.) Voss, *B. nepalensis* Stapleton, *B. nutans* subsp. *cupulata* Stapleton, *B. tulda* Roxb., *B. vulgaris* Vittata, *Cephalostachyum latifolium* Munro, and *Dendrocalamus strictus* (Roxb.) Nees, in this part of Nepal, of which eight species were used for agriculture, five for medicine, and four for construction, food, fodder, artifacts and religious purposes. The phytochemical screening leaf-extract of *B. balcooa*, *B. tulda* and *B. nutans* subsp. *cupulata* in methanol

showed the presence of alkaloids, glycosides, saponins, phenols, terpenoids, flavonoids and steroids while *B. balcooa* exhibited steroids in hexane extract. Both the flavonoids and phenolic content of *B. balcooa* (65.11±1.33µg QE/ml and 16.05µg GAE/ml) were found to be higher than that of *B. tulda* (57.97±0.22µg QE/ml and 11.53 µg GAE/ml) and *B. nutans* subsp. *cupulata* (31.45±0.01µg QE/ml and 22.98±1.76µg GAE/ml). Highest DPPH radical scavenging activity was shown by *B. balcooa* (IC_{50} = 26.05±0.09). It concluded that the traditional utilization of all kinds of bamboo in this area is huge despite less prominent diversity of bamboo. Species such as *Bambusa balcooa*, B. tulda, and *B. nutans* subsp. *cupulata* were found to have a wide spectrum of pharmacological agents and support for the development of bamboo-based anti-oxidant food. Furthermore, the nutrient distribution in bamboos has also enormous potential to become a quality fodder for livestock animals. Considering the wider aspect of overall uses of bamboo in the study area, it is worthwhile to encourage local people to promote bamboo plantation in their fallow land which would contribute to uplift their livelihood. Furthermore, in light of the "monkey terror" prevalent in these areas, that has contribute to gradually erase traditional agricultural practices, bamboo cultivation can prove to be an efficient means of restoration of barren and riverine land and generation of economic revenue.

Key Words: Bamboo, Monkey terror, Nepal, Pharmacological, Traditional knowledge

Diversity, evolution, systematics, and conservation status of Podocarpaceae

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Among conifer families, Podocarpaceae is the second largest, with amazing diversity and functional traits, and it dominates the Southern Hemisphere. However, comprehensive studies on diversity, evolution, systematic, and ecophysiological aspects of the Podocarpaceae are sparse. We aim to outline and evaluate the current and past diversity, distribution, systematics, evolutionary adaptations, endemism, and conservation status of podocarps.We analysed data on the diversity and distribution of living and extinct macro-fossil taxa and combined it with genetic data to reconstruct an updated phylogeny, cone evolution, and understand historical biogeography. We also evaluated the biodiversity hotspots, ecophysiological, ecological, and conservation aspects of Podocarpaceae by analysing the available data. Podocarpaceae today contains 20 genera and about 219 taxa (201 species, 2 subspecies, 14 varieties, and 2 hybrids) placed in three clades plus a paraphyletic group/grade of four distinct genera. The family originated about early mid Permian, while most of the living genera show long branches and relatively recent diversification of species in the Eocene-Miocene. *Podocarpus* is the largest (about 120 species) and widely distributed genus. Indonesia, Papua New Guinea, Malaysia, the Philippines, New Caledonia, and New Zealand are the current centre of diversity of podocarps. The IUCN conservation status shows that 8 species and one variety are Critically Endangered (CR), and 27 species and 2 varieties are Endangered (EN). Macrofossil records show the presence of more than 100 podocarp taxa globally, dominantly from the Eocene-Miocene. Australasia (New Caledonia, Tasmania, New Zealand, and Malesia) is the hotspot of living podocarps diversity. The inclusion of macrofossils provides a new insight into the historical biogeography of Podocarpaceae. Podocarps also show remarkable adaptations from broad to scale leaves, fleshy seed cones, animal dispersal, shrubs to large trees, from lowland to alpine regions, and a rheophyte to a parasite (the only parasitic gymnosperm, *Parasitaxus*), and a complex pattern of functional trait evolution.

Key Words: conservation; conifers; climate change; fossils; historical biogeography; IUCN red list; paleo-endemism; physiology; phylogenetics.

Taxonomy, Species Richness, and Distribution Patterns of Cyperaceae in Nepal

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The family Cyperaceae, commonly known as the sedge family, is one of the most diverse and ecologically significant plant families worldwide; however, its taxonomy and distribution in Nepal remain poorly understood. This study presents a comprehensive taxonomic revision and spatial analysis of Cyperaceae in Nepal, a country with exceptional physiographic and ecological diversity along the Himalayas. An integrative approach was employed, combining intensive field surveys, living plant observations, and the examination of more than 4700 herbarium specimens. The spatial distribution of Cyperaceae species across Nepal was also mapped. Cyperaceae in Nepal occupy a wide range of habitats, including agricultural lands, wetlands, rangelands, and alpine ecosystems, from approximately 60 m to above 6000 m elevation. The study recognizes 244 species and six infraspecies of Cyperaceae in Nepal, representing 20 genera, 15 tribes, and one subfamily, including seven endemic taxa. Spatial analysis reveals a non-linear relationship between species richness and elevation, with diversity declining from lowlands to 1000 m, increasing to a peak at 2700–2800 m, and decreasing above 3000 m. The mid-hills and highlands of Central and Eastern Nepal harbor the highest species richness, whereas Western Nepal exhibits comparatively lower diversity. This research provides the first comprehensive and up-to-date taxonomic and ecological framework for Cyperaceae in Nepal. The findings offer an essential baseline for biodiversity conservation, biogeographic analyses, and future taxonomic and evolutionary studies of Himalayan sedges.

Key Words: Endemic, Himalayas, Sedge family, Spatial distribution, Taxonomic revision

Characterizing the genome evolution and demographic history underlying a reversal of dioecy in *Amaranthus*

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Dioecy, the reproductive system comprised of separate unisexual male or female individuals, is found in only 6% of flowering plant species. Puzzlingly though, the distribution of this trait across the angiosperm phylogeny indicates it has evolved independently hundreds or even thousands of times. Elevated extinction risk among dioecious lineages was once the leading hypothesis for this "tippy" pattern, but recent work calls that into question. Instead, the widespread reversal of dioecy back to cosexual states (i.e. hermaphroditism or monoecy) may offer a more compelling explanation. Here, we closely examine one such reversal as inferred in *Amaranthus*, a genus of ~70 species including both important crops and weeds, where dioecy has arisen twice from monoecy. Nested in the larger clade of derived dioecious plants is *A. pumilus*, or seabeach amaranth — a monoecious, predominantly selfing, species that has reverted from dioecy; this species is a rare endemic of sandy beaches in the northeastern United States, where it persists in a fugitive, often mate-limited, dynamic. Using both newly generated and previously published reference genomes, we characterize genome evolution and demographic history underlying a transition away from dioecy in *A. pumilus*. We further delineate evolutionary strata at the sex-linked regions of two of *A. pumilus's* dioecious relatives, comparing gene content and loss, substitution rates, and structural variation with the reverted species. Separately, using whole-genome sequencing data from wild *A. pumilus* populations, we estimate the age of the transition away from dioecy against the backdrop of different scenarios of demographic change and divergence. These results offer insights into how and when reversals of dioecy may proceed, providing an empirical look at the decay of sex-linked regions following a return to cosexuality.

Key Words: dioecy, comparative genomics, Amaranthus

Biogeography and diversification of the tropical amphi-Pacific disjunct genus *Dendropanax* (Araliaceae) based on phylogenomics and machine learning algorithms

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Dendropanax constitutes one of the most species-rich genera of the ginseng family (Araliaceae), with nearly 100 species with a tropical amphi-Pacific biogeographic distribution. Approximately 75% of the species are found across Mexico and the Neotropics, with the rest distributed across east to southeast Asia, including Malay and Borneo in the Malesian region. Despite its diversity and unique distribution, the factors explaining its evolution and diversification remain mostly uncertain. Only one previous phylogenetic study based on limited genetic and species (c. 30%) sampling has focused on its evolution, supporting two geographic clades (Asia and Neotropics). In addition, the taxonomy of *Dendropanax* is complex as a consequence of the high phenotypic plasticity, and several taxonomic novelties have been published during the last decades. However, many of these taxa have never been explored from a phylogenetic perspective. Here, we used the next generation sequencing technique Hyb-Seq, combining target-enrichment with genome skimming, to obtain hundreds of nuclear loci and plastome sequences from silica-gel dried and herbarium specimens representing an extensive sampling of *Dendropanax* species and close allies (c. 300 samples representing 75% of *Dendropanax* species and all closely related genera), as well as accurately representing their geographic distribution. These data were used to obtain highly resolved nuclear and plastid phylogenetic reconstructions that were time-calibrated and used to perform biogeographic and diversification analyses. In addition, these genomic data were used alongside traditional morphological examination to improve species delimitation of *Dendropanax*

and closely related genera. Lastly, we compiled information from herbarium specimens to obtain a database of taxonomically reviewed occurrences of *Dendropanax* and used it to explore climatic preferences of the species. These herbarium specimens were also used to obtain leaf morphological traits through cutting-edge machine learning algorithms, and the relationships between diversification, climatic preferences, and morphology were explored. Our results support the existence of five main geographic clades in *Dendropanax* in both nuclear and plastid analyses (Asian clade, Caribbean clade, South American clade, and two Mesoamerican clades), with several polyphyletic taxa in the Neotropics according to their current circumscription (e.g., *D. arboreus*, *D. tessmannii*, and *D. umbellatus*). Two Asian *Dendropanax* species are now supported to constitute a new genus. Biogeographic analyses with increased species sampling supported early colonization from eastern Asia to Mexico and Mesoamerica, from where the Caribbean was colonized several times, and an eastward pattern of colonization in South America. In addition, they support a recent colonization of Malesia from eastern Asia during the Miocene. Preliminary diversification analyses support a general decrease in diversification across the genus since the Eocene both in Asia and the Neotropics, and suggest higher extinction in Asia linked to the Oligocene global cooling. Preliminary climatic analyses suggest there was a shift towards warmer climatic preferences after the colonization of the Americas, which was also linked to a wider variability in leaf traits. In summary, our research provides significant insights into the evolution, biogeography, diversification, ecological preferences and morphological variability of *Dendropanax* and closely related genera. The phylogenetic framework and evolutionary hypotheses from this study will significantly benefit subsequent integrative taxonomic studies and promote research on the tropical amphi-Pacific biogeographic disjunction pattern.

Key Words: Araliaceae, Dendropanax, amphi-Pacific disjunctions, machine learning, phylogenomics

Unveiling the pantropical evolutionary history of the largest genus of the grape family using an integrative approach of phylogenomics, ecology and machine learning

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The pantropical disjunctions in plants have fascinated botanists for decades. These disjunctions have been sometimes associated with the breakup of Gondwana, but dispersal events after the fragmentation of the supercontinent often explain this pattern in other taxa. *Cissus* (Vitaceae) is one example of the pantropical disjunction explained by long-distance dispersal events. The c. 300 species of *Cissus* occur in tropical areas of the Americas, Asia, Africa, and Australia, with a divergence of the genus long after the fragmentation of Gondwana. Despite being the largest genus in the family, encompassing almost one-third of the Vitaceae species, its evolutionary history is still poorly understood. Previous phylogenetic analyses of *Cissus* analyzed less than a 20% of the species with limited genetic sampling. In addition, the highly variable morphology of *Cissus* resulted in a complex taxonomy. As a consequence, several species of *Cissus* were transferred to other genera (e.g., the transfer of the *Cissus striata* clade into *Clematicissus*), resulting in the recognition of *Cissus* as a monophyletic genus after the recent establishment of *Apocissus*. However, there is still a huge gap in knowledge on the evolutionary history of this genus, as it is unknown how such a large number of species (especially in Africa, which harbors about half of the species) and a high morphological variability could be produced. This study aims to unveil the biogeography and evolutionary history of this intriguing genus of the grape family. To achieve that, hundreds of herbarium specimens were sampled in four major herbaria in the United States (the US National Herbarium in the Smithsonian Institution, the New York Botanical Garden, the Missouri Botanical Garden, and the Harvard University Herbaria) and sequenced using the target-enrichment Hyb-Seq procedure with a Vitaceae-specific bait set of 1,013 nuclear loci, also obtaining the plastomes. These data were used to perform the most complete phylogenomic

reconstructions of *Cissus*, containing molecular data for c. 50% of its species. For the first time, these phylogenies resolved the backbone of *Cissus*, that includes nine main clades. In addition, the machine learning approach was used to explore the morphospace of the genus, that recognized several morphological groups. The biogeographic reconstruction supports the two earliest divergent clades (*C. barbeyana* and *C. integrifolia* clades) endemic to Africa, diverged during the early evolution of the genus in the Paleocene (c. 60 mya). Most of the other clades diverged c. 45 mya in Africa, with a significant increase of diversification rates of *Cissus* during this period associated with the expansion of the boreotropical vegetation in the Middle Eocene Climatic Optimum. The New World was colonized through a single dispersal event from Africa (c. 40 mya), while Asia and Australasia were colonized several times since the Miocene (c. 20 mya). The previously recognized Neotropical lineage is now divided into four main clades (*C. trifoliata*, *C. alata*, *C. patellicalyx,* and *C. verticillata* clades), which display different ecological affinities and diverse morphologies. In particular, for the *C. verticillata* clade, species diversification was associated with the aridification of western Mexico during the Middle Miocene Climatic Optimum. This period is also related to the significantly high diversification rate of the *C. quadrangularis* clade in Africa, with a high proportion of succulent species associated with the aridification of African deserts. In summary, this study sheds light on the evolutionary history of *Cissus* and highlights the utility of phylogenomics in resolving complex, widely distributed plant groups. Furthermore, this study also showcases that a high proportion of its species diversity remains hidden, supported by the recent discovery of several undescribed species in the Neotropics, particularly in Mexico. Additional integrative studies are still needed to fully understand the patterns and processes of the evolutionary diversification of the pantropical biogeographic disjunctions in plants.

Key Words: biogeography, Cissus, diversification, Hyb-Seq, machine learning, pantropical disjunction, Vitaceae

Which came first? A modeling approach for examining the role of preadaptation in plant evolution onto harsh soils

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Preadaptation can facilitate the evolution of plants into extreme environments, but this process can be challenging to study. Harsh soil habitats such as gypsum, saline, and calcareous soils feature numerous stressful conditions which make them inhospitable to most plants. Preadaptation to one or more of these conditions may account for the impressive capacity some plant clades show for parallel evolution into these habitats. To better characterize the role of preadaptation in this process, I will employ an integrative modeling approach designed to investigate not just evolutionary associations between traits, but the order in which they evolved. I will use multiple established methods for studying multistep evolutionary processes such as hidden Markov models with precursor states, phylogenetic independent contrasts of stress tolerance traits at nodes prior to harsh soil evolution, and the threshold model. I will also modify traditional tests for correlated trait evolution to assess if the presence of certain stress tolerance traits precedes habitat transitions. I will implement these methods across North American *Allium* subgenus *Amerallium* and non-orchid Asparagales, two clades that span phylogenetic scales and feature numerous transitions into harsh soil habitats. This comprehensive modeling approach will contribute to our understanding of the pace and pattern of evolution onto multiple harsh soils and the role of preadaptation in the evolution of lineages that are adapted to numerous stressful conditions.

Key Words: onion, phylogenetics, stress tolerance, modeling

Winners and losers of urbanization: citizen-science records reveal how urbanization reshapes the flora of the Netherlands

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Urbanization is one of the most intense global change drivers, transforming landscapes, altering habitat availability and reshaping biological communities. However, we still lack large-scale, temporally explicit assessments of how urbanization affects plant species distributions across entire national floras. Here, we evaluate how urban growth has shaped the flora of the Netherlands by combining historical and contemporary plant occurrence records with spatially explicit urbanization data.We use the nationwide plant records collected from citizen-science and included in the FLORON database, together with Kadaster/BAG building data to reconstruct urbanization gradients across the Netherlands. By linking species occurrences to building cover at the 1 × 1 km grid scale, we estimate species-specific urban affinity and identify taxa that are positively, negatively or neutrally associated with urban environments. We further aim to compare these associations through time to evaluate whether species have become winners or losers of the urbanization process. Preliminary analyses show clear species-specific responses to urbanization. Some species are positively associated with increasing building cover, suggesting that urban environments may favor widespread, ruderal or disturbance-tolerant taxa. In contrast, other species show negative associations with urbanization, indicating potential sensitivity to habitat transformation, fragmentation or urban environmental filtering. These contrasting responses suggest that urbanization does not simply reduce or increase plant diversity uniformly, but instead reshapes floristic composition by filtering species according to their ecological strategies. This project provides a data-rich framework to understand how urbanization affects plant biodiversity at both species and community levels. By integrating citizen-science records, historical floristic data and high-resolution spatial information, we can move beyond local case studies to assess how plant communities are assembled, reorganized and filtered across an entire urbanizing landscape. Such integration is essential to understand not only which species persist in cities, but how urban ecosystems are built.

Key Words: citizen science, FLORON, global change, plant communities, species distributions, urban ecology, urbanization

Digital Ethnobotany 5.0: Integrating Artificial Intelligence, Traditional Ecological Knowledge and Biocultural Diversity for the Future of Plant Sciences

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As the world confronts accelerating biodiversity loss, climate uncertainty, and the erosion of cultural knowledge systems, plant sciences are entering a new era in which technological innovation must be coupled with ecological wisdom and cultural understanding. This paper introduces **Digital Ethnobotany 5.0**, a transformative framework that integrates Artificial Intelligence (AI), Traditional Ecological Knowledge (TEK), and biocultural diversity to redefine the future of plant sciences. Moving beyond conventional ethnobotanical documentation, Digital Ethnobotany 5.0 envisions dynamic knowledge networks in which indigenous and local ecological knowledge is preserved, analysed, and mobilized through advanced digital technologies, including machine learning, geospatial analytics, remote sensing, digital archives, and predictive ecological modelling. Drawing upon ethnobotanical research from the Himalayan cultural landscapes of India, the study demonstrates how centuries of community-based knowledge embedded in oral traditions, sacred landscapes, folk classifications, and resource-use practices can complement contemporary scientific datasets. The paper argues that TEK provides long-term ecological insights that are often absent from technology-driven approaches, while AI offers unprecedented capacities for pattern recognition, biodiversity monitoring, and conservation planning. The convergence of these knowledge systems creates new opportunities for documenting biocultural heritage, forecasting ecological change, enhancing climate resilience, and supporting community-led conservation. By positioning biocultural diversity at the centre of technological innovation, Digital Ethnobotany 5.0 challenges the separation of nature, culture, and technology and proposes a more inclusive, ethical, and sustainable paradigm for plant sciences. The paper contends that the future of biodiversity conservation and ecological stewardship lies not merely in smarter technologies, but in creating meaningful partnerships between artificial intelligence and the accumulated ecological intelligence of human societies. Such an integrative approach

represents a new horizon for global plant sciences in the Anthropocene.

Key Words: Ethnobotany 5.0, Artificial Intelligence, Traditional Ecological Knowledge, Biocultural

Phylogeny and Plastome Evolution of Orobanchaceae

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Robust phylogenetic hypotheses are essential for studies of trait evolution and diversification, yet phylogenomic incongruence persists even with genome-scale data, leaving critical thresholds for stable inference undefined. The parasitic plant family Orobanchaceae, characterized by extensive plastome reduction through repeated transitions to holoparasitism, provides an ideal natural system to address this gap. We generated 112 new plastomes and assembled a dataset of 113 species spanning all nine tribes and nine outgroups, systematically evaluating the effects of dataset type, inference method, alignment trimming, and sampling coverage on topological stability. Our analyses

consistently recovered nine major clades with high congruence across RAxML, IQ-TREE, MrBayes, and TNT, revealing that overly stringent trimming (-gt > 0.8) destabilized topologies, while moderate trimming (-gt 0.2–0.6) yielded optimal results. Resampling identified critical thresholds for backbone stability, requiring ≥30% species sampling and ≥40% sequence length, with stability linked to the retention of 22 universally conserved CDS rather than overall missing data. Parallel analyses of plastome evolution demonstrated predictable degradation of gene function with decreasing dependence on intrinsic photosynthesis, most evident in NDH complex genes, while housekeeping genes remained conserved. This degradation was associated with relaxed selection (elevated dS/dN ratios), though instances of purifying selection suggested selective pressure to maintain a minimal plastome. Genome-level traits—including GC content, plastome size, structural variation, and SSR abundance—were correlated with dependence on intrinsic photosynthesis and divergence time since the last autotrophic ancestor.

Key Words: Orobanchaceae; plastome evolution; phylogeny

Reassessing the taxonomy of Chinese *Dasiphora* (Rosaceae): Integrative evidence reveals discordance between petal color and genomic data

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Dasiphora Raf. is a genus in the Rosaceae family, native to southwestern China but widely distributed across the Northern Hemisphere's alpine regions. Despite its economic importance and use in landscaping, the taxonomy of *Dasiphora* remains unresolved, with species counts varying across sources. Guided by an integrative framework, this study tests whether the traditional two-species delimitation in China, *D. fruticosa* (yellow-petaled) versus *D. glabra* (white-petaled), is supported by plastome, nuclear ribosomal, and morphological evidence, rather than presuming that petal colour reflects distinct evolutionary lineages. Our results show that the plastomes of *Dasiphora* species exhibit a typical quadripartite structure with variation in size and gene content. Notably, *D. fruticosa* plastomes ranged from 152,881–153,552 bp, whereas *D. glabra* showed greater variation (152,907–187,012 bp). Phylogenetic analyses based on whole plastomes, protein-coding and non-coding regions, and nrITS did not recover monophyletic groups corresponding to petal colour, with yellow- and white-flowered individuals frequently intermixing across clades. Divergence-time estimates indicate a late Miocene origin for crown *Dasiphora*, with early splits involving North China populations, and biogeographic reconstruction infers a vicariance event between North and Southwest China followed by dispersal and additional vicariance events. Morphological analyses of 12 characters showed that only a

few traits (e.g., leaflet area, leaflet lamina length, leaflet pairs, flower colour) accounted for most variation. Yet, morphometric clustering also failed to separate the two colour groups. Together, these findings indicate that petal colour is unreliable for species delimitation in *Dasiphora*, likely due to hybridisation, polyploidy, and phenotypic plasticity. We recommend population-level nuclear genomic studies across the genus's full distribution to resolve species limits and clarify the role of ploidy in diversification.

Key Words: Dasiphora; integrative taxonomy; plastome structural variation; phylogeny; morphology; biogeography; petal colour

A Preliminary Study on the Orchid Flora of Yintiaoling National Nature Reserve in Chongqing

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Many orchid species possess important ornamental, medicinal, scientific research and conservation values. Being sensitive to changes in ecological environments, orchids are regarded as flagship groups in plant conservation. Located in the southeastern section of the Daba Mountains, Yintiaoling National Nature Reserve of Chongqing lies within the biodiversity hotspot of eastern Sichuan and western Hubei, and harbors abundant orchid resources. Entrusted by the reserve, our research team launched a special survey on orchids in 2021. Based on field survey data, specimens and literature references, the orchid flora of the reserve was systematically sorted out. The main results are as follows: 1. A total of 78 orchid species were recorded in the reserve, including 23 national key protected species and 3 municipal key protected species of Chongqing. 2. One new orchid species, *Cephalanthera yintiaolingensis*, and nine new record species for Chongqing were discovered. 3. In terms of ecological habits, there are 66 terrestrial orchids, 12 epiphytic orchids and 6 saprophytic orchids. 4. Orchids are distributed across the entire reserve, mainly concentrated in evergreen broad-leaved forests and humid valleys at an altitude of 500–1400 m in Lanying Gully, Qingyan River and other areas. 5. Taxa with high ornamental and medicinal values such as Dendrobium, Bletilla, Pleione, Cymbidium, Gastrodia and Bulbophyllum have suffered severe human disturbance, while other species maintain favorable growth status. 6. Corresponding conservation suggestions were put forward: strengthen patrol and management within the reserve and ban arbitrary digging; carry out publicity and education on relevant laws and regulations to raise public awareness of protection; conduct collaborative research with scientific research institutions on endangerment mechanisms, artificial propagation and population reintroduction for species with low reproduction rate and poor natural regeneration, including *Cypripedium fargesii*, *Cypripedium flavum* and *Cephalanthera yintiaolingensis*.

Key Words: Orchidaceae; flora; Chongqing; Yintiaoling; nature reserve

Soil nutrient heterogeneity, clonal integration, and AMF symbiosis: effects on growth and invasion of *Solidago canadensis*

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Soil nutrient heterogeneity is common in natural habitats, and clonal plants often perform better in such conditions through clonal integration. However, little attention has been paid to how soil nutrient heterogeneity and clonal integration jointly affected the arbuscular mycorrhizal fungal (AMF) symbiosis of a clonal plant, and consequently influence its growth, and even its invasion success. To address this, we conducted a greenhouse experiment to examine the effects of soil nutrient heterogeneity and physiological integration (rhizome connection *vs.* severance) on the growth performance and root AMF colonization of an invasive clonal plant *Solidago canadensis*. Our results showed that clonal integration marginally promoted root mass and significantly increased height, body size, and basal diameter in both homogeneous and heterogeneous nutrient soils, but reduced ramet number. We further evaluated root foraging strength based on root mass and found that clonal integration enhanced foraging strength, which was significantly and positively correlated with aboveground mass and stem mass. Interestingly, although no evidence was found that either soil nutrient heterogeneity or clonal integration affected overall AMF colonization rate, higher total infection rate and lower spore infection rate were observed in nutrient-rich patches than in nutrient-poor ones within heterogeneous nutrient soil, suggesting that soil nutrient availability is a key factor influencing AMF colonization. These findings indicate that a rhizomatous clonal plant such as *S. canadensis* can flexibly adjust its survival strategy via clonal integration, regardless of soil nutrient heterogeneity, and that AMF symbiosis may contribute to its performance when nutrients are patchily distributed, thereby facilitating its invasion success.

Key Words: clonal plant, AMF, physiological integration, invasive plant

Genomic Adaptive Signals Underlying Flower Color and Shape Homoplasy in *Pedicularis* (Orobanchaceae)

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Phenotypic homoplasy, the independent evolution of similar traits, provides a powerful framework for understanding how repeated ecological pressures shape phenotypic similarity. A central goal in studying phenotypic homoplasy is to investigate the underlying molecular basis: to what extent do similar phenotypes arise through shared genetic mechanisms? The hyper-diverse alpine genus *Pedicularis* (>500 species), centered in the Hengduan Mountains biodiversity hotspot, exhibits extensive homoplasy in flower color and shape driven by bumblebee-mediated selection and assortative mating. This system offers an exceptional opportunity to investigate the genomic basis of repeated floral evolution.We generated transcriptome data for 77 samples representing 51 *Pedicularis* species, focusing on clades with frequent transitions in flower color and shape, and reconstructed the first genome-scale phylogeny for the genus. Using ancestral state reconstruction, we inferred repeated independent transitions in both flower color and shape and estimated their evolutionary rates. We then applied comparative genomic approaches to detect adaptive molecular convergence at both substitution and gene levels and evaluated patterns of gene tree-species tree discordance to assess the potential contribution of introgression. Our phylogenomic framework improved resolution of relationships within *Pedicularis* and revealed numerous independent origins of similar floral phenotypes, with transition rates higher for flower color than for flower shape. We identified multiple candidate genes associated with both traits that exhibit signatures of positive selection and adaptive molecular convergence, indicating that repeated floral evolution is associated with a mosaic of hierarchical genetic mechanisms. Together, these results provide the first genome-wide insights into the molecular basis of floral evolution in *Pedicularis* and advance our understanding of the evolutionary processes that drive rapid phenotypic diversification in species-rich plant radiations.

Key Words: homoplasy, adaptive molecular convergence, floral traits, Pedicularis Orobanchaceae

Forecasting the Future: Longleaf Understory Community Responses to Climate Change

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Longleaf pine (*Pinus palustris*) ecosystems are some of the most species-rich in North America, but they have been reduced to a fraction of their historical range. They are characterized by an overstory of predominantly longleaf pine, but harbor incredibly diverse understory plant communities containing many endemic and endangered species with densities of more than 30 species per square meter. Climate projections show that the southeastern US will likely see longer dry seasons, lower average dry season precipitation, and increased overlap between high-lightning and dry season days. When combined with projected higher mean temperatures, hotter droughts will likely increase the frequency and severity of lightning-ignited fires. Since both fire heterogeneity and seasonality influence species diversity and composition of longleaf understory communities, we urgently need to understand how heat, drought, and hotter drought impact these communities. We imposed drought, heat, and hotter drought treatments in an established fire-managed longleaf ecosystem two months before a prescribed fire, reinstalled them after the fire, and conducted monthly community surveys over a span of nineteen months. We observed community simplification and reduced biomass in treated plots both over the course of the experiment and compared to control plots. Over the nineteen months of the experiment we observed 54 species across all 24m^2. Our manipulations have resulted in heated treatments being 5.8C warmer during the day and 2.8C warmer at night on average than non-heated treatments over 19 months. While long-term comparisons of soil volumetric water content are difficult in this experiment due to very sandy, rapidly draining soils, we did observe smaller jumps in soil moisture in drought treatments during precipitation events than in non-drought treatments. We are currently assessing the impacts of heat, drought, and hotter drought on the physiology of abundant and important understory species to assess the tolerance of the most biodiverse aspect of this vital ecosystem. This experiment reimposed treatments one week after a prescribed fire, so all of the above-ground growth we are examining has grown under treatment conditions. This provides a unique opportunity to examine the impacts of stress on new growth from well-established individuals in an ecosystem adapted to low-severity fires as well as more annual species. Analysis is still ongoing, but we believe that differences we're already observing in turgor loss point

between control and treated plants show physiological acclimation, and we are also examining anatomy, leaf dry matter content, and stomatal density to understand the various ways these 54 species have changed in response to heat, drought, and hotter drought. This is important as we hope to find species that can indicate stress and better understand the impacts of global climate change on this iconic ecosystem. This understanding can be used to choose more resilient species in conservation and restoration activities and better understand how to prepare these systems and our management of them for potential future conditions. While the longleaf pine trees are iconic and well-known, the plants of the understory lay the groundwork for this to be one of the most diverse ecosystems in North America. We believe studying this diverse level and its potential responses to climate change is essential to understanding some of the future of the southeastern United States.

Key Words: longleaf pine, OTCs, climate manipulation, field experiment, hotter-drought, ecophysiology, community ecology

Evolutionary history and future development of the Arctic flora

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The Arctic is warming at rates 3–4 times higher than the global average, highly sensitive to global warming, and serves as the barometer of the climate of the whole world, with dramatic implications for climate feedbacks, vegetation change and global biogeochemical cycling. However, the historical dynamics of the Arctic flora, its future spatial and temporal development, and whether Arctic plants can adapt to future warming through migration remain unknown. Here, we investigate the origin and evolutionary dynamics of the Arctic flora by sampling 32 angiosperm clades that together encompass 3626 species. Using species distribution models (SDMs), we predict potential changes of the Arctic flora in the 21st century based on 1,187 (~58.2%) Arctic vascular plant species under four shared socioeconomic pathways (SSPs), and further assess climate-informed range shifts and extinction risks for 574 Arctic seed plant species with available dispersal traits based on SDMs developed dispersal processes. We show that dispersal into the Arctic and in situ diversification within the Arctic have similar trends through time, initiating at ~10–9 Ma, increasing sharply around 2.6 Ma, and peaking around 1.0–0.7 Ma. Additionally, we discover the existence of a longterm dispersal corridor between the Arctic and western North America. Our results suggest that the initiation and diversification of the Arctic flora might have been jointly driven by progressive landscape and climate changes and sea-level fluctuations since the early Late Miocene. Looking to the future, we find widespread but heterogeneous changes in the Arctic flora throughout the 21st century, with some surprising trend reversals. A large gap between habitat availability and accessibility exists for ~77.4–99.3% of Arctic seed plants, and 10.3–70.0% of sampled species are projected to experience range contraction under low- to high-emission scenarios. Depending on the emission scenario, 4.9–58.4% of species, 2.2–41.5% of genera, and 1.6–21.3% of families will be at risk of extinction, critically endangered and/or endangered. Species extinction risks show a phylogenetic signal, meaning that species with similar evolutionary histories tend to have similar risk levels. Importantly, if we do not act now to limit future climate

change, the changes in Arctic floristic composition and extinction risks from rapid warming are expected not only to increase but to accelerate over time as greenhouse gas emissions rise. These findings provide critical insights into the long-term dynamics of the Arctic flora, emphasizing the urgent need for global collaboration in climate change mitigation to afford Arctic seed plants the time needed to adapt.

Key Words: Arctic flora, evolutionary history, future spatiotemporal development, climate change, biodiversity, extinction risk

The emergence of deciduous forests during the angiosperm terrestrial revolution

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The question of where, when, and under what climatic conditions did deciduousness evolve in flowering plants (angiosperms) has long been debated for decades. Ancestral reconstructions of 103 families and 14,157 species coded with biome occupation and leaf habit show that deciduousness first emerged in the tropics by the Mid-Cretaceous, likely as an adaptation to seasonal aridity. Subsequently, deciduous lineages gradually spread into temperate and boreal environments during the warmest intervals of the Late Cretaceous. In Angiosperms, deciduousness more often evolved before, rather than after, lineages colonized temperate biomes. Global cooling during the Cenozoic subsequently accelerated the *in-situ* diversification of deciduous lineages in temperate biome, contributing to the expansion of deciduous forests at higher latitudes.

Key Words: deciduousness, Angiosperms, pre-adaptation, biogeography

Integrative utilization of genomic resources for improved phylogenetic resolution in Sonerileae (Melastomataceae)

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Next-generation sequencing (NGS) has revolutionized plant phylogenetics over the past decade. A variety of sequencing strategies have been developed and applied in both phylogenetic and non-phylogenetic studies, yet it remains insufficiently explored whether genomic data generated by these different approaches can be effectively integrated. In this study, we addressed this challenge in Sonerileae, the second-largest tribe of Melastomataceae, by combining newly generated Hyb-Seq and deep genome skimming data with publicly available NGS datasets, including RNA-Seq, target enrichment data from different probe sets, genome skimming data, Hyb-Seq data, and annotated genomes from 184 accessions representing 41 of the 47 genera in the tribe. Using a newly developed reference comprising 5626 loci, we generated a well-supported and near-comprehensive phylogeny of Sonerileae, providing new insights into relationships within the tribe, especially the long-unresolved Asian Sonerileae. This approach shows promise for integrating heterogeneous NGS data generated through different sequencing strategies and can be broadly applied to other groups, including non-plant lineages, facing similar challenges. By maximizing the reuse of existing genomic data, it can also reduce the need for additional sequencing, which makes phylogenomic research more cost-effective and environmentally sustainable.

Key Words: Data integration, phylogenomics, systematics, taxonomy

Expert-led biodiversity data curation unmasks range distortions and cryptic extinction risk driven by widespread misidentification in a megadiverse hotspot

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Accurate biodiversity data are essential for effective conservation, yet taxonomic errors and inaccurate occurrence records remain pervasive across digitized collections and citizen-science platforms, particularly in megadiverse tropical hotspots. To investigate and address these challenges, we compiled an occurrence dataset of *Begonia* section *Petermannia* in the Philippines, a hyperdiverse lineage within one of the world's most threatened biodiversity hotspots. This dataset integrated rigorously curated records from 1,902 herbarium specimens, 195 crowd-sourced photographs, 161 online observations, and targeted field surveys. We found that only 44% of historical specimens and 47–55% of online records were correctly identified, resulting in substantial range contractions or expansions subsequent to verification. Applying IUCN Red List criteria to 76 taxa indicated that 72% are threatened, with 42% raised to higher threat categories, including many karst micro-endemics. Although 89% of species occur within legally protected areas, 11% persist entirely outside reserves, and only 18% are represented *ex situ*. These results demonstrate that expert-led biodiversity data curation functions as proactive conservation intervention transforming fragmented digital archives into robust, actionable baselines for

safeguarding hyperdiverse tropical floras in the Anthropocene.

Key Words: archipelago, Begonia, Biodiversity shortfalls, GBIF, Philippines

The Impact of Frequent Wildfire on Subalpine Forest Understory Recovery

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High-severity wildfires are increasing in frequency across western North America, threatening forests' resilience. As the intervals between wildfires shrink to a time period shorter than dominant tree species require for maturation, changes in fire frequency can interact with vegetation to determine postfire forest trajectories. Successive fires an order of magnitude shorter than the historic-return-interval can alter subalpine conifer forests capacity to regenerate by reducing tree regeneration and establishment. In altering the structure and composition of the overstory community, short-interval-fires (<30years) can also facilitate changes in understory plant community by decreasing litter and duff layers, increasing sunlight quantity reaching the understory, and increasing below-ground resource availability. These changes can translate into significantly different understory plant community compositions, richness, and evenness. Yet, few studies have examined the mechanisms underlying how increasingly short-interval fires affect understory plant recovery despite these communities' crucial role in ecosystem functioning and future fire activity. By assessing fuel loading, tree regeneration, and understory community composition across sites with variable time-since-fire (TSF) and fire-return-interval (FRI) we assessed how subalpine lodgepole forests understory communities respond to anomalous short-interval fires in Montana's Sapphire Mountain Range. We find that fuel loading and tree regeneration were different between sites that had burned twice within 30 years. We also found that species richness was highest at sites with intermediate fire frequency, where in richness peaks in sites burned 13 years ago (TSF) and with 21 years between fires (FRI) relative to sites experiencing either shorter or longer TSF and FRI. Four species were primarily responsible for variation in our community composition data: *Lupinus argenteus* (Fabaceae; Silvery Lupine), *Gayophytum diffusum* (Onagraceae; Spreading Groundsmoke), *Chamaenerion angustifolium* (Onagraceae; Fireweed), and *Vaccinium scoparium* (Ericaceae; Whortleberry). We plan to further investigate the

demographic response of these species to shortened fire frequency, investigating how the historically overlooked understory plant community is altered in light of increasingly short-interval wildfires under climate change.

Key Words: wildfire, short-interval fire, fire-return interval, time-since-fire, subalpine forest, understory plant community

Genomic insights into deep reticulation and introgression-driven adaptability in *Camellia* (Theaceae)

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Hybridization and introgression have long been recognized as important sources of genetic variation and evolutionary forces for species diversification and adaptation. Yet, published examples of reticulation likely represent only the tip of the iceberg across the tree of life. Moreover, studies of the functional characterization of introgressed genomic regions and how introgression might facilitate adaptability remain limited. We used whole-genome resequencing to conduct a comprehensive phylogenomic analysis of *Camellia* to better understand patterns of reticulation. Integrated approaches were applied to disentangle the relative contributions of ILS (incomplete lineage sorting) and introgression to phylogenetic discordance. Putative functional features of high-frequency introgression regions were identified, particularly focusing on potential adaptive introgression of oil biosynthesis-related genes. We detected extensive phylogenetic discordance across the genome and topological incongruence between nuclear and organellar datasets. Both ILS and post-speciation introgression contributed to this discordance; ILS appears to be the dominant contributor, and introgression was highly concentrated in the radiation of core clades. The topology recovered from low-recombination regions is more likely to reflect the true evolutionary relationships of *Camellia*, this genus represents one of the "thorniest nodes" in the angiosperm Tree of Life, compounded by the pervasive problem of misidentification of cultivated materials, which is exacerbated by the ease of sampling from gardens. We have resolved eight major clades within the genus. Furthermore, in contrast to previous

studies in which many subgenera or sections unsupported by chloroplast data were often recovered with strong support when large-scale nuclear gene data were employed, no single section as defined by either Chang's or Ming's classification systems is monophyletic. Putatively introgressed genes were mainly associated with central biological processes, particularly DNA repair and mitochondrial function; both processes could improve organismal fitness. Intriguingly, numerous core oil biosynthesis-related genes were represented in the high-frequency introgression regions. Our findings demonstrate the important role of introgression as a generative process in plant evolution and provide new insights into how environmental adaptability of *Camellia* might be facilitated by introgression through the incorporation of adaptive loci and beneficial alleles.

Key Words: phylogenetic discordance, reticulation, incomplete lineage sorting, introgressed genes, adaptability, Camellia

The contribution of recent and historical demographic histories to genomic diversity and conservation status in plant species

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Demographic factors are intrinsically crucial to evaluate species' extinction risk. However, measuring them remains difficult and time-consuming and the use of genomic summary statistics has been advocated to assess the conservation status of a species. In the present study, we estimated (i) the census number (N_c), (ii) effective population size (N_e) over three different time periods, recent, historical and ancient, (iii) neutral genetic diversity (π_4), and (iv) a measure of the efficacy of purifying selection (π_0/π_4) for 101 plant species using population genomic sequencing data. Twenty-one species are from the Plant Species with Extremely Small Populations (PSESP) program of SW China. Threatened species exhibited significantly lower N_e, N_c, π_4, and weaker purifying selection, but had a higher N_e/N_c ratio than non-threatened ones. N_c was the main determinant in identifying conservation status, and contemporary neutral genetic diversity was predominantly influenced by historical N_e. In the absence of demographic information, genetic parameters are a good proxy of conservation status, likely because currently threatened species also had a low historical population size. In summary, our findings suggest that direct estimates of N_c are more useful than π_4, although the latter remains a valuable conservation indicator. Hence, efforts such as the PSESP should be extended.

Key Words: demographic history, census size, genetic diversity, IUCN threatened, PSESP

The Dynamic UV Sex Chromosomes Of Liverworts

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How sex chromosomes evolve and attain their sex-determining function is a major question in evolutionary biology. In plants, sex determination is increasingly recognized as dynamic, with sex chromosomes having evolved and been lost multiple times, particularly in angiosperms. In contrast, the U and V sex chromosomes of plants with haploid sex determination have long been thought to be less dynamic, an assumption that has also been applied to liverworts, whose sex chromosomes originated more than 400 million years ago. However, this view relies mainly on studies of *Marchantia polymorpha*, the model liverwort species, and the lack of genomic resources across liverworts has so far limited a broader understanding of sex chromosome evolution in this group.

To address this gap, we sequenced and analyzed the genomes of multiple liverwort species. In particular, we generated chromosome-scale genome assemblies for *M. paleacea*, *Lunularia cruciata*, *Blasia pusilla*, and *Apopellia endiviifolia*, which diverged from *M. polymorpha* between 10 and 420 million years ago. Comparative analyses across chromosome-scale assemblies from 34 species spanning all major liverwort taxa allowed us to investigate sex chromosome evolution in this group of plants at an unprecedented scale. Specifically, we found that collinearity decays more rapidly on sex chromosomes than on autosomes, accompanied by the accumulation of repetitive elements. Strikingly, we identify a core set of sex chromosome-linked genes conserved for over 400 million years, but this set is far smaller than previously inferred based primarily on *M. polymorpha*. Together, our results challenge the long-standing view of static liverwort sex chromosomes and instead show that they combine deep conservation with extensive dynamism in collinearity, gene content, and repeat composition.

Key Words: bryophytes, liverworts, sex chromosomes, evolution, genomics

Salt-tolerant plants and the future of saline ecosystems

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Salt-tolerant plants define saline ecosystems from mangroves and salt marshes to inland salt flats, saline wetlands, and arid basins. Although salinity is their common ecological axis, these systems are changing through different processes, including sea-level rise and coastal squeeze along shorelines, aridification and groundwater alteration in inland basins, and land-use pressure across both coastal and inland landscapes.This presentation examines halophytes as a botanical framework for understanding changing saline landscapes through their species, lineages, and ecological patterns. It considers how taxonomy, herbarium collections, field observations, vegetation studies, phylogenetic evidence, environmental variables, and remote sensing can be brought together to study the distribution, dominant lineages, and vulnerability of salt-tolerant floras. Examples from Salicornioideae (Amaranthaceae), mangroves, and other halophytic groups will illustrate why species-level knowledge remains essential for interpreting saline ecosystems under global change. The future of these systems depends not only on physical change, but also on the diversity and ecological meaning of the plants that define them.

Key Words: halophytes, saline ecosystems, Salicornioideae, mangroves, global change

AI and Public Policy shaping a new horizon for Plant diversity and Conservation Research!

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In the modern era of Technological intervention, it is extremely significant to apply AI in the studies related to Plant diversity and Conservation. Further By looking into deeper insights these interventions can shape for a better Public Policy research for the benefit of Humanity! I will present here, some of the examples of plant diversity from Western Himalaya. I will answer, how AI and Public Policy is relevant to create novel models and Policy documents! With my this approach, I will combine the field and lab based research to Technology and Industry!

Key Words: AI, policy, plant diversity, conservation

Seed and seedling function traits assessment to improve ex-situ conservation and ecological restoration of the Kenyan Coastal forest

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Many indigenous forest plant species along the Kenyan coast remain poorly understood, particularly with respect to their seed and seedling functional traits, such as dormancy, growth rate, and mortality. While numerous restoration initiatives are underway in this region, challenges persist. During my involvement in Kaya Connect—one of the largest restoration programs coordinated by Botanic Gardens Conservation International—I served as the seed bank manager and technician. One major challenge we encountered was that some species failed to germinate under standard nursery conditions. As a result, restoration efforts often prioritize species without seed dormancy, overlooking others that are ecologically important and listed as threatened by the IUCN. In other cases, certain species achieved shoot emergence rates above 80%, only to experience over 70% mortality during early growth stages. Notably, many of these species, such as *Uvaria puguensis* and *Dialium orientale*, are listed as critically endangered or vulnerable on the IUCN Red List. These plants hold significant cultural and ecological value for coastal communities, serving as sources of medicine, food, and as sacred species in traditional worship. These challenges inspired me to focus on understanding seed and seedling traits to ensure that restoration efforts along the Kenyan coast are more inclusive of all native plant species, especially rare, vulnerable, or culturally significant ones. This also supports the government of Kenya objectives of planting 15 billion trees by 2032. To assess dormancy, seed coat permeability tests will be conducted using four replicates of 10 seeds each. Seeds will be weighed and fully put in humid conditions at room temperature for 72 hours. They will be reweighed at 2, 4, 6, 10, 24, 48, and 72 hours, with water paper towels being replaced every 12 hours to maintain hydration and avoid fungal activity (Kildisheva et al., 2020). Species showing 20–30% water uptake will be considered imbibed (ISTA, 2024). Seeds with permeable coats will be planted in seed trays and lightly covered with forest soil. This will be four replicates of 10 seeds per species. Germination will be checked daily. Emergence below 50% within forty days will be considered physiologically dormant (ISTA, 2024), while those exceeding 50% emergence will be non-dormant (ND). Seeds showing less than 30% water uptake (ISTA, 2024) will be classified as physically dormant. Depending on seed size and family, dormancy will be broken by nipping, hot-water treatment, or hammering, followed by rinsing and placing in water paper towels for 24 hours before weighing and

sowing. Physically dormant species that still have an emergence below 50% after 40 days will be considered to have combined physical and physiological dormancy. For physiologically dormant (PD) species, new samples will be treated with gibberellic acid (GA) at 185 millimoles. Seeds will be soaked for 24 hours at room temperature, rinsed, and sown immediately. Emergence will be monitored for four weeks, with records taken every 24 hours. 16 rectangular structures (4 m × 6m) will be built to provide 0% 35%, 50%, and 75% shade levels. Each treatment will have four replicates of 10 seeds per species, each seed in its own planting bag. Cylindrical nylon planting bags of (15 cm diameter, 20 cm depth) will be filled with soil, and treated seeds will be planted individually, covered lightly, and watered regularly. Shade treatments will simulate the shade levels of the Arabuko Sokoke Forest, the surrounding KAYAs, and the Shimba Hills Forest. Emergence, identified by protrusion of the shoot from the soil, will be recorded every 24 hours. A full-light treatment (0%) will serve as the control. Relative growth rate (RGR), mortality, number of leaves, and stem diameter will be measured every ten days for four months. A total of 30 indigenous plant species were collected from Arabuko Sokoke National Park. The first objective focuses on seed functional traits, including seed shape, seed weight, imbibition capacity, dormancy type, and germination performance. These traits provide insight into key ecological functions such as dispersal strategies, germination behavior, seed persistence, seedling establishment, and germination timing. For the second objective, the number of species is reduced from 30 to 10 due to space limitations and project timelines. This phase evaluates seedling functional traits, including height growth rate, chlorophyll content, stem diameter, and leaf production. These traits inform understanding of early establishment potential, resource-use strategies, and overall survival capacity. The project is in the data analysis phase. The project determines the type of seed dormancy, the method of alleviation, and the shoot emergence light niche. This enables the local community, restoration groups, and the government forest department to learn how to propagate different native species and which seedlings to consider planting as pioneers, intermediates, or climax species. This is made possible by focusing on traits that lead to germination (dormancy), growth, and survival. Many restoration efforts are underway in the region, but the main challenges are 1) mortality—planting pioneers greatly reduces mortality—and 2) propagating over 500 different Kenyan coastal species, most of which have unique germination methods. Among these species, some are listed by the IUCN as critically endangered to vulnerable, highlighting the urgency of proper propagation and planting

From Colonisation to Radiation: Historical Drivers of *Inga* Diversification across Neotropical Rainforests

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Tropical rainforests harbour extraordinary plant diversity, yet the evolutionary processes that determine why some lineages diversify extensively after colonising a region whereas others remain species-poor are still not well understood. In tropical plant lineages, arrival in a new region may result either in limited persistence or in extensive in situ diversification. However, the conditions under which a successful colonisation event becomes an evolutionary radiation remain unresolved. Here, we address this question using *Inga* Mill. (Leguminosae), one of the most species-rich tree genera in the Neotropics and an important component of wet tropical forests. We used a densely sampled phylogeny of more than 200 *Inga* species, combined with divergence-time estimation and ancestral-area reconstruction, to evaluate the timing, directionality, and evolutionary consequences of colonisation across major Neotropical rainforest regions. We focused on regional radiations in the Chocó, Central America, and the Atlantic Forest, asking whether these radiations share common historical and ecological conditions or represent independent outcomes of colonisation. Our results suggest that *Inga* diversity across the Neotropics was assembled through repeated dispersal events among rainforest regions, followed in some cases by local diversification. However, not all colonisation events resulted in radiation. Instead, species-rich regional lineages appear to be associated with repeated occupation of wet forest environments, geographic connectivity that enabled dispersal, and subsequent isolation promoted by major landscape barriers such as the Andes, and dry vegetation formations. These findings indicate that evolutionary radiations in tropical rainforests may depend not

only on dispersal into suitable habitats, but also on the interaction between ecological opportunity, regional connectivity, and long-term geographic isolation.

Key Words: Inga, biogeography, phylogenomics, colonisation, evolutionary radiation

Phenotypic Diversity and Resource Allocation of *Ottelia acuminata* in Response to Environmental Factors

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This study on *Ottelia acuminata* has primarily focused on physiological and biochemical processes, while the comprehensive adaptive mechanisms involving phenotypic differentiation, nutrient accumulation, and resource allocation between male and female individuals across heterogeneous habitats remain unclear. Therefore, this study selected O. acuminata as the research subject and investigated eight typical habitat populations in northwestern and central Yunnan, China. In each habitat, 20 male and 20 female individuals were randomly collected, resulting in a total of 320 individuals from the eight sampling sites. Field surveys and laboratory experiments were conducted to obtain data on nine key phenotypic traits, as well as the nitrogen (N), phosphorus (P), and potassium (K) concentrations and biomass allocation patterns of roots, stems, leaves, and reproductive organs. Combined with physicochemical data from simultaneously collected water and sediment samples, correlation analyses were performed to explore the adaptive strategies of male and female O. acuminata individuals under different environmental conditions and to identify the key environmental factors driving resource allocation patterns.The degree of variation differed among traits. Leaf-related traits exhibited relatively high variability, whereas plant height showed the highest stability. Phenotypic differentiation was mainly attributed to variation within populations, with intra-population variation exceeding inter-population variation. The phenotypic differentiation coefficient of root length reached 44.99%, higher than those of plant height (40.77%) and functional leaf number (35.42%), indicating a strong adaptive capacity of the root system to sediment environments. Overall, male individuals exhibited lower trait repeatability than female individuals, suggesting that male traits were more susceptible to environmental influences.Correlation analysis of environmental factors revealed strong associations among multiple environmental variables. Water conductivity and water pH showed a highly significant positive correlation ($r = 0.916$, $P < 0.01$), while mean annual temperature (MAT) and altitude (ASL) exhibited a highly significant negative correlation ($r = -0.873$, $P < 0.01$). Water depth (WD) was significantly negatively correlated with total nitrogen (TN) concentration in water (r =

−0.753, $P < 0.05$). Correlation analysis between environmental factors and phenotypic traits indicated that water depth was the primary factor driving phenotypic variation in O. acuminata, with a stronger influence than other environmental variables. Plant height, leaf traits, and stem traits of male and female individuals exhibited significant sexual differentiation in their responses to water depth, with stem traits showing the most pronounced sex-specific responses. Male stem traits were more sensitive to changes in water depth, emphasizing enhanced mechanical support and competitive ability for resources, whereas female individuals exhibited more stable responses, with photosynthetic products preferentially allocated toward reproductive development.To cope with environmental stress, O. acuminata flexibly adjusted nutrient accumulation proportions among different organs. This study identified water nitrogen concentration, sediment pH, and light availability as the key environmental factors influencing nutrient allocation. Under nutrient-poor conditions, plants allocated more nutrients to roots to enhance anchorage and nutrient absorption capacity. Moreover, male individuals showed greater flexibility than females in nutrient utilization strategies.When growing under unfavorable conditions, such as deeper water and reduced light availability, O. acuminata allocated more biomass to shoot organs (leaves and stems) under deep-water and low-light conditions, while reducing investment in root growth or reproduction. This strategy prioritizes vegetative growth and enhances competitive ability for spatial resources. Such dynamic adjustment of resource allocation represents a crucial survival strategy that enables O. acuminata to maintain optimal fitness along elevation and hydrological gradients.This study advances the theoretical understanding of environmental adaptation in dioecious submerged plants. The results demonstrate that water depth, water physicochemical properties, and sediment physicochemical properties all influence the growth, development, and reproduction of O. acuminata. However, water depth was identified as the key factor regulating trait variation and resource allocation. The high phenotypic plasticity and flexible nutrient utilization strategies of O. acuminata represent critical mechanisms allowing this species to maintain stable growth and reproduction under heterogeneous habitats. These findings reveal the environmental factors associated with the persistence of endangered O. acuminata populations and provide scientific guidance for selecting suitable sites for ex situ conservation and restoring biodiversity in plateau lakes.

Key Words: Ottelia acuminate, phenotypic traits, diversity, resource allocation, environmental factors

Towards A Systematic Analysis on Flower and Inflorescence Morphology in the context of the Synflorescence

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Angiosperm flowers are modified shoots of inter-connected phytomers that bear modified leaves for sexual reproduction. The perianth organs are modified sterile leaves that cover the fertile leaves (i.e. stamens and carpels) in a flower. They have been lost and re-acquired multiple times during evolution. The perianth can derive from stamens or from lower vegetative leaves, both part of the structure of the 'whole flowering region'—the synflorescence—where flowers and inflorescences are nested within. However, the synflorescence has received little attention. Besides, botanical terms describing perianth and synflorescence/inflorescence structure lack consistency and often 'force' continuous traits into discrete categories, thus making systematic comparisons across distantly-related clades difficult. To resolve these problems and better understand perianth evolution, I developed a phytomer-based, consistent reference frame that systematically describes and compares perianth and synflorescence structure, and generates evolutionary hypotheses. The reference frame includes a new 'synflorescence formula' and a revised 'floral formula'. The formulae can describe the continuous natural variation on synflorescence branching pattern, potential sources of different perianth whorls and organ orientation within and among whorls. This reference frame has multiple advantages over previous morphological descriptions on flowers and inflorescences: (1) The consistent definitions and analytical methods based on synflorescence structures provides a holistic view of plant sexual reproductive structures, and enables morphological comparison among distantly-related clades across all angiosperms; (2) The morphological data generated from the reference frame will facilitate future computer modelling on synflorescence structures, geometric morphometric analysis; (3) The data will generate better character matrices for ancestral reconstruction in phylogenetic studies; (4) It better connects morphology with evo-devo, which can reinterpret and compare developmental data from model and non-model organisms. This reference frame was then applied to Caryophyllineae, a clade with complex perianth evolution and diverse synflorescence structures. Based on morphological data from various sources, I wrote a family-based monograph for Caryophyllineae which

describes synflorescence branching pattern and develops hypotheses on the origin and morphological modifications of the perianth. The perianth-related hypotheses stem from comparing position, shape and development among different perianth whorls, stamens and various vegetative leaves in the synflorescence within and across closely related taxa. The main hypotheses include (1) for re-acquired stamen-derived perianth, the thecae, connective and filament are modified differently on a ‘spectrum’;(2) for re-acquired vegetative leaf-derived perianth, they can derive from original floral prophylls, prophylls of partial inflorescences, leaves in synflorescences and even the inhibition zone below the synflorescence. In future studies, I aim to apply this reference frame to other angiosperm taxa, providing more insights on their morphology, development and evolution.

Macroecological effective migration reveals replicated divergence across landscape barriers in the Hengduan Mountains

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The Hengduan Mountains Region (HMR) is one of the world's richest temperate hotspots of plant diversity. Its exceptional richness and endemism are often attributed to extreme topographic and environmental heterogeneity, which restricts dispersal, isolates populations, and creates opportunities for ecological specialization. However, most landscape-genomic studies examine individual species independently, making it difficult to distinguish general landscape effects from lineage-specific histories. We introduce the concept of macroecological effective migration, the shared structure of genetic connectivity inferred across replicated species-level datasets, and use it to identify landscape barriers that consistently shape plant divergence across the HMR. We investigated these patterns in *Pedicularis* (Orobanchaceae), one of the most diverse plant radiations in the region. The genus includes narrowly distributed endemics as well as widespread and geographically variable species, providing replicated natural experiments for examining how a shared landscape structures genetic variation. We assembled a large genomic and community dataset combining 12 replicated phylogeographic studies of population-level genomic variation, a regional phylogenetic dataset representing more than 150 *Pedicularis* species, and occurrence records for more than 230 species across hundreds of sampled *Pedicularis* communities. To estimate macroecological effective migration, we developed MEADOW (Multispecies EstimAtion of Dispersal On netWorks), a new algorithm and software framework for jointly analyzing patterns of genetic connectivity across species. MEADOW represents populations and their potential connections as a spatial network and infers a hierarchical model of effective migration shared among replicated phylogeographic datasets. This approach identifies migration boundaries that are

repeatedly supported across taxa while allowing individual species to differ in the strength and spatial scale of their responses. It therefore separates general features of landscape permeability from the demographic histories and sampling patterns of particular lineages. MEADOW reveals a shared, hierarchical set of barriers to effective migration across the HMR. Although the 12 focal Pedicularis lineages differ in their geographic distributions and evolutionary histories, they exhibit replicated reductions in genetic connectivity across many of the same landscape boundaries. These results demonstrate that macroecological effective migration is highly structured rather than idiosyncratic: different species repeatedly diverge across a common landscape template. We then asked whether this shared structure extends beyond recent or ongoing effective migration. Barriers identified by MEADOW correspond closely to the geographic structure of divergence across more than 150 Pedicularis species, indicating that many landscape features restricting genetic connectivity within species have also shaped diversification over deeper evolutionary timescales. The same migration structure also predicts turnover of species in plant assemblages. Thus, boundaries inferred solely from replicated population-genomic datasets coincide with broader transitions in community composition involving hundreds of co-occurring species. Our results establish macroecological effective migration as a framework for connecting processes across biological scales. In the HMR, shared barriers link population divergence, the diversification of a major plant radiation, and the assembly of ecological communities. These findings suggest that the region's extraordinary biodiversity has arisen not simply from independent responses by individual lineages, but from repeated evolutionary and ecological responses to a persistent, hierarchically structured landscape. More broadly, MEADOW provides a transferable approach for discovering shared barriers in other biodiverse regions and for identifying landscape connections whose disruption may have consequences extending from genetic diversity within species to the composition of entire communities.

Key Words: Hengduan Mountains, Gene Flow, Phylogeography, Pedicularis, Landscape, Biodiversity, Alpine

Ancient legacies and emerging radiations: Linking evolutionary history and conservation priorities in African plants

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Africa harbours extraordinary plant diversity shaped by complex geological histories, climatic fluctuations, and contrasting evolutionary processes. However, understanding how this diversity has accumulated requires moving beyond species richness to reveal the evolutionary mechanisms that generate and maintain biodiversity. Plant diversity may reflect the persistence of ancient lineages through geological time or recent diversification associated with ecological opportunity and environmental change. Here, we integrate phylogenetic, biogeographic, and macroevolutionary approaches across two complementary African systems—Madagascar, an ancient island centre of endemism, and mainland Africa, a continent shaped by diverse climatic and geological histories—to investigate the evolutionary processes underlying plant diversity and conservation priorities. First, we examine Madagascar's unique flora through a dated phylogenetic framework incorporating 3,950 vascular plant species and 1,621 genera. By integrating phylogenetic diversity, phylogenetic endemism, and geographic distributions, we reveal strong spatial variation in evolutionary history across the island. Humid forests of eastern and central Madagascar harbour concentrations of paleo-endemism and ancient evolutionary lineages, whereas dry and spiny forests in western and southern Madagascar contain high levels of neo-endemism associated with recent diversification. These contrasting evolutionary patterns highlight the importance of conserving both regions preserving deep evolutionary history and those supporting ongoing diversification. Extending this evolutionary perspective to mainland Africa, we investigate continental-

scale patterns of plant diversity using large-scale occurrence datasets, phylogenetic information, diversification estimates, and environmental variables. We reveal substantial spatial mismatches among species richness, evolutionary history, and diversification rates. While tropical forests contain exceptional evolutionary history, mountain systems and seasonally dry regions coincide with elevated diversification rates, demonstrating that African landscapes contribute to biodiversity through distinct evolutionary pathways. Together, these studies reveal that African plant diversity has been assembled through multiple evolutionary processes operating across islands and continents. Integrating evolutionary history into biodiversity assessments provides a framework for conservation strategies that protect both ancient lineages and regions where evolutionary processes continue to shape future biodiversity.

Key Words: African flora; phylogenetic diversity; neo-endemism; paleo-endemism; diversification; evolutionary history; conservation biogeography

Phylogenomic resolution among Australian bush tomatoes suggests a reversal from dioecy to cosexuality via leaky males

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Just 1% of Solanaceae species exhibit a dioecious sexual system; nearly all of these occur within the "spiny solanums" of the Australian Monsoon Tropics in which morphologically cosexual individuals produce inaperturate pollen that renders them functionally female. The "*S. dioicum* group," which includes functionally dioecious taxa and andromonoecious relatives, has been studied for decades yet the relationships among groups of species and patterns of sexual system evolution are still unresolved. We aim to illuminate the evolutionary history of the lineage using targeted enrichment data, evaluate areas of phylogenetic conflict, reconstruct the evolution of sexual systems, and revisit previous hypotheses regarding phylogeny, fruit and calyx morphology, and seed dispersal. Our sampling includes 172 individuals representing 102 taxa. We report on data obtained via the universal Angiosperms 353 probe set and illustrate discordance among subsets of loci. We assembled 340 loci that ultimately support some previously reported species-level relationships while also revealing substantial conflict among subclades and areas of rapid radiation where processes such as incomplete lineage sorting and hybridization have occurred. Our character state reconstructions detect one origin of andromonoecy, one origin of dioecy, and one reversal to the ancestral cosexual state (likely via sex inconstancy among male flowers) within the "*S. dioicum* group". The study provides a framework for future studies inclusive of the Australian spiny *Solanum* species, where diverse reproductive traits and systems are more common than previously thought and reflect ongoing *Solanum* diversification on the Australian continent.

Genomic architecture and evolutionary dynamics of the S-locus in *Cratoxylum cochinchinense*: a hemizygous heterostyly region in Hypericaceae

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Intraspecific variation is a fundamental feature of biological diversity and elucidating the genetic basis of such variation is therefore a central goal in evolutionary biology. Heterostyly is a classic form of intraspecific floral polymorphism that has multiple origins in angiosperms. Although the molecular mechanisms underlying heterostyly have been characterized in several plant groups, they have not yet been investigated in Hypericaceae. Notably, species of *Cratoxylum* exhibit stylar dimorphism rather than typical heterostyly, raising the question of whether their floral morph differentiation is governed by molecular mechanisms similar to those identified in typical heterostylous systems. In this study, we investigated *Cratoxylum cochinchinense* (Hypericaceae) through long- and short-styled flower genome assembly, population genomics, and comparative genomic analyses to elucidate the structure and evolutionary features of the S-locus governing stylar dimorphism in Hypericaceae. We first generated genome assemblies for the long- and short-styled morphs of *Cratoxylum cochinchinense*, with assembled genome sizes of 406.39 and 412.98 Mb, respectively. We identified a hemizygous region on chromosome 8 of the short-styled genome that represents the putative *S*-locus and contains nine short-styled-specific genes (LG08.544–LG08.552). Molecular evolutionary analyses revealed an extensive accumulation of repetitive sequences within this region, consistent with reports in other heterostylous lineages. Transcriptomic analyses further showed that LG08.546 and LG08.547, which are associated with cell-wall formation and auxin biosynthesis, respectively, were specifically expressed in short-styled flowers, making them strong candidate genes for the regulation of style length. Together, these findings suggest *Cratoxylum* with stylar polymorphism shares a common genetic mechanism with typical heterostyly.

Key Words: Heterostyly, S-locus, Hemizygous, Hypericaceae, *Cratoxylum cochinchinense*

Homoeologous exchanges stimulate incipient speciation in allopolyploid rice

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Polyploids formed from hybridization often show instantaneous reproductive isolation from parental taxa, potentially leading to saltational speciation. Whether different derivatives of the same polyploid hybrid can rapidly diverge from each other, thereby forming multiple distinct lineages, remains unknown. Here we report that a swarm of stabilized and self-sustaining tetraploid recombinant inbred lines (TRILs), descended from a single genome-doubled hybrid between subspecies *indica* and *japonica* of rice (*Oryza sativa*), exhibit immediate variation in flowering-phenology that enables pre-mating isolation, and poor germination or hybrid dysgenesis facilitating postzygotic isolation. Reduced fitness and fertility are likely caused by germline aneuploidy in hybrids due to disruption of newly evolved meiotic stability in the parental TRILs as a result of incompatible interactions between the mosaic genomes. Our results reveal that when homoeologous recombination occurs rampantly and precipitates divergent mosaic genomes in a polyploid hybrid swarm, rapid reproductive isolation may emerge and potentiate formation of multiple evolutionary lineages from a single hybridization event.

Key Words: Hybridization, polyploidy, homoeologous exchange, reproductive isolation, speciation

Patterns of clonality within and among species: Impact of population disturbance in three partially clonal *Vaccinium*

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Many plants exhibit a combination of sexual and vegetative reproductive strategies, referred to as partial clonality. Within the broad category of partially clonal plants, a given species may rely on vegetative reproduction to a greater or lesser extent as a growth strategy, leading to taxonomic differences in population clonality. Moreover, within a species, a population's reliance on sexual vs. vegetative reproduction is predicted to vary in response to multiple eco-evolutionary pressures, including the position of the population relative to the range edge, population age, and disturbance levels. In this study, we documented plot-scale and population-scale clonal richness (*R*) in three perennial *Vaccinium* species that are broadly sympatric in northeastern Minnesota (US): *Vaccinium angustifolium* (lowbush blueberry), *Vaccinium cespitosum* (dwarf bilberry), and *Vaccinium vitis-idaea* (lingonberry). Between 11 and 14 populations were surveyed for each species, and the populations differed based on their disturbance history due to either logging or prescribed burns. Populations with a history of disturbance were expected to be less dependent on clonal reproduction, due to the opportunity for new seedlings to establish. However, clonality levels did not correspond to predictions based on histories of population disturbance for any of the three species. In fact, the most intensely studied disturbed/undisturbed population pair with the best-documented disturbance history showed the opposite of the predicted pattern. Overall, this study reveals the range of reproductive strategies exhibited at the intra- and interspecific levels within a geographic region and indicates that the disturbance history of a population alone is not sufficient to predict the relative level of clonality.

Key Words: clonal, Vaccinium, blueberry, lingonberry, diversity

Genome Duplication and Regulatory Innovation Underpin Contrasting Life-History Strategies in Cryptic *Cassytha filiformis* Lineages

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Parasitic plants have evolved extreme adaptations, but the origins of these innovations remain poorly understood. *Cassytha filiformis* is a leafless stem hemiparasite representing an ancient angiosperm lineage with pantropical distribution. Plastome studies revealed cryptic lineages in South China and Southeast Asia, but the nuclear genomic basis remains unclear. We combined comparative transcriptomics, phylogenomics, and common-garden phenotypic assays to investigate genome dynamics and cryptic divergence. We quantified transcriptomic divergence via orthologous gene family comparisons, detected gene duplications using *Ks* distributions, and assessed functional enrichment of parasitism-related duplicates; germination and parasitic vigor were measured under greenhouse conditions. Nuclear phylogenomic analyses showed that morphologically indistinguishable lineages diverged in the Late Miocene, significantly later than plastid-based estimates, indicating decoupled organellar and nuclear evolutionary rates. The lineages exhibited highly asymmetric transcriptomic divergence, with less than 30% of gene families forming a conserved core transcriptome. We identified recent, lineage-specific gene duplications (Ks=0.2–0.4) that provided raw material for parasitism, with 67% and 76% of known

parasitism-related genes in each lineage arising from these duplicates. Functional enrichment highlighted convergence in hormone signaling and regulatory pathways. This genomic divergence mirrors distinct life-history strategies, one lineage invests more in propagule establishment (higher germination), while the other prioritizes rapid host exploitation (greater parasitic vigor). Our study demonstrates that regulatory innovation and gene duplication underpin ecological divergence and parasitic adaptation in this ancient hemiparasitic lineage.

Key Words: Parasitic plants, phylogenomics, gene duplication, cryptic species.

Climate-driven genomic signatures in *Toxicodendron vernicifluum*: A landscape genomic approach with RAD-seq

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Toxicodendron vernicifluum is an economically important tree species in East Asia, valued for its lacquer, medicinal properties, and timber. To gain a systematic understanding of the genetic variation and adaptive evolution of its natural populations, we applied restriction-site associated DNA sequencing (RAD-seq) to 175 individuals representing 39 populations across China. An average of 5,697,771 clean reads per individual was obtained, with a mean mapping rate of 85.47%. Through principal component analysis, ADMIXTURE, and phylogenetic analyses, the Chinese populations of *T. vernicifluum* were assigned to eight genetic groups: Nujiang, Yunnan (NUJ); Guizhou Plateau (GZP); Qinling–Daba Mountains 1 (QB1); Qinling–Daba Mountains 2 (QB2); Taihang Mountains (THS); eastern China (EAS); Xingdoushan, Hubei (XDS); and Zigui, Hubei (MPX). Among these, the latter three groups exhibited genetic admixture of two ancestral components. Demographic simulations revealed that the eastern China and western China lineages diverged approximately 2.66 Ma, and the XDS population originated from an admixture event between the GZP and EAS lineages. Latent factor mixed models identified 205 SNP loci significantly associated with environmental variables, predominantly related to altitude and temperature factors. Gradient forest analysis further demonstrated that altitude, isothermality, temperature seasonality, and precipitation of the wettest month were key environmental drivers of adaptive genetic variation. Under future climate warming scenarios, populations in eastern China, the Yunnan–Guizhou Plateau, and the Xingdoushan region are projected to experience substantial genetic offset, indicating elevated climate vulnerability. This study elucidates the lineage divergence and adaptive genetic basis of *T. vernicifluum* at the nuclear genome level, providing a scientific foundation for the management and conservation of its germplasm resources.

Key Words: *Toxicodendron vernicifluum*; adaptive evolution; population genetics; landscape genomics; phylogeography.

Morphological, molecular and geographical evidence support the recognition of *Salvia nipponica* subsp.zhejiangensis as a distinct species

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Salvia L., the largest genus in the family Lamiaceae, comprises approximately 1000 species worldwide. East Asia, particularly China, is recognized as a major center of diversity for the genus. Based on extensive field observations and morphological examinations of taxa within *Salvia* sect. *Glutinaria* in East Asia, this study elevates *Salvia nipponica* subsp. *zhejiangensis* to species rank. The taxonomic assessment was conducted using an integrative approach combining detailed morphological comparisons, phylogenetic analyses, and plastid genomic data. *Salvia nipponica* subsp. *zhejiangensis* is elevated to species rank as *Salvia zhejiangensis*. Morphologically, *S. zhejiangensis* resembles *S. nipponica* but differs in corolla coloration, indumentum characteristics, calyx pubescence, and leaf shape. Specifically, *S. zhejiangensis* is characterized by pale yellow corollas with reddish-purple spots on both the inner and outer surfaces, corollas with an indumentum composed of long erect hairs and short glandular hairs, calyx tubes covered with long erect hairs and short glandular hairs, and triangular leaves. In contrast, *S. nipponica* possesses uniformly yellow corollas without spots, corollas covered only with glandular hairs, calyx tubes with long villous hairs along the ridges and margins, and sagittate leaves. Geographically, *S. zhejiangensis* is clearly isolated from other members of *Salvia* sect. *Glutinaria*. Phylogenetic analyses recovered *S. zhejiangensis* as a strongly supported independent lineage within an East Asian clade comprising taxa distributed in Japan and Korea. Furthermore, the plastome of *S. zhejiangensis* was characterized and compared with those of closely related species. The integration of morphological and molecular evidence supports the recognition of *S. zhejiangensis* as a distinct species. This taxonomic revision contributes to a better understanding of species diversity within *Salvia* and provides new insights into the biogeography and evolutionary history of the genus in East Asia.

Key Words: Salvia; Lamiaceae; Sino-Japanese flora; taxonomic revision; species delimitation; plastome phylogenomics

Phylogeny and biogeography of Smilacaceae in the world and classification revision of Asian Smilacaceae

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Smilacaceae is a monocot family of shrubs and herbs widely distributed across the world. The family comprises two genera (*Smilax* and *Heterosmilax* in traditional taxonomy) and more than 200 species characterized by climbing habit, reticulate leaf venation, paired petiolar tendrils, unisexual flowers, and berries. Our molecular phylogenetic studies have clearly revealed the framework of phylogeny and biogeography in Smilacaceae. This family consists of only one genus (*Smilax*), which is composed of five lineages: 1) the Old World's woody *Smilax* group, 2) the Old World's stingless, herbaceous and near herbaceous *Smilax* groups (including the former genus *Heterosmilax*), 3) the Old World's Southwest China-Himalaya *Smilax* group, 4) the Old World's *Smilax aspera* group, 5) the New World's woody *Smilax* group. It reveals eight long-distance transcontinental dispersals during the Miocene, including the herbaceous *Smilax* from East Asia to North America, the needled *Smilax* from North America to East Asia, the spicate *Smilax* from East Africa to South Asia, the *Smilax* of Australia from Southeast Asia, the *Smilax* of Africa from South Asia, and the close connection between North American *Smilax* and Europe and South America *Smilax*. It reveals that the *Smilax aspera* group and the *Smilax elegans* group are the basal lineages of the Eurasian branch. On the basis of more than twenty years' research on morphology, molecular phylogeny and DNA barcoding of Smilacaceae, we present here a comprehensive taxonomic revision of Smilacaceae in Asia, one of the diversification centers of the family. Our results show that: 1) the combination of ITS, *rbcL*, and *matK* serves as a high-resolution DNA barcode for Smilacaceae, resolving species boundaries for approximately 80% of Asian taxa and revealing 11 species complexes affected by incomplete lineage sorting, most of which were confirmed by morphometric analyses as morphologically distinguishable, independent species; 2) a new classification

system of Asian Smilacaceae is proposed, recognizing one genus, five subgenera, and 19 sections, comprising about 118 species and 7 subspecies, with seven species reduced to subspecies, eight names treated as synonyms, five new species described, and ; 3) ten difficult-to-delimit or rare species are provisionally treated as species inquirendae pending future investigation. The morphology and distribution of all species of Asian *Smilax* are described, and an identification key is provided.

Key Words: Smilacaceae; Phylogeny and Biogeography; Revision of Asian Smilacaceae

Strong phylogeographic structure in major plastid lineages of East Asian Cerris oaks (*Quercus* subsection *Campylolepides*, Fagaceae): Insights from a 761-plastome analysis

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In angiosperms, plastomes are typically maternally inherited and transmitted primarily through seeds, leading to limited gene flow of plastid DNA. This restriction often results in a stronger geographic structure for plastid DNA compared to nuclear DNA, especially in wind-pollinated plants with large seeds, such as oaks. However, previous studies on East Asian Cerris oaks (*Quercus* subsection *Campylolepides*; *Q. acutissima*, *Q. chenii*, and *Q. variabilis*) found only three deep-diverging plastid lineages distributed randomly across their range, obscuring any clear phylogeographic structure. In this study, we performed a comprehensive sampling of whole plastomes to re-examine the phylogeographic pattern of East Asian Cerris oaks. Across 761 samples, we identified 163 haplotypes clustered into 15 clades, 11 of which were shared among species. The crown-group radiation of the *Campylolepides* core plastid clade appears to predate the formation of modern-day species, suggesting that the previously identified deep-diverging plastid lineages may reflect the retention of ancestral polymorphism. Under this interpretation, these lineages are expected to be randomly distributed across the species' range. Within eight plastid clades occurring in more than five populations, we detected a significant phylogeographic structure. The consistent east-west differentiation observed in several widely distributed clades reflects allopatric divergence followed by localized gene exchange among sympatric species in multiple isolated refugia. Additionally, we found that different oak species co-occurring at the same site exhibited higher levels of haplotype sharing compared to those in nearby populations. The haplotypes shared within mixed-species populations displayed narrow distributions and were estimated to have originated well after the speciation events, likely due to Pleistocene plastome capture. Our findings highlight that in East Asian Cerris oaks, strong phylogeographic structure is evident primarily within major plastid clades rather

than within individual species. Both shared ancestral polymorphism and historical introgression may have contributed to shaping the phylogeographic patterns of these species.

Key Words: introgression; phylogeography; plastome capture; *Quercus acutissima*; *Quercus chenii*; *Quercus variabilis*

From Species Coexistence to Genomic Adaptation in *Rhododendron*: A Multi-scale Perspective on Plant Diversity and Conservation in Mountain Ecosystems

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Mountain biodiversity hotspots provide exceptional opportunities to understand how ecological and evolutionary processes generate and maintain plant diversity. The Hengduan Mountains, one of the world's richest centers of temperate plant diversity, harbor remarkable species radiations of *Rhododendron* across steep elevational gradients. By integrating evidence from community ecology, trait evolution, and population genomics, this study explores how adaptive processes at multiple scales contribute to the assembly and persistence of mountain plant diversity. First, community-wide surveys show that co-occurring among closely related species is primarily associated with divergence in flowering phenology rather than vegetative morphology, suggesting that temporal niche partitioning promotes reproductive interference and coexistence. Second, analyses of multidimensional floral traits further reveal that floral diversification and community-level shifts is strongly constrained by evolutionary history but also shaped by environmental filtering along elevational gradients in this generalized pollination system.

Finally, population genomics of one alpine shrub *R. intricatum* uncover widespread genomic signatures of local adaptation across elevations. Genome–environment associations, coordinated phenotypic variation, and projections of increasing genomic offset under future climate scenarios together demonstrate adaptive responses to environmental heterogeneity while highlighting the vulnerability of alpine populations to climate change. Together, these findings link species coexistence, phenotypic diversification, and genomic adaptation within a unified multiscale framework. They illustrate how ecological and evolutionary processes jointly shape mountain biodiversity and provide insights for conserving plant diversity under ongoing environmental change.

Key Words: adaptation, coexistence, mountain ecosystems, Rhododendron

From Collection to Identification:
A Complete Workflow for DNA Barcoding Studies of Bryophytes

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Bryophytes hold significant value and broad development potential in ecological, ornamental, and medicinal fields. However, challenges exist in specimen collection, preservation, morphological identification, and DNA barcoding. This study proposes a technical solution based on experimental research and data analysis across diverse bryophyte groups: 1. Use mobile applications to geolocate each specimen during collection; dry specimens using hot-air drying methods (recommended at 40-80°C). 2. Classify molecular specimens into two categories: macroscopic materials stored in herbaria are vacuum-sealed with desiccants and oxygen absorbers for ambient temperature storage; purified DNA is cryopreserved at ultra-low temperatures. 3. Employ an optimized mCTAB method specific for bryophytes to extract DNA from micro-sample. 4. Improve direct PCR protocols to enable DNA barcoding from as little as 0.01 mg of dried material. 5. Based on moss chloroplast genomic data, screen highly variable candidate barcodes; design universal primers and validate resolution across diverse representative taxa; recommend seven core candidate barcodes for mosses: *atpB-rbcL*, *psaI-accD*, *ycf1*, *ycf2*, *matK*, *rpoB-trnC*, and *clpP*.

Key Words: mosses, biodiversity, environmental DNA, taxonomy, molecular specimens

Genomic Diversity and Evolutionary History of Medicinal Licorice (*Glycyrrhiza glabra* s.l.)

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Medicinal licorice (*Glycyrrhiza glabra* s.l.) holds profound pharmacological and ecological significance in arid and semi-arid environments; however, a comprehensive global-scale genomic landscape resolving its evolutionary history and lineage diversification has remained elusive. Here, high-coverage (~20×) whole-genome resequencing was conducted on 436 globally collected accessions. By integrating ADMIXTURE, principal component analysis, and phylogenetic reconstruction, fine-scale population structure and evolutionary dynamics were systematically delineated. The accessions were distinctly partitioned into four geographically differentiated genetic lineages (K = 4), exhibiting a prominent East–West divergence pattern driven by macro-geographic isolation between the Western (Group 2) and Eastern (Group 4) Tethys lineages. Concurrently, pronounced genetic isolation and ecological specialization were identified within the Central Asian arid zone, as evidenced by the highest degree of differentiation observed between the Central Asian core (Group 1) and Eastern Central Asia (Group 3) (F_{ST} = 0.5344). Furthermore, divergent evolutionary trajectories were revealed across lineages: the Western Tethys lineage harbored the highest nucleotide diversity (π) and most rapid linkage disequilibrium (LD) decay, whereas the Central Asian lineage displayed the lowest diversity and slowest LD decay, indicating that historical bottlenecks or directional selection coupled with subsequent demographic expansion shaped its genomic architecture. Collectively, this study establishes a high-resolution genomic framework for medicinal licorice, providing crucial genetic foundations for lineage-specific germplasm conservation, core collection construction, and marker-assisted breeding.

Key Words: Medicinal licorice, Whole-genome resequencing, Population structure,

Genetic diversity

Rheophytes: diversity, evolution, and conservation in fast-flowing rivers

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Rheophytes are plants specialized for life in fast-flowing rivers and streams, where strong currents, rocky substrates, and seasonal fluctuations in water level impose distinctive environmental constraints. This lifestyle has evolved independently across multiple plant lineages, often accompanied by remarkable morphological and ecological adaptations. Yet rheophytic diversity remains incompletely understood, partly because these plants occupy highly specialized, fragmented, and often inaccessible habitats. Our studies of Hydrostachyaceae and Podostemaceae, two distantly related angiosperm families independently adapted to fast-flowing waters, provide complementary insights into the diversity, evolution, and habitat specialization of rheophytes. Taxonomic and molecular investigations continue to uncover previously unrecognized diversity, including a recently described species of *Hydrostachys* from Madagascar and previously underestimated diversity of Podostemaceae revealed by molecular evidence in China. Large-scale phylogenetic analyses have also resolved the long-debated placement of Hydrostachyaceae within Cornales, providing an evolutionary context for its highly modified morphology and specialized lifestyle. At the habitat level, rheophytes occupy only a restricted subset of river systems, making their distributions difficult to characterize from broad-scale environmental conditions alone. Multi-scale habitat analyses of Podostemaceae further demonstrate how integrating regional climate, riverine characteristics, and local habitat information derived from remote sensing can refine the identification of potentially suitable habitats. Human disturbance, flow regulation, and road construction increasingly threaten rheophytes and their specialized habitats, emphasizing the need to conserve both these distinctive plants and the dynamic river systems that sustain them. Together, these findings highlight the close links among rheophyte diversity, evolutionary history, habitat specialization, and conservation, and underscore the value of integrating these perspectives to guide future exploration and protect their specialized riverine habitats.

Key Words: Hydrostachyaceae; Podostemaceae; rheophytic adaptation; habitat

specialization; plant conservation

Phylogenomic Investigations of Trait, Gene and Genome Evolution Across the Green Tree of Life

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"Phylogenomics" research includes the application of genome-scale data to infer species relationships and comparative analyses of genome structure and gene content within the context of a species phylogeny. Genome and transcriptome data are resolving relationships among plant species and guiding comparative genomic analyses of the evolution of gene content and genome structure across the green plant phylogeny. Moreover, comparative and functional genomic analyses are elucidating the molecular basis of variation in functional traits. I will discuss how we are using comparative and functional genomics to identify genes contributing to parallel evolutionary innovations in a variety of metabolic, physiological and reproductive plant traits. Implications for plant diversification and synthetic plant biology will be discussed.

Phylogenomic study revealed stepwise evolution of the root nodule symbiosis

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Some plants in ten families of the nitrogen fixing clade of angiosperms form root nodules through symbiosis with nitrogen fixing bacteria, converting atmospheric inorganic nitrogen into ammonia nitrogen that plants can assimilate, thus playing a critical role in the nitrogen cycle of terrestrial ecosystems. However, whether root nodule symbiotic nitrogen fixation arose once and was subsequently lost multiple times, or arose multiple times independently, remains controversial, and the formation and evolutionary trajectory of the gene regulatory network underlying symbiotic nitrogen fixation are also unclear. By whole genome sequencing of representative species from ten key nitrogen fixing lineages, combined with comparative genomic and phylogenetic analyses on 194 published genomes, this study constructed, for the first time at the single gene level, the evolutionary architecture of the gene regulatory network for root nodule symbiosis. The key breakthrough lies in revealing that three "gene innovations" gave rise to the capacity for nodulation and symbiotic nitrogen fixation. First, the gamma (γ) paleohexaploidy event in core eudicots generated numerous duplicated genes, providing the genetic raw material for subsequent functional differentiation and neofunctionalization of nodulation inducible genes and key nitrogen fixation genes (e.g., NIN, CNGCa, NFP). Second, the common ancestor of the nitrogen fixing clade modularly recruited and rewired genes from the arbuscular mycorrhizal symbiosis, nitrate response, and stress response pathways, establishing an initial gene regulatory network for symbiotic nodulation and nitrogen fixation. Finally, legumes evolved efficient root nodule symbioses through convergent evolution, with two key genes, NPL and SymSTK, playing decisive roles. This study not only reconciles the "single origin" and "multiple origin" debates at the level of gene regulatory network evolution, but also systematically compiles a core "gene inventory" of the nodule symbiosis network, providing precise targets for engineering nitrogen fixation into non legume crops.

Key Words: root nodule symbiotic nitrogen fixation; nitrogen fixing clade; gene regulatory network; symbiosome

Facing the Paradox — Exploring the Strange Realities of Fern Genomics

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The publication of the first whole plan genome, the genomic of the derived eudicot Arabiopsis thaliana arguably enabled plant sciences to enter the post-genomic area. Since, a rapidly enhancing number of plant species have been added to the plant genome resources available with the current state including more than 1,500 species of land plants having at least on e whole genome released. While all major plant lineages have now several genomes made available, ferns have been for some time the last frontier in plant genomics as a consequence of challenges such as medium to large sized genomes, high chromosome numbers, and in general low economic value. In turn, the uniqueness of fern genomics have not been fully exploited such ferns include the record holders of largest genome and largest chromosome number. However, major breakthroughs have been achieved in the recent years as a consequence of the publication of several whole genome sequences and the utilisation of other approaches enabling to integrate the wast amount of cytological information available to explore the key hypotheses introduced recently such as the “centromere drive”. This presentation outlines some of the emerging conclusions in the context of comparison with the paradigms of genome evolution founded by the study of angiosperms genomes. Similar to the findings in bryophytes revealing different trends in genome evolution among the three lineages, vascular plant lineages appear to be not only distinct in their species richness and morphological disparity but also in the trends shaping their genomic disparity. As predicted by the “centromere drive”, divergent trajectories of genome architecture and chromosome evolution shape the genome disparity in homosporous and heterosporous plants. Taking the recent findings in the context of abbot 100 years research on fern genetics, the presentation aims to identify the key questions to be addressed in the post-genomic era of fern studies including the role of polyploidy in fern speciation and the fixation of ancient whole genome duplication in some but not all early diverging lineages of ferns. Special attention has to be also given to the consequences of the maintenance of medium to large sized genomes with large chromosome numbers and its consequences of the evolvability of ferns.

The evolution of high-order genome architecture revealed from 1,000 species

Kai Ye

Spatial genome organization plays a crucial regulatory role, but its evolutionary development remains unclear. Leveraging Hi-C data from 1,025 species, we trace the evolutionary trajectories of genome organization through 2 higher-order architectures, ‘‘global folding’’ (spatial organization of the karyotype) and ‘‘checkerboard’’ (spatial organization of chromatin compartments). Earlier unicellular life forms mostly displayed random genome configurations. Throughout the evolution of plants, global folding became and remained the prominent architecture. However, animals progressively developed more pronounced checkerboard architectures; these are also apparent during early embryogenesis, which suggests that they act as a conserved mechanism of gene regulation. In contrast, plants exhibit comparatively weaker checkerboard patterns and instead preferentially organize co-regulated genes into linear genomic clusters. Both strategies of gene arrangement reinforce the biological principle that ‘‘structure determines function’’: divergent evolutionary paths converge on architectural solutions that reflect gene regulatory requirements over time.

Polyploidy and 3D genome remodeling in driving angiosperm diversity

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Angiosperms comprise approximately 350,000 extant species, accounting for over 90% of terrestrial plant diversity. The underlying causes of their evolutionary success have long been a central question in evolutionary biology. By comparative genomic studies, we identified and named 22 polyploidization events (designated ζ, ε, τ, and others) associated with the origin and diversification of major land plant lineages. We further demonstrated that polyploidization was a primary factor enabling the survival of more than ten major plant clades through the Cretaceous–Paleogene (K-Pg) mass extinction event approximately 65 million years ago. In contrast, we found that the lineage leading to *Aristolochia fimbriata* experienced no additional polyploidization events since the origin of angiosperms. Despite this genomic simplicity, this lineage evolved a highly specialized floral architecture and a complex trapping–imprisonment–release pollination system. Our results showed that, although the genome of *A. fimbriata* was compositionally simple, it evolved an extensive and sophisticated long-range regulatory network via 3D genome remodeling, which drive floral organ specialization and adaptive evolution. Collectively, these findings revealed the role of polyploidization in the origin and proliferation of angiosperms, and also found that, in the absence of polyploidization, plants can achieve complex trait innovations through three-dimensional genome remodeling and long-range regulatory networks, thereby deepening our understanding of the mechanisms underlying plant diversity.

Key Words: angiosperm diversity, genome evolution, trait innovation, 3D genome

Decoding genomic diversity across the green plant tree of life

Tong Wei

Rapid growth in green plant genome sequencing is outpacing our ability to deliver high-quality, lineage-aware gene annotations across Viridiplantae. We present OrionGeno, a phylogeny-aware deep learning framework that jointly predicts plant gene architectures (exons, introns, UTRs) and repetitive elements directly from genomic DNA, without requiring RNA-seq or protein homology evidence. By fine-tuning OrionGeno on a taxonomically balanced training set spanning chlorophyte and streptophyte algae, bryophytes, lycophytes, ferns, gymnosperms, and angiosperms, we capture both conserved and lineage-specific features of plant gene structure and repeat landscapes. We further apply OrionGeno to annotate hundreds of plant family exemplars, revealing substantial variation in genome completeness among major groups and substantially expanding gene-model coverage for previously uncharacterized families. Collectively, we provide a scalable, evidence-independent framework for advancing plant genome annotation, enabling robust downstream studies in plant evolutionary genomics, functional biology, and biodiversity conservation.

From Reads to Evolution: An Integrated Phylogenomic Framework for the Plant Tree of Life

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Unlike plastid genomes, which trace only a single maternal lineage, nuclear genomes retain biparental evolutionary histories and therefore capture signals of hybridization, introgression, incomplete lineage sorting, and trait evolution. These processes have played central roles in the diversification of flowering plants, yet they remain difficult to study at broad taxonomic scales. Although high-throughput sequencing has greatly expanded the availability of nuclear data, progress is still constrained by three practical challenges: making full use of existing genomic resources, analysing increasingly large datasets in a reproducible manner, and translating phylogenomic datasets into evolutionary insights. In this presentation, I'll describe how we (in my lab) have addressed these challenges through three complementary studies and demonstrate their application in a phylogenomic study of *Prunus* sensu lato (Rosaceae).We first asked whether large amounts of publicly available sequencing data could be repurposed for target-enrichment phylogenomics. Using the universal Angiosperms353 probe set, we showed that hundreds of nuclear loci can be recovered not only from target-capture data, but also from transcriptomes, whole-genome sequencing, and genome-skimming datasets. Even relatively shallow sequencing datasets often recover sufficient loci for robust phylogenetic analyses. These results demonstrate that existing sequencing resources can substantially increase taxon sampling while reducing the need for additional laboratory sequencing. We next developed HybSuite, an integrated workflow for hybrid-capture phylogenomics that automates the analytical steps from raw reads to species trees. The pipeline combines quality control, locus recovery, assembly, orthology inference, alignment, gene-tree estimation, species-tree reconstruction, and downstream analyses within a single reproducible workflow. By reducing manual intervention and standardizing data processing, HybSuite makes large phylogenomic analyses easier to reproduce and scale across different study systems. Finally, we applied these approaches to reconstruct the evolutionary history of *Prunus* s.l. using approximately 5,500 lineage-specific nuclear genes along with universal Angiosperms353 genes. The

resulting robust phylogeny indicates an early Paleocene origin (~63 million years ago, Ma), followed by accelerated diversification near the Paleocene–Eocene boundary (~55 Ma). Integrative macroevolutionary analyses further revealed that diversification rates are strongly associated with paleo-temperature and historical atmospheric CO_2 concentration, while transitions in inflorescence architecture and ploidy level contributed to lineage diversification through interactions with changing environmental conditions. These findings illustrate how intrinsic biological traits and extrinsic environmental drivers jointly shape the evolutionary history of one of this economically and horticulturally important lineage. Taken together, these studies show how publicly available sequencing data, reproducible analytical workflows, and nuclear phylogenomics can be combined to address questions that were previously difficult to tackle at scale. As genomic resources continue to accumulate, our strategy illustrated here can be readily extended to other plant groups, enabling phylogenomic studies at increasingly broader taxonomic scales. Beyond resolving phylogenetic relationships, integrating these components provides a practical roadmap to investigating the timing, mechanisms, and ecological drivers of diversification across the angiosperm Tree of Life.

Key Words: Nuclear phylogenomics Angiosperms353, Hybrid capture sequencing, Phylogenomic pipelines, Prunus, Macroevolution, Tree of Life

The uplift of the Qinghai-Xizang Plateau and global climate cooling triggered spatiotemporal evolution of *Lonicera* (Caprifoliaceae)

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The distribution patterns of plants in the Northern Hemisphere are closely linked to their evolutionary history. The genus *Lonicera*, commonly referred to as honeysuckle, is widely distributed across the northern temperate zone, making it an ideal model for exploring the distribution patterns and driving factors of plants in the Northern Hemisphere. This study, based on 108 globally distributed *Lonicera* samples (57 species), covered 22 of the 25 subsections of *Lonicera* recognized by Rehder (1903) and Nakai (1938), analyzed 485 orthologous loci and plastid genomes to investigate phylogenetic relationships, and observed phylogenetic incongruence. QuIBL and *f*-branch analyses revealed that incomplete lineage sorting (ILS) is the primary driver of phylogenetic discordance, accompanied by widespread but weak introgression, with only a small proportion of triplets showing strong support for introgression with relatively high mixture weights. Biogeographic and diversity distribution analyses suggest that Lonicera originated in the Qinghai-Xizang Plateau (QXP) and/or East Asia, spread to North America and Europe, and established diversity centers in East Asia, Central Europe, and western North America. Our results support the hypothesis that the uplift of the QXP and global climate shift of the Eocene-Oligocene transition (EOT) were both evolutionary drivers, with varied ecological

adaptability among various *Lonicera* lineages. This study provides new insights into the phylogeny and biogeographic evolution of *Lonicera*, while also serving as a reference for studies on the evolutionary history of plant and animal lineages.

Key Words: biogeography, Caprifoliaceae, ecological analyses, phylogenomics, species diversification.

Evolutionary and Domestication Genomics Facilitate Solanaceae Crop Breeding

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With the rapid advancement of sequencing technologies, the Solanaceae family ranks as the third most sequenced plant family in terms of species number, with genomes sequenced for 131 species and abundant multi-omics data, offering extraordinary opportunities for comparative evolutionary genomics. To understand how evolution and domestication facilitate breeding, we integrated Solanaceae data and specifically analyzed a potato progenitor panel and landrace panel including 502 accessions as well as a tomato population comprising 706 accessions. Through comparative genomics at both the interspecific and population levels, viewed through the lenses of evolution and domestication, we identified functional genes, lncRNA-PEL8 and Tw1, that underlie metabolites and yield-related agronomic traits. Furthermore, we incorporated multi-omics data to improve genomic prediction of potato and tomato metabolites and yield. Together, these approaches further validate that evolutionary genomics facilitates breeding efforts by increasing genomic prediction accuracy and enabling genomic design breeding. However, the efficient extraction and use of evolutionary insights, such as evolutionarily conserved sites, sequence divergent loci, and cross-species expression patterns, remains challenging for researchers without extensive bioinformatics expertise. To bridge this gap, we developed the Solanaceae Evolution Multi-Omics Database (SolEvoDB), a user-friendly web-based platform designed for rapid and intuitive exploration and interactive visualization of genomic and transcriptomic conservation and variation across the Solanaceae phylogeny. By unlocking the legacy of evolution and domestication, coupled with genomic selection and genome design, our study provides a transformative framework for harnessing naturally occurring genetic variation, thereby enabling breeders to design vigorous cultivars.

Key Words: Solanaceae, potato, tomato, evolution, domestication, breeding

Genetic consequences of hybridization between Fagaceae species

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Hybridization is common between modern oak species and presumably occurred among their ancestral lineages. To investigate the deep history and genetic consequence of hybridization in oak species, we used phylogenomic analyses of nuclear and plastid genomes to detect signatures of hybridization across the Fagaceae. We showed that introgression resulted from historical hybridization events between ancestral species representing three oak sections, *Ponticae*, *Quercus* and *Virentes*. Identity-by-descent (IBD) analyses based on whole-genome SNP data clearly detected a large number of shared haplotypes between these sections. These shared haplotypes apparently originated during hybridization, and most of them are significantly longer than expected under neutrality. These results suggested that shared haplotypes were maintained by natural selection, providing convincing evidence for the persistence of adaptive introgression. Current hybridization also may provide an additional genetic pathway for species to repeatedly adapt to similar environments via molecular parallelism. To test this hypothesis, we studied a pair of sympatrically distributed East Asian oak species, *Q. variabilis* and *Q. acutissima*. Population genomic analyses revealed an east-west divergence within *Q. variabilis*, and detected a ~270kb region showing a strong signal of selection. This region contains 20 genes, including 10 members of ethylene-responsive factor (ERF) family, which are involved in the response to abiotic stress. To investigate the origin of advantageous variation in this region within *Q. variabilis*, we first performed forward simulations to reject models of selection acting on *de novo* mutations or standing variation. Next, a battery of tests including phylogenetic analysis, efficient local ancestry inference, and gene flow analysis revealed multiple lines of evidence supporting beneficial alleles in this region originated through introgression from *Q. acutissima* into *Q. variabilis*. Finally, we found that the same ~270 kb region was under selection in *Q. acutissima*, suggesting that adaptive introgression has contributed to molecular parallelism in repeated climate adaptation in oaks. These studies underscore the importance of hybridization in the evolution of oak species across time scales.

ASTER: Phylogenomic Tools for the Era of Plant Tree of Life 2.0

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The plant Tree of Life is entering its 2.0 era, driven by unprecedented volumes of genomic data. However, reconstructing a robust species phylogeny from genome-scale datasets remains challenging due to widespread incomplete lineage sorting (ILS), gene duplication, and interspecific hybridization — all of which are especially prevalent in plants. Accurate Species Tree EstimatoR (ASTER) is a unified, open-source software package that addresses these challenges through a family of ILS-aware methods. All ASTER tools share a common algorithmic philosophy: using the fastest and simplest counters to achieve ILS-aware inference, scalable to thousands of whole genomes — a scale that complicated and bulky tools cannot reach. ASTRAL-IV — the flagship method for single-copy gene trees — infers a species tree from unrooted gene tree topologies. It incorporates CASTLES-II for branch length estimation in substitution units and achieves orders-of-magnitude speedups over ASTRAL-III, routinely handling tens of thousands of genes across thousands of species. Weighted ASTRAL (wASTRAL) extends this framework by leveraging branch lengths and support values from input gene trees, up-weighting signals from reliable gene tree regions. This weighted approach consistently outperforms the common practice of collapsing low-support branches. For plant genomes where whole-genome duplications are ubiquitous, ASTRAL-Pro3 handles multi-copy gene family trees without requiring homology assignment between copies; it automatically distinguishes speciation from gene duplication events, excludes noise from paralogous genes, and integrates CASTLES-Pro for branch length estimation. Moving beyond gene trees, CASTER bypasses gene tree reconstruction entirely by inferring species trees directly from whole-genome alignments or aligned sequences. On benchmark datasets, CASTER is 60–150× faster than concatenation-based maximum likelihood while achieving higher accuracy under ILS. For researchers working without assemblies, WASTER infers species trees directly from raw short reads at coverage as low as 1.5×, using k-mer–based identification of variable sites to bypass genome assembly and alignment altogether — a capability that dramatically lowers the learning curve and financial barrier for non-model

plant species. All of the above tools are available as precompiled binaries for Linux, macOS, and Windows, installable via Bioconda, and integrated into PhyloSuite. The ASTER ecosystem further includes a set of unpublished tools: D* statistic, which detects interspecific hybridization signals up to 50 Mya; SISTER, which infers phylogeny using synteny; TRIAL, which reduces reference bias by integrating alignment signals based on different reference genomes; and AFRESH, which refines errors in calling orthologous genomic sequences in large-scale analyses. To help fellow scientists navigate this growing toolbox, we provide a decision chart mapping common data scenarios — from raw reads to whole-genome alignments, from single-copy to multi-copy genes, from intra-genic to inter-class levels — to the most suitable tool, along with recommended execution parameters. We are also developing agent-friendly workflow guides that encode this decision logic into executable instructions, so that researchers can select, configure, and run the appropriate ASTER tool interactively with an agent using simple natural-language queries. With its unified framework, exceptional scalability, and coverage of diverse data types, ASTER is uniquely positioned to accelerate the reconstruction of the plant Tree of Life 2.0 at unprecedented scale and resolution.

Key Words: ASTER, ASTRAL, CASTER, WASTER, phylogeny

Global phylogeny and taxonomy of Artemisia

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Big plant genera account for ca. 25% of the flowering plant species. Despite their critical role in shaping plant diversity, their global-scale phylogenetic and taxonomic research are significantly behind compared to other genera. *Artemisia*, a big genus comprising ~500 species, holds immense medicinal and ecological importance. Despite decades of efforts, establishing a comprehensive phylogeny and taxonomy for global *Artemisia* has remained a formidable challenge. Here, we reconstruct the most comprehensive phylogeny of global *Artemisia* to date using a gigamatrix approach. We also analyze evolutionary patterns of 20 morphological characters of *Artemisia* worldwide to evaluate their taxonomic utility. Based on these findings, we propose a global taxonomy for *Artemisia*, recognizing 24 sections in 8 subgenera. This study provides a robust framework to advance understanding of the evolution and ecology of *Artemisia*, and to promote the sustainable utilization of its rich resources. Meanwhile, it introduces an exemplary case for taxonomic research on big genera in the genomic era.

Building Plant Genomics Resources: High-Quality Genome Annotation, Data Management, and Data Mining

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Long-read sequencing has improved the completeness of genome assemblies. However, annotation errors and fragmented data management still limit functional studies and breeding applications. We analyzed the genomes of rice, litchi, pineapple, and other plant species. Multiple types of evidence were integrated for gene model curation. GSAman and Simple Genome Hub were developed, and TBtools-II was used for genome annotation and analysis. Manual curation of seven plant genomes showed that about 8%–70% of exon structures required correction. In rice, the completeness of conserved single-copy genes increased from 86.9% to 99.6%. Simple Genome Hub supports standardized management and workflow-based analysis of genome-related data. We also developed an automated pipeline for pineapple fruit phenotyping. Accurate annotation, standardized data management, and efficient analysis can improve the quality and use of crop functional genomics resources. These resources provide a reliable basis for gene discovery and molecular breeding.

长读长测序提升了基因组完整度，但注释错误和数据分散仍限制功能解析与育种应用。以水稻、荔枝、菠萝等植物基因组为对象，整合多类证据，开发 GSAman、Simple Genome Hub 并结合 TBtools-II 开展基因结构校准与分析。七种植物基因组校准显示，约 8%～70%的外显子结构被修订，水稻保守单拷贝基因完整度由 86.9%提升至 99.6%。Simple Genome Hub 实现基因组及相关数据的标准化管理和流程化分析，并建立菠萝果实表型自动分析流程。精准注释、规范管理与智能分析可提高作物功能基因组资源质量和利用效率，支撑功能基因发现与分子育种。

Genome evolution in angiosperms: a phylogenomic perspective of gene structure conservation

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Angiosperms are the most species-rich group of land plants and have highly complex structures and functions of great importance for the human society and ecosystems. Protein-coding genes in plants usually contain introns and proteins often have functionally defined and/or structural conserved domains. Among all plant exons in different size, micro exons (<51 bp) and small exons (51~100 bp) are two previously defined size categories; micro and small exons are present in *Arabidopsis* floral homeotic genes (such as members of MADS-box and AP2 gene families) and encode portions of DNA-binding or protein-interaction domains. Recent studies indicate the specific protein factor(s) are needed for proper retention of micro exons in multiple floral homeotic genes and also for retention of other micro and small exons. Despite the importance of micro and small exons in the floral homeotic genes and other members of the MADS-box and AP2 gene families, the genome-wide gene exon-intron organizations and their conservation across many representative angiosperms are largely unknown. Here we selected genomes from 46 angiosperms representing 29 orders and four representative gymnosperms and estimated the number of the exons in different size categories for protein-coding genes. Among exons of protein-coding genes from these 50 genomes, ~35% are micro and small exons affecting most genes and the remaining exons are defined here as medium, large, or super exons. Exon-intron structural comparison using our new bioinformatic tool, ExonEvo, reveals that, ~69% of conserved exons in homologous genes are found in two or more major angiosperm subgroups, including ~47% as the seed plant-wide conserved exons that are present in most genes in individual species. An examination of domain-exon correspondence revealed that most conserved protein domains match two or more conserved exon families and genes encoding the same domain family members can have different domain-exon correspondence. Moreover, most flower-preferential genes contain conserved exons and most exons with exon skipping during splicing are shared by seed plants, suggesting that alternative splicing of the exons could be a conserved mechanism for regulating protein

structure. Our phylogenomic landscape of exon structure and domain-exon organization supports a model for conservation of exon/domain structure in relation to post-transcriptional regulation of gene/protein function.

Key Words: angiosperms, phylogenomics, gene structure conservation

Tree of Life and Spatio-Temporal Evolution of Urticaceae

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The Urticaceae is a large, globally distributed angiosperm family with high morphological-ecological diversity and considerable economic value, yet its phylogenetic backbone and evolutionary history remained poorly resolved for decades. This presentation summarizes our serial advances in reconstructing the Urticaceae tree of life and dissecting its spatio-temporal diversification across family, genus and species levels. Based on extensive field sampling covering major biomes worldwide, we deployed multi-layer molecular markers, ranging from traditional DNA fragments, plastid genomes to genome-scale nuclear data, to build a robust, upgraded phylogenomic framework for Urticaceae, achieving 96.3 % generic coverage. We formally proposed a revised classification system comprising four subfamilies and seven tribes, resolving long-standing taxonomic ambiguities of 21 controversial genera and establishing one new tribe and one new genus. Biogeographically, our time-calibrated phylogenies support a Late-Cretaceous Eurasian origin of Urticaceae, whose modern distribution was shaped by at least 92 independent long-distance dispersal events rather than vicariance. At the genus level, we uncovered repeated continental-island dispersals within Oreocnide and Debregeasia, triggered by palaeoclimatic and geological shifts. At the species level, population-genomic investigations on riparian *Debregeasia orientalis* demonstrated that climate-driven niche filtering constrains gene flow and post-dispersal establishment even with strong dispersal capacity. For the domesticated fibre crop ramie (*Boehmeria nivea*), human-mediated long-distance dispersal has driven its global spread and rapid adaptive divergence among wild-cultivated-feral populations. Collectively, these multi-scale findings highlight the intertwined roles of long-distance dispersal, geological-climatic change and human activity in shaping the extraordinary biodiversity of Urticaceae.

Key Words: Urticaceae; tree of life; spatio-temporal evolution; long-distance dispersal

Revisiting evolutionary relationships in the Neotropical radiation of the mega-diverse genus *Begonia* using genome-scale nuclear loci

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The Neotropics represent a major center of plant diversity, harboring more than 650 species of *Begonia*, one of the most species-rich angiosperm genera. However, evolutionary relationships within Neotropical *Begonia* remain incompletely resolved, largely due to reliance on a limited number of plastid markers. Here, we revisit evolutionary relationships in Neotropical *Begonia* using a phylogenomic dataset comprising over 1,200 nuclear loci and representatives from all 36 Neotropical sections. This genome-scale dataset provides a substantial expansion over previous frameworks and enables a direct comparison with earlier phylogenetic hypotheses based on plastid data. By contrasting nuclear and plastid-based phylogenies, we assess the extent to which previous relationships are supported, revised, or contradicted, and identify areas of conflict that may reflect processes such as incomplete lineage sorting or hybridization. This approach provides a more robust backbone for the Neotropical radiation of *Begonia* and offers new insights into the evolutionary history of this group. This phylogenomic framework establishes a foundation for future work on diversification in Neotropical *Begonia*, including ongoing population genomic analyses of Andean taxa and the development of genomic resources such as a reference genome for *Begonia ferruginea*. Together, these efforts contribute to a more comprehensive understanding of diversification in one of the most diverse tropical plant lineages.

Key Words: Andean Flora, Begoniaceae, molecular systematics, Neotropics, target enrichment

Untangling reticulate evolution and whole-genome duplication in *Alchemilla* s.l. and Fragariinae (Rosaceae)

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Alchemilla in the broad sense (s.l.) is one of the most species-rich and evolutionarily complex lineages of Rosaceae, with at least 350 species and more than 1,100 subspecies distributed mainly in alpine and temperate regions worldwide. Together with Aphanes, Afromilla, Eualchemilla, and Lachemilla, the group is characterized by extensive morphological diversity, frequent hybridization, high levels of polyploidy, and, in many lineages, apomixis. Previous plastid, nuclear ribosomal, and target-enrichment studies revealed strong cytonuclear and gene-tree discordance in the backbone of Alchemilla s.l. and Fragariinae. In particular, earlier analyses identified recurrent hybridization and allopolyploidy in Lachemilla, elevated proportions of gene duplication at four backbone nodes in Alchemilla s.l., and a putative polyploid origin of the group. Here, we revisit the backbone of Fragariinae, with emphasis on Alchemilla s.l., using a phylotranscriptomic dataset of 37 transcriptomes and 10 genomes, including 25 newly sequenced transcriptomes, 20 of them from Alchemilla s.l. We use species-tree, gene tree discordance, whole genome duplication, and coalescent-based species-network analyses to evaluate the relative roles of incomplete lineage sorting, hybridization, and recurrent genome duplication in shaping the evolutionary history of the group. The new phylotranscriptomic analyses recover WGD patterns broadly consistent with previous target-enrichment results, supporting a polyploid origin of Alchemilla s.l., but also reveal important differences. These include an additional WGD shared by Eualchemilla and Aphanes, no clear WGD signal for Lachemilla, and a potential new WGD in the backbone of Fragariinae. Coalescent-based PhyloNet analyses further suggest that reticulation is not restricted to Alchemilla s.l., but may characterize several major Fragariinae lineages, with Comarum, Sibbaldia, Farinopsis, Fragaria, and Alchemilla s.l. each showing evidence consistent with independent hybrid origins. Together with newly generated genome assemblies of Sibbaldia and Aphanes, these results provide a broader framework for understanding how hybridization, polyploidy, and subsequent diploidization have shaped the backbone of

Fragariinae and the diversification of Alchemilla s.l.

Key Words: Alchemilla s.l.; Phylotranscriptomics; Gene tree discordance; Hybridization and whole-genome duplication

Decoding genomic diversity across the plant tree of life

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Rapid growth in green plant genome sequencing is outpacing our ability to deliver high-quality, lineage-aware gene annotations across Viridiplantae. We present OrionGeno, a phylogeny-aware deep learning framework that jointly predicts plant gene architectures (exons, introns, UTRs) and repetitive elements directly from genomic DNA, without requiring RNA-seq or protein homology evidence. By fine-tuning OrionGeno on a taxonomically balanced training set spanning chlorophyte and streptophyte algae, bryophytes, lycophytes, ferns, gymnosperms, and angiosperms, we capture both conserved and lineage-specific features of plant gene structure and repeat landscapes. Across diverse benchmark plant genomes, OrionGeno achieves the highest mean CDS and ORF F1 scores and superior BUSCO completeness relative to state-of-the-art ab initio methods such as Helixer, Tiberius, ANNEVO, and AUGUSTUS, with particularly large gains in structurally complex or non-model plant lineages. We further apply OrionGeno to annotate hundreds of plant family exemplars, revealing substantial variation in genome completeness among major groups and substantially expanding gene-model coverage for previously uncharacterized families. Collectively, these results establish OrionGeno as a scalable, evidence-independent framework for advancing plant genome annotation, enabling robust downstream studies in plant evolutionary genomics, functional biology, and biodiversity conservation.

Key Words: Plant genomics; Genome annotation; deep learning; Repetitive elements; Comparative genomics

Convergent evolution of heterostyly in the largest heterostylous plant family through recruitment of different floral genes

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The evolution of similar phenotypes by convergent evolution usually results from adaptive responses to similar selective pressures. An enduring question is whether convergent phenotypic evolution relies on the same or distinct molecular mechanisms, especially among closely related lineages where developmental and genomic backgrounds are more likely to be similar. Here, we address this question by investigating the genetic architecture of the floral polymorphism heterostyly across Rubiaceae—the angiosperm family with the greatest number of heterostylous species. By integrating chromosome-scale genome assemblies, multiomics and functional assays in six heterostylous species, we uncover the *S*-locus underlying heterostyly originated at least twice independently in Rubiaceae, with distinct genetic pathways and structures. In five species, style length is regulated by *IAA* genes originating from a single duplication predating radiation of the family. Among the five species *Dunnia sinensis* has additionally recruited *DuEXOC3* in style length control. By contrast, in *Luculia pinceana*, the ancestral *IAA*-based *S*-locus was apparently lost and replaced by newly assembled polygalacturonase (*PG*) genes controlling style length thus representing an independent origin of heterostyly. The hemizygous or partially hemizygous *S*-locus supergene in Rubiaceae exhibits striking architectural variation, ranging from 75 kb to 1.2 Mb in size with lineage-specific repeat accumulation. Transgenic experiments with tobacco provided evidence that six candidate genes identified in three species likely play a role in regulating style elongation. Our findings demonstrate that among related lineages of a single family convergent adaptive traits controlled by supergenes can originate through a mosaic of shared ancestral components and lineage-specific innovations.

Key Words: Heterostyly, Convergent evolution, S-locus, Rubiaceae

SolEvoDB: A Phylogeny-Aware Evolutionary Multi-Omics Platform for Translating Evolutionary Insights into Functional Gene Discovery Across Solanaceae

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The Solanaceae family comprises major crops including tomato, potato, pepper, eggplant, and tobacco, whose extensive phenotypic and genomic diversity has arisen through approximately 80 million years of evolution. Although multi-omics datasets from Solanaceae species now provide resources for comparative evolutionary studies, translating evolutionary signals into functional gene discovery remains challenging because phylogeny-aware evolutionary analyses and extraction require substantial bioinformatic expertise, limiting their accessibility to the broader research community. Here, we present the Solanaceae Evolution Multi-Omics Database (SolEvoDB; https://solevodb.cpolar.top/), a web-based, programming-free platform integrates evolutionary genomics with multi-omics data to facilitate the exploration of genome and transcriptome evolution, functional gene discovery, and comparative analyses across the Solanaceae. SolEvoDB integrates 143 genome assemblies of 119 species, 5.53 million gene models and annotations, 83,380 ortholog groups, 5.22 million orthologous genes, 5.34 million syntenic genes, and genome-wide evolutionary constraint level as well as 454 tissue-specific transcriptomes, within a unified phylogenetic platform. The platform enables users to translate evolutionary signatures into functional hypotheses by integrating evolutionary constraint, sequence conservation and divergence, syntenic relationships, and expression conservation and divergence across the Solanaceae phylogeny through interactive visualization and comparative analyses, thereby facilitating the identification and prioritization of candidate genes and regulatory loci. By transforming evolutionary

information into an accessible framework for functional inference, SolEvoDB bridges comparative evolutionary genomics and crop genetics, accelerating functional gene discovery, genetic dissection of complex traits, and precision breeding across Solanaceae.

Key Words: Solanaceae, evolution omics, phylogeny, ortholog, synteny, functional gene discovery

Seed Plants – an update in the phylogeny of a 400-million-year-old lineage

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The evoluMonary lineage that includes seed plants is among the most impac^ul players in the history of life, as its innovaMons, diversificaMon and radiaMon led to the establishment of predominant terrestrial biomes nearly since the onset of its differenMaMon. While the lineage itself can be traced to ca. 400 Ma, seeds evolved ca. 20 myr later. The fossil record documents a vast diversity of seed plant lineages, only five of which, i.e., cycads, *Ginkgo*, Gnetales, conifers and angiosperms, survived to the present. DelimiMng natural groups and the relaMonships among them has represented a substanMal challenge. With the goal of synthesizing informaMon on phylogeneMc relaMonships among extant seed plants, we reviewed available molecular phylogenies, summarized esMmated phylogeneMc arrangements, and evaluated recurrent results. We examined 41 studies that include seed plants published for 30 years, that together comprise ca. 400 esMmated phylogenies. We summarized the frequency of phylogeneMc results according to types and treatment of molecular data, and phylogeneMc esMmaMon method. We found that there is a single result that seems solid, which is the phylogeneMc closeness between Gnetales and conifers. Lingering quesMons are the exact relaMonship between Gnetales and conifers, the phylogeneMc posiMon of cycads and of *Ginkgo*, and whether extant gymnosperms are closer to each other than what any is to angiosperms. Recent discoveries and new interpretaMons from careful examinaMon of the fossil record might provide informaMon about relaMonships and evoluMon that can contribute to solve some of these lingering quesMons. A deep understanding of seed plant relaMonships will require integraMon of informaMon from fossil lineages, and to do this, the first inescapable step is a criMcal evaluaMon of their morphological agributes, interpreted with an evoluMonary vision.

Key Words: conifers, fossil record, Gnetales, molecular phylogeny, morphology, phylogeneMc uncertainty

Genomic and morphological data help resolving phylogenetic conflicts and set revised stable classifications: A synthetic insight into *Carex* sect. *Mitratae* s.l. (Cyperaceae)

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Phylogenetic incongruences and taxonomic discrepancies often go hand in hand, confounding taxonomic classifications due to the conflicting signals between molecular and morphological data. The internal organization of *Carex* (Cyperaceae), a genus with over 2,200 species, presents substantial phylogenetic and taxonomic challenges due to pervasive homoplasy of key morphological characters. Although sequence data from hyb-seq approaches have recently provided a preliminary infrageneric framework, the underlying causes of deep gene tree discordance and unresolved relationships in rapidly radiating shallow lineages remain insufficiently understood, thereby introducing uncertainty into taxonomic classifications. In this study, we focused on the alliance known as *Carex* sect. *Mitratae* s.l., a typical shallow rapid phylogenetic radiation, to address these issues. Leveraging deep genome skimming data comprising 4,975 single-copy orthologs (SCOs), we reconstructed a robust phylogenetic backbone of the group and its relatives. We demonstrated that incomplete lineage sorting (ILS), introgression, and hybridization collectively explain the pervasive gene tree discordance affecting sect. *Mitratae*. Integrating phylogenetic and morphological evidence, we propose a revised taxonomy of the group recognizing five monophyletic sections within the alliance: sects. *Foraminatae* (sect. nov.), *Cryptostachyae*, *Digamae*, *Truncatiglumae*, and *Mitratae*. Our study not only resolves the long-standing taxonomic controversies regarding the limits of sect. *Mitratae* s.l., but also provides an empirical case demonstrating how integration of genomic data, phylogenetic methods, and morphological evidence can help decipher the complex

evolutionary history of a rapid radiation in a megadiverse genus, ultimately establishing a stable, revised classification.

Key Words: deep genome skimming; gene tree discordance; ILS; integrative taxonomy; sedges; taxonomic treatment.

Potential Evolutionary Significance of Polyploidy-Associated Aneuploidy in Higher plants

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Aneuploidy is intrinsically associated with nascent polyploidy, yet its evolutionary relevance in this specific biological context remains unknown. We performed experimental evolution to address this issue in a synthetic allotetraploid wheat. We assessed evolvability, defined as 'progeny fitness', of transgenerationally selected aneuploid and euploid tetraploid cohorts under both regular condition and three abiotic stresses (salinity, low nitrogen and endoplasmic reticulum stress). We find ca. 30% of the aneuploid tetraploid-cohorts manifested higher evolvability than all the euploid tetraploid-cohorts even under regular normal condition. Moreover, nearly all individuals of both tetraploid sets, which survived any of the three stresses, were aneuploidies with loss/gain of a limited, and apparently nonrandom, set of defined chromosomes, whereas the few euploid survivors were all progenies of stress-tolerant parental aneuploidies, which contained the same multiple structural variants. Whole-genome resequencing confirmed aneuploidy, rather than de novo occurred nucleotide sequence variation, underpins the higher evolvability and stress tolerance phenotypes. Physiological assay revealed a striking pattern of stress-induced shifting of cellular physiological processes in the stress-tolerant aneuploidies towards or surpass those of the more tolerant diploid parent. RNA-seq-based global gene expression comparisons revealed that although the different kinds of aneuploidies manifested the same stress-tolerate phonotypes, they appeared to employ distinct regulatory circuits involving different genetic pathways. Our findings suggest that aneuploidy may serve as a transit genetic springboard facilitating the establishment of nascent polyploidy especially under stressful environments by imparting its stress-tolerance properties to euploid progenies. By analogy, we surmise that aneuploidy may also play similar roles during the process of rediploidization of paleopolyploids wherein cyclic chromosome fission and fusion or descending dysploidy occurs, with intertwined aneuploidy and chromosomal rearrangements being inevitable intermediates. Thus, our study unveils a previously unheeded force, i.e., polyploidy-associated aneuploidy, in the

evolution of multicellular higher organisms.

Key Words: polyploidy, aneuploidy, stress, evolvability, synthetic allotetraploid wheat
Tracing the continental biogeographic history of *Mahonia*

(Berberidaceae) using molecular and fossil evidence

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The East Asia-western North America floristic disjunction is a major biogeographic pattern in the Northern Hemisphere, but the relative roles of geological history, climatic change, and trait evolution in shaping this pattern remain poorly resolved. *Mahonia* (Berberidaceae) is widely distributed in East Asia and western North America and has a rich Cenozoic fossil record, making it an ideal lineage for examining the origin and evolution of intercontinental disjunctions. In this study, we reconstructed the phylogeny, divergence times, biogeographic history, climatic niches, and leaf trait evolution of *Mahonia* by integrating plastome data, fossil occurrences, morphological characters, and species distribution records.Phylogenomic analyses based on plastome data resolved the major lineages of *Mahonia* and provided a framework for integrating fossil taxa through total-evidence dating. Divergence-time estimation under the fossilized birth-death model indicated that the evolutionary history of *Mahonia* was closely linked to Cenozoic environmental change. Biogeographic reconstruction suggests that the genus was formerly more widespread across the Northern Hemisphere and that its present East Asia-western North America disjunction likely resulted from a combination of intercontinental floristic exchange, regional extinction, and range contraction. Climatic and trait analyses further suggest that differences in leaf morphology, particularly venation-related characters, may have contributed to lineage persistence and diversification under contrasting environmental regimes.

Our study provides an integrated view of the continental biogeographic history of *Mahonia* and emphasizes that intercontinental plant disjunctions cannot be fully explained by geological and climatic factors alone. Instead, lineage-specific trait evolution may have played an important role in mediating responses to Cenozoic environmental change.

Key Words: Mahonia, biogeography, plastome phylogenomics; fossil evidence; East Asia-western North America disjunction; leaf venation

Establishing *Actaea purpurea* as a model for studying pollinator-driven speciation in Ranunculaceae

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Ranunculaceae is an economically important family because of its remarkable diversity of bioactive secondary metabolites and has become an important model for evolutionary developmental biology owing to its extraordinary diversity in vegetative and floral morphology. Despite this diversity, convincing examples of pollinator-driven speciation remain scarce in the family, limiting our understanding of how floral trait divergence contributes to reproductive isolation in basal eudicots. Developing suitable study systems is therefore essential for dissecting the genomic and evolutionary mechanisms underlying pollinator-mediated diversification. *Actaea purpurea* represents an exceptional candidate for such a model system. It is sister to *A. japonica* and *A. biternata*, yet exhibits striking floral innovations, including persistent purple sepals, purple filaments, concealed yellow nectaries, and a distinctive floral architecture that differs dramatically from the white, open flowers typical of its closest relatives. Previous field observations and pollinator exclusion experiments demonstrated that *A. purpurea* is primarily pollinated by the hornet *Vespa bicolor*, whereas its sister species are mainly pollinated by large flies. Furthermore, reproductive isolation between *A. purpurea* and *A. japonica* is nearly complete. These observations suggest that floral trait divergence, particularly flower colour and floral architecture, may have facilitated a pollinator shift and contributed to reproductive isolation, making *A. purpurea* an ideal system for investigating pollinator-driven speciation. To establish the genomic resources required for this system, we generated a chromosome-level reference genome of *A. purpurea* (11.84 Gb), currently the largest assembled genome in Ranunculaceae. Comparative genomic analyses showed that genome expansion was primarily driven by massive proliferation of long terminal repeat (LTR) retrotransposons rather than lineage-specific whole-genome duplication. Despite an approximately 38-fold genome size difference between *A. purpurea* and the model ranunculaceous species *Aquilegia coerulea*, chromosome-scale synteny remained highly conserved, indicating that genome expansion largely resulted from extensive accumulation of repetitive sequences within intergenic regions while preserving overall genome organization. These genomic

resources provide an essential foundation for evolutionary and functional studies in giant-genome Ranunculaceae.To investigate the molecular basis of floral colour divergence, we integrated comparative genomics, transcriptomics, metabolite profiling, and functional assays. Cyanidin-3-O-glucoside was identified as the predominant anthocyanin responsible for the characteristic purple pigmentation of sepals and filaments. Transcriptome analyses identified multiple anthocyanin biosynthetic genes showing elevated expression during floral development, together with two candidate R2R3-MYB transcription factors. Yeast one-hybrid and dual-luciferase assays demonstrated that ApMYB1 directly binds to the promoter of ApF3H and activates its transcription, identifying ApMYB1 as a key upstream regulator controlling anthocyanin biosynthesis and floral pigmentation in *A. purpurea*. These results establish a mechanistic link between regulatory evolution and one of the most distinctive floral traits differentiating *A. purpurea* from its sister species. Finally, population-level genotyping-by-sequencing (GBS) reconstructed the evolutionary history of *A. purpurea* and its close relatives. Demographic modelling indicated that *A. purpurea* initially diverged from *A. japonica* in a small, geographically isolated population with little or no early gene flow, supporting an allopatric origin. Secondary contact occurred only after divergence had been established. These results suggest that the evolution of distinctive floral traits likely occurred after initial geographic isolation rather than initiating species divergence. Consequently, floral colour evolution and pollinator shifts probably reinforced reproductive isolation during later stages of speciation rather than serving as its primary trigger.Together, this work establishes *A. purpurea* as a powerful emerging model for studying the interplay between genome evolution, floral trait diversification, pollinator shifts, and reproductive isolation in basal eudicots. More broadly, it provides important genomic resources for Ranunculaceae and offers a framework for investigating how ecological interactions shape plant diversification through the integration of genomics, evolutionary biology, and pollination ecology.

Key Words: flower color, genome size, pollinator-triggered speciation, Ranunculaceae

Allohexaploidy Facilitates Aquatic Adaptation and Ecological Success in the Submerged Macrophyte *Myriophyllum spicatum*

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Aquatic angiosperms have repeatedly re-evolved from terrestrial ancestors, but life under water imposes profound constraints on plant growth, morphology, and environmental response. Successful adaptation to submerged habitats requires coordinated changes in photosynthesis, mechanical support, gravitropism, and stress tolerance. Understanding the genomic basis of these changes is therefore important for explaining how plants persist and expand in freshwater ecosystems. *Myriophyllum spicatum*, a cosmopolitan submerged macrophyte, is a representative example of an aquatic plant with remarkable ecological plasticity and widespread invasive success. Despite its ecological importance, the evolutionary mechanisms underlying its adaptation to submerged environments remain poorly understood. In this study, we generated a chromosome-scale genome assembly of *M. spicatum* and investigated how polyploid genome evolution contributed to aquatic adaptation and ecological success. Our analyses revealed that *M. spicatum* possesses a high-quality allohexaploid genome composed of three differentiated subgenomes (AABBCC). This genomic architecture provides an opportunity to examine how polyploidy can create evolutionary novelty in plants occupying challenging environments. Comparative analyses showed that the three subgenomes are not evolutionarily equivalent. Instead, they exhibit substantial asymmetry in gene structure, expression regulation, and functional retention, indicating that post-polyploid genome evolution in *M. spicatum* involved subgenome differentiation. We identify subgenome-asymmetric expression, including a set of Subgenome B-suppressed genes enriched for photosynthesis-related functions and a set of Subgenome C-suppressed genes enriched for genome stability/DNA damage response-related functions. TE insertions are significantly enriched in these suppressed gene sets and coincide with structural simplification, including shorter and fewer exons, together with reduced expression, supporting subgenome regulatory asymmetry during post-polyploid genome evolution. Gene family evolution analyses also

revealed genomic signatures consistent with submerged adaptation. Core flavonoid-related gene families have undergone tandem expansion, whereas several cell wall-related gene families show contraction. These changes are compatible with the ecological requirements of submerged plants, which experience different oxidative environments, reduced structural demands, and modified light interception compared with terrestrial species. In addition, we identified adaptive substitutions in genes such as *FLS1* and *SGR2*, which are likely associated with cold tolerance, photomorphogenic adjustment, and gravitropic response. These changes may have contributed to the characteristic flexible morphology and canopy-forming growth habit of *M. spicatum*, traits that are advantageous for efficient light capture and competitive performance in freshwater habitats. Taken together, our results support a model in which allohexaploidy promoted aquatic adaptation in *M. spicatum* through multiple interacting mechanisms, including subgenome-asymmetric evolution, TE-associated regulatory remodeling and gene family reorganization. This study provides a valuable genomic resource for aquatic plant research and offers new insight into how genome evolution can facilitate plant persistence and expansion in submerged environments. More broadly, our findings highlight the importance of polyploid genome evolution in enabling ecological innovation in non-model plants and provide a comparative framework for understanding how plants adapt to challenging habitats in a changing world.

Key Words: *Myriophyllum spicatum*, polyploidy, aquatic adaptation, subgenome asymmetry, genome evolution

Scale-dependent Reversal of Mountain Biodiversity: Geoclimatic and Ecological Drivers in the Hengduan-Himalaya Mountains and the European Alpine System

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Mountain ecosystems harbor disproportionately high biodiversity shaped by the interplay between contemporary ecological conditions and long-term evolutionary history.Previous comparisons among mountain systems have largely focused on regional species richness, whether biodiversity differences remain consistent across spatial scales, and the ecological and evolutionary processes underlying these patterns, remain poorly understood. Here, we conducted a comprehensive assessment of taxonomic and phylogenetic diversity from local to regional spatial scales in two Eurasian mountain systems with striking species richness disparities: the European Alpine System (EAS) and the Hengduan-Himalaya Mountains (HHM). We selected two species-rich representative plant groups, *Saxifraga* and *Androsace*, that co-occur across both mountain systems, allowing us to assess both shared and lineage-specific patterns of biodiversity assembly. To address bias arising from uneven occurrence sampling, we developed a modelling framework tailored to mountain biotas for inferring species potential distributions, combining ensemble species distribution models with ecological connectivity constrained and spatial filtering methods for rare species. Our multi-scale analysis revealed a pronounced scale-dependent reversal in biodiversity patterns between the two mountain systems. The EAS demonstrated a higher local taxonomic alpha diversity at fine spatial grains, but this contrast progressively reversed with increasing grain size, culminating in higher gamma diversity in the HHM, consistent with its greater regional species richness. This scale-dependent shift was driven by the more rapid spatial accumulation of beta diversity within the HHM, dominated by spatial species turnover. Zeta diversity decay curves further revealed a faster loss of compositional similarity across space in the HHM. This elevated spatial turnover strongly aligned with

greater geographic isolation and environmental niche differentiation among HHM species, particularly within subalpine-alpine lineages, consistent with the more heterogeneous topography and habitat mosaic in the HHM relative to the EAS. From a macroevolutionary perspective, the two mountain systems showed deep divergence in evolutionary patterns within the subalpine-alpine zone. In the EAS, high-altitude lineages exhibited a strong lineage-specific response, reflecting divergent evolutionary possibly response to multi-phase orogeny and intense Quaternary climatic oscillations in this region. By contrast, *Saxifraga* and *Androsace* showed broadly congruent evolutionary patterns in the HHM, suggesting shared extrinsic drivers, particularly sustained tectonic uplift, on lineage diversification. In conclusion, this study links deep-time evolutionary trajectories with contemporary ecological processes to explain how mountain biodiversity emerges across spatial scales. Our results show that present-day spatial patterns of biodiversity reflect the legacy of regional geoclimatic history, expressed through species' ecological responses to the heterogeneous physical environments of mountain landscapes.

Key Words: Mountain biodiversity, ESDMs, Biodiversity scaling, historical biogeography, macroevolution, macroecology

Spatial patterns and determinants of plant diversity in the Qaidam Basin

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The Qaidam Basin, located in the northern Qinghai-Tibet Plateau, is an arid closed basin serving as a crucial ecotone with a unique desert flora. This study integrated multi-source data to compile a checklist of wild vascular plants and construct a functional trait dataset. Based on a phylogenetic framework, we analyzed plant diversity patterns and community assembly mechanisms across taxonomic, phylogenetic, and functional dimensions. The results showed that the basin harbors 510 species of wild vascular plants. Taxonomic and phylogenetic α-diversity exhibited a radial pattern, being higher in the east and lower in the west, with lower values at the center and higher values at the margins. The standardized effect size of phylogenetic diversity (SES.PD) was higher in the central area and lower at the margins, indicating a non-random pattern of community assembly. Environmental analyses revealed that water availability and soil physicochemical properties dominate community assembly through deterministic environmental filtering. Taxonomic and phylogenetic β-diversity was primarily driven by turnover components, with the eastern region showing significantly higher community heterogeneity than the west. Environmental variables explained 49.3% of the variation in phylogenetic β-diversity turnover, with the pure effects of climate, soil, and topography constituting the main sources of β-diversity variation. Local species pool and environmental filtering jointly serve as the core drivers of plant diversity formation in the Qaidam Basin.

Key Words: Qaidam Basin, Functional Diversity,Taxonomic Diversity, Phylogenetic Diversity, Patterns of plant diversity

The transcriptional and epigenetic regulation of *Arabidopsis* male fertility

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Anther and pollen development are important for plant male fertility, including crop yield. Transcription factors and receptor-like protein kinases are the two known types of important regulators of anther development in *Arabidopsis thaliana*, but regulation by other factors is less understood. In addition, the expression of meiosis-specific genes and pollen-developmental genes, which are required for male fertility and agricultural productivity, are largely unknown. Our work identified key transcriptional regulators for cell-type specific expression of meiotic genes and uncovered their mechanisms coordinating with histone modifications. Moreover, we also discovered essential transcriptional regulators for metabolic processes in anther and pollen development and revealed the potential role of histone modifications in the metabolic synthesis for plant reproduction. Together, our data demonstrated the crucial and conjugate roles of transcriptional and epigenetic regulations in plant male fertility.

Key Words: transcriptional regulation, epigenetic regulation, meiosis-specific genes, pollen-developmental genes, male fertility

Conserved Plastome Architecture and Uneven but Concordant Phylogenetic Signal across *Prunus* sensu lato

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Plastomes are structurally conservative and usually inherited as a single linked unit, but their structural characters and phylogenetic information may evolve unevenly. These issues are particularly relevant to *Prunus* sensu lato, whose evolutionary history has been shaped by rapid diversification, hybridization, and cytoplasmic introgression. We examined whether plastome variation across *Prunus* sensu lato is concentrated in particular genomic regions and whether its phylogenetic relationships are broadly supported or driven by a few influential genes.Thirty-nine representative plastomes were uniformly reannotated for structural comparison. All plastomes retained the typical quadripartite organization and high IR identity, without widespread large inversions or rearrangements. Structural variation was largely restricted to IR/SC junctions, particularly configurations involving *ycf*1, *rps*19, *rpl*2, *rpl*22, and *psb*A, indicating a conserved genomic backbone accompanied by localized IR-boundary dynamics. A quality-controlled dataset of 119 accessions, including 116 *Prunus* samples and three outgroups, was used to infer the whole-plastome phylogeny. To assess phylogenetic signal within the plastome, we constructed a complete matrix of 70 shared single-copy protein-coding genes (Core70) for all 119 accessions. Every strongly supported branch in the Core70 nucleotide tree was also present in the whole-plastome tree, and the whole-plastome topology could not be rejected by an approximately unbiased test using the Core70 data. Although gene concordance factors were low for many branches, most individual genes contained insufficient information to resolve those relationships. All branches with sufficient decisive sites supported the reference topology, and none was dominated by an alternative relationship. Ten candidate influential loci were identified, but their removal did not recover a different strongly supported backbone and instead reduced phylogenetic resolution. These results show that *Prunus* plastomes combine strong structural conservation with limited IR-boundary variation. Their phylogenetic information is unevenly distributed among loci, but sufficiently informative signals are broadly concordant and the principal topology is not controlled by a few genes. Low gene concordance in the linked plastome should therefore

not be interpreted automatically as evidence of conflicting evolutionary histories.

Key Words: Prunus; plastome evolution; IR boundary; phylogenetic signal; gene-tree conflict

Regulation of Target Gene Expression by Chromatin-associated Protein-coding Transcripts in Plants

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Protein-coding transcripts are regarded as intermediates that mediate DNA-to-protein information flow, leaving their non-coding regulatory potential largely underappreciated. Genome-wide profiling of RNA–chromatin interactions in Arabidopsis has uncovered widespread associations between protein-coding transcripts and distinct genomic loci, implying that they possess regulatory functions. Here, we found that *BT2* and *GSL8* transcripts modulate target gene transcription independently of their protein products through distinct mechanisms. The *BT2* transcript represses transcription of its targets *CEP2* and *MRF4* by forming RNA–DNA triplexes, thereby restricting root growth and promoting flowering, whereas *GSL8* acts through a triplex-independent pathway. Our findings unveil intrinsic regulatory activities of protein-coding transcripts, challenging the canonical definition of mRNA function and blurring the functional distinction between coding and non-coding RNAs in the context of genome evolution.

Key Words: Protein-coding transcript; regulatory RNA; RNA–chromatin interaction; RNA–DNA triplex; gene expression

Ecological and Evolutionary Systems Biology of Plant Resilience: Insights from Wild Legume Species

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Understanding how plants evolve resilience to environmental challenges remains a central question in both evolutionary biology and sustainable agriculture. Although crop domestication has dramatically improved productivity, it has also narrowed the genetic diversity available for adaptation to emerging biotic and abiotic stresses. In contrast, wild legume species have evolved across diverse environments and preserve extensive natural variation that remains largely unexplored. Rather than viewing these species simply as reservoirs of beneficial alleles, we propose that they represent naturally evolved biological systems whose molecular, metabolic, and cellular organization has been shaped by long-term selection. Recent advances in multi-omics integration and single-cell technologies now allow us to investigate these adaptive systems across multiple biological scales with unprecedented resolution. Here, I present two complementary case studies that illustrate how wild diversity and integrative omics can address both fundamental biological questions and agricultural challenges. The first focuses on wild soybean (*Glycine soja*), where integrated transcriptomic, proteomic, and metabolomic analyses reveal how naturally resistant genotypes establish coordinated defense networks against soybean cyst nematode through constitutive preparedness and rapid defense activation. The second highlights the emerging wild legume model sand bean (*Strophostyles helvola*), where reference genome assembly and annotation, together with single-nucleus transcriptomics, uncover the cellular architecture of adaptation to coastal saline environments and identify cell-type-specific regulatory programs associated with stress resilience. Despite representing distinct biotic and abiotic challenges, these systems converge on a common principle: resilient plants are not simply more responsive to stress but often occupy distinct molecular and cellular states before stress occurs. Integrating ecological and evolutionary perspectives with systems biology provides a framework for understanding how complex adaptive traits emerge from coordinated regulatory networks, metabolic pathways, and specialized cell types. Importantly, systems-level understanding does not replace gene

discovery; instead, it provides a roadmap for identifying regulatory hubs, key genes, and evolutionary mechanisms most likely to control complex adaptive traits. By integrating the evolutionary diversity preserved in wild legumes with next-

generation omics technologies, we can move beyond cataloging adaptive variation toward identifying the regulatory mechanisms and key genetic factors that govern plant resilience. This systems-level framework will accelerate the discovery of high-impact targets and enable more effective strategies for developing climate-resilient crops for future agriculture.

Key Words: crop wild relatives, multi-omics, single-cell transcriptomics, systems biology, plant resilience, sustainable agriculture

Genetic Control of Maize Flowering Synchrony under Drought Stress

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Drought severely threatens maize yield stability, especially during flowering. As a monoecious species, its pollination and seed set depend on the synchronous development of male and female inflorescences. Drought, however, often disrupts this synchrony, resulting in a prolonged anthesis–silking interval (ASI) and substantial yield loss. This report presents our recent research progress on genetic dissection of maize drought resilience. Through QTL mapping, we cloned a quantitative trait locus *qDR9* and identified *ZmSAUR72*, which promotes silk growth by activating H^+-ATPase activity. This shortens ASI and stabilizes yield under drought. Additionally, the pan-genome analysis of 25 newly assembled and 31 existing maize genomes, revealed the natural variations in *ZmASI3* are associated with ASI prolongation under drought stress. The functional transcript of *ZmASI3* acts as a chromatin remodeler and confers drought resilience at the flowering stage by alleviating ASI extension. Thus, the finding offers new insights into the genetic control of maize drought resilience and provides strong candidate genes to breed maize cultivars with enhanced yield stability under water-deficit conditions.

Key Words: Maize, Drought resilience, Flowering synchrony, Yield, Gene Cloning

De Novo Design of Functional Micropeptides

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We discovered microRPG1, a 31-amino-acid micropeptide encoded by a previously non-coding region of the maize genome that delays kernel dehydration. This peptide originated de novo approximately 650,000 years ago, representing a novel, lineage-specific, and non-homologous protein exclusive to the Zea genus. These findings raised two fundamental scientific questions: whether microRPG1 retains functional conservation across diverse species, and whether numerous uncharacterized novel micropeptides with biological functions remain hidden within the vast and complex 2031 sequence space? Cross-species studies revealed that microRPG1 retains a conserved dehydration - delaying function in model plants, including Arabidopsis and rice. Notably, this micropeptide exhibits cross-kingdom conserved anti-aging functions in model animals (Caenorhabditis elegans and Drosophila melanogaster) and human cells, and also confers conserved thermotolerance under high-temperature stress in rice, C. elegans and D. melanogaster. Mechanistic exploration revealed that microRPG1 can specifically enter various animal cells, including human HEK293T cells, mouse NIH3T3 cells, and C. elegans embryonic cells. Its cellular entry relies primarily on extracellular matrix glycosaminoglycans (GAGs) and endocytosis, with the peptide ultimately localized to the Golgi apparatus. Furthermore, we initially constructed an integrated research platform combining chaos theory based design, high-throughput single-cell characterization, and automated phenotype verification. This platform enables large-scale de novo design of functional micropeptides and provides a powerful framework to explore the emergent mechanisms of novel biological functions in complex living systems.

Intronic lariat RNA turnover in plants

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Lariat RNAs are formed from introns during pre-mRNA splicing, after which they are degraded by the debranching enzyme DBR1. Impairment of DBR1 leads to developmental arrest, yet the mechanism remains unclear. Here, we show that debranching of lariat RNA prevents production of 21- and 22-nt lariat-derived siRNAs (lasiRNA), which causes the burst of exonic siRNAs, thereby safeguarding development and defense response. LasiRNA biogenesis relies on RNA-dependent RNA polymerases (RDRs) and Dicer-like proteins (DCLs).Upon pathogen infection, DBR1-dependent lariat RNA removal is accelerated and these lariat RNAs are processed by DCL4 and DCL2 into siRNAs, particularly targeting immunity genes, ultimately disrupting plant defense responses. Collectively, DBR1-dependent lariat RNA removal serves as a protective mechanism to prevent the activation of a small RNA-based defense system in plants.

Towards soybean molecular breeding 大豆分子设计育种探索

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大豆是重要的粮油饲作物，我国大豆消费对外依存度长期高达80%以上，已经成为我国农业领域最大的“卡脖子”问题。提升我国大豆基础和应用基础研究水平，推动大豆分子设计育种，是解决我国大豆危机、保障国家粮食安全的重大需求。针对大豆基因组研究基础薄弱的科学瓶颈问题，构建了国产大豆“中黄13”高精度基因组序列，建立了利用共表达网络结合数量遗传学鉴定重要性状调控基因新方法，通过对26个具代表性大豆高质量基因组的组装和比较基因组分析，突破传统线性基因组的存储形式，在植物中首次实现了基于图形结构泛基因组的构建，为大豆功能基因组发展奠定了坚实基础。针对大豆农艺性状调控基因被挖掘数量少和鉴定困难的瓶颈，开发出基于基因组、转录组等多组学数据的群体遗传分析方法，高效鉴定并功能解析多个复杂农艺性状功能基因，为大豆分子设计育种提供了重要的基因资源。针对大豆遗传演化规律不清限制了大豆品种创新的重要问题，通过群体基因组学对大豆种质资源演化中遗传变异的系统研究，揭示了大豆在驯化、改良、传播中的基因选择路径，通过系统全基因组关联分析和遗传网络构建，解析了84个大豆重要农艺性状的分子基础以及多性状遗传调控耦合网络，发现了不同性状协同调控的关键调控位点，建立了大豆分子设计育种理论和技术体系，合作培育出科豆10、科豆2号、科豆7号、科豆17、晋大88号等一系列大豆新品种。

The plant disease resistance against Phytophthora pathogen

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Phytophthora species infect a wide range of plant hosts and threaten global food security. The majority of Phytophthora resistance genes deployed in agriculture belong to the NLR family, which encode nucleotide-binding domain and leucine-rich repeat immune receptors that recognize pathogen effectors. Nevertheless, rapid pathogen evolution has rendered most of these resistance genes ineffective. Phytophthora infestans, the notorious pathogen responsible for the Irish Great Famine, has been established as the primary model species for Phytophthora research. We aim to identify new disease resistance genes, dissect resistance mechanisms, and rational utilize resistance genes. Recently, we have elucidated the durable resistance mechanisms of RB and Rpi-vnt1.1 and identified novel late-blight resistance genes including Rpi-cjm1 and Rpi-brk1. Meanwhile, we found novel elements in plant NLRs and proposed a novel plug-in design strategy for disease resistance breeding. Recently, we identified an N-terminal extension encoded by an intron in the late-blight resistance protein Rpi-vnt1.1. This extension acts as a molecular safety lock that suppresses resistosome function and prevents autoactivation of NLR. Upon pathogen infection, plants trigger precise excision of this intron to remove the inhibitory module, priming the NLR for rapid activation. Upon effector recognition, the NLR promptly assembles into a resistosome to initiate immune responses. Pan-genomic analysis suggests that such a molecular safety lock may represent a conserved regulatory mechanism for a subset of NLRs. Our study provides new insight for crop disease resistance improvement.

From Single Cell to Whole Plant: Multi-Omic Profiling of Protoplast Regeneration

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Single differentiated plant cells, such as leaf mesophyll cells, can regenerate into whole plants after cell wall removal (protoplasting). Distinct from standard explant regeneration, this process provides a direct demonstration of cellular totipotency and is widely used in plant biotechnology, but its molecular basis is poorly understood. Here we show that cell wall removal triggers global nucleosome disassembly and epigenetic erasure, accompanied by widespread transcriptional pausing. Using single-cell and spatial transcriptomics, we find that protoplast-derived callus cells enter a fate-labile “limbo” state with mixed identities and no spatial patterning. Over time, these cells gradually resolve into vascular, shoot, and root lineages. The competitive balance among these fates determines whether regeneration succeeds; shifting this balance away from vascular fate promotes shoot regeneration. Our findings suggest that the cell wall acts as a structural guardian of epigenetic identity, providing a mechanistic basis for protoplast totipotency, and informing strategies to improve crop transformation.

Mitochondrial Dynamics in Plant Immunity: From Organelle Homeostasis to Stomatal Defense

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线粒体是高度动态的细胞器，其形态和功能会随细胞状态及外界环境发生快速变化，但线粒体动态如何参与植物免疫调控仍缺乏深入认识。我们近期的研究发现，病原相关分子模式诱导植物细胞中线粒体发生快速动态重塑，并揭示了细胞骨架与线粒体动态协同调控植物免疫的分子机制。进一步研究表明，免疫信号可促进线粒体融合，推动线粒体膜电位和细胞能量状态的恢复，并调控线粒体活性氧信号，从而促进气孔关闭和植物抗病反应。这些研究揭示了细胞骨架、线粒体稳态与免疫信号之间的紧密联系，表明线粒体动态重塑是植物免疫应答的重要组成部分。

TGW1a locus simultaneously shortens growth duration and boosts grain yield in rice

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Balancing short growth durations with high grain yields remains a key objective for crop breeders aiming to maximize total annual crop yields per unit area. Mining genes with pleiotropic effects on flowering and yield has the potential to balance growth duration and yield. Through QTL mapping of heading date and thousand-grain-weight (TGW) in rice, we identified a major locus *qTGW1a* (*LOC_Os01g11940*) encoding a florigen-like, phosphatidyl ethanolamine-binding protein (PEBP). In vegetative tissues, TGW1a physically binds to NUE enhancer proteins Hd1 and Ghd7, preventing their 26S proteasome–mediated protein degradation. Stabilized Hd1 and Ghd7 elevated the direct transcription of NUE-related genes, thereby conferring higher NUE. During reproductive transition, TGW1a activates transcription of MADS-box genes in the shoot apical meristem, thereby promoting flowering. Among the three major haplotypes, the rare, ancestral haplotype $TGW1a^{JZ}$, which contains an intact promoter, is strongly selected in the *aus* ecotype. A 12.9-kb retrotransposon insertion and a 993-bp deletion in the promoter gave rise to the divergence of *TGW1a* between *indica* and *japonica*. $TGW1a^{JZ}$ maintained an intermediate transcription level conferring early maturation and higher grain yield. However, because of its genetic linkage with the *Gn1a* controlling grain numbers, the yield benefit of $TGW1a^{JZ}$ could have been masked by the linked weak allele $Gn1a^{JZ}$, making $TGW1a^{JZ}$ underutilized in modern cultivars. By introgression of the superior $TGW1a^{JZ}$-$Gn1a^{HHZ}$ block in breeding, we achieved 3 to 8 days shorter growth duration and 4.22 to 11.00% higher grain yield in five modern inbred cultivars and derived F_1 hybrids.

Molecular mechanisms underlying chilling resilience in rice

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In this talk, Luo will present his recent work published in Nature on chilling resilience in rice. Tiller regeneration after chilling stress is critical for restoring growth and yield. We defined this post-chilling recovery capacity as chilling resilience and developed a quantitative evaluation system to assess this trait. Using this system, we identified CHILLING PHOENIX (CHPO) as a key regulator that dynamically controls downstream genes to coordinate chilling tolerance and nitrogen-use efficiency, thereby promoting tiller regeneration and yield recovery after chilling stress.

Legume–rhizobium symbiotic intracellular infection: mechanisms and insights into engineering nitrogen fixation in non-legume crops

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Colonization of plant roots by symbionts requires substantial morphodynamic reorganization. Examples are actin-scaffolded micro-compartments called infection pockets formed during root nodule symbiosis (RNS) by legumes. Here, we demonstrate that the actin-binding formin SYFO2 is indispensable for rhizobial infection in *Medicago truncatula*, where it drives actin polymerization in phase-separated and symbiosis-specific nanodomains. Being evolutionarily conserved, SYFO2 also regulates symbiotically active arbuscules formed during mycorrhizal symbiosis (AMS) outside the nodulating clade, indicating that it was additionally recruited to promote rhizobial infections in legumes. Following our aim to enable nitrogen fixation in non-legumes, we additionally succeeded in activating endogenous *SYFO2* by stably introducing the RNS master regulator NIN into the natural non-host tomato. This demonstrates the possibility of recruiting AM-related genes into an engineered nodulation-specific pathway.

How Plants Cope with Flooding Stress

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Frequent extreme weather events exacerbate flooding, and the resulting hypoxia stress severely constrains crop production; however, the plant regulatory network governing the response to such stress remains elusive. In this study, using *Arabidopsis thaliana* and *Brassica napus*, we combined forward and reverse genetics approaches to identify several key genes, including RAP2.12, WRKY22, ACBP4, HPCA1 and ETP2, and dissected the molecular mechanisms by which their allelic variations modulate adaptation to flooding-induced hypoxia stress. In different Arabidopsis ecotypes, the promoter cis-elements of RAP2.12 exhibit divergence, enabling differential binding of transcription factors to mediate tolerance to both drought and flooding; phosphorylation of ACBP4 induces nuclear translocation of WRKY70, thereby enhancing hypoxia response; a TA deletion in the WRKY22 promoter attenuates the repression by ARRs and, upon activation by WRKY70, promotes flooding tolerance; An insertion variation in the HPCA1 promoter recruits activating histone modifications and upregulates HPCA1 expression, thereby negatively regulating hypoxia adaptation; whereas a promoter variation in ETP2 reduces its expression level to promote hypoxia tolerance. These genes display functional interactions and coordinately regulate environmental adaptation. Our findings enrich the theoretical framework of hypoxia signal transduction and provide key genetic resources and allelic targets for molecular breeding of flood-tolerant crops.

Cellular Compartmentalization Mediated Environmental Signal Response and Metabolic Regulation in Plants

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Cells ensure efficient and orderly internal metabolism and signal transduction through compartmentalization. Focusing on how cellular compartmentalization responds to environmental signals, we conducted two tiers of progressive studies spanning from signal perception to metabolic execution. First, at the membrane-less compartment level, we discovered that the phytochromeB (phyB) forms photobody via liquid-liquid phase separation (LLPS) in the nucleus, selectively recruiting transcription factors and enriching signaling components to markedly enhance light signal transduction. Furthermore, phyB achieves the co-perception of light and temperature by coupling light-controlled reversible conformational changes with temperature-sensitive phase separation. Extending from signal perception, at the membrane-delimited compartment level, we found that plastoglobules (PGs) in maize chloroplasts dynamically respond to nitrogen. Quantitative proteomics precisely identified two key enzymes, ZmNIR2 and ZmGLN1, which assemble into a metabolon on the PG platform, efficiently driving nitrogen assimilation. The functional divergence driven by alternative splicing of *ZmNIR2* provides a genetic paradigm linking gene regulation with metabolic compartmentalization, and reshapes the functional understanding of PGs as a hub for primary nitrogen assimilation. Together, these two studies extend from membrane-less signaling compartments for light perception to membrane-delimited metabolic compartments for nitrogen execution, systematically revealing a regulatory logic by which plants employ compartmentalization strategies at distinct hierarchical levels to coordinately respond to environmental signals, and offering a conceptual framework and theoretical reference for the precise improvement of crop environmental adaptability.

Key Words: Cell compartmentalization, Environmental signals, Liquid-Liquid phase separation, plastoglobules

Beneficial plant-microbe interactions in P nutrition

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Scarcity of soil available Pi and low P fertilizer efficiency are major bottlenecks for agriculture. Excessive P fertilizer input leads to serious ecological contamination, creating an urgent need for green and sustainable alternative solutions. The plant microbiome plays essential roles in plant growth, development, and stress adaptation. It remains unknown whether plants establish mutualistic relationships with any bacteria to cope with P limitation. We characterized root-bacterial microbiome members to show that many of them may cooperate with *Arabidopsis* to promote seedling P nutrition and growth. In-depth analyses uncovered an intricate interaction between *Arabidopsis* and *Acinetobacter* bacteria during P deficiency. Instead of a direct role in P-mining, malate secreted by P-deprived roots acts as a call-for-help signal that recruits bacteria to the rhizoplane, where *Acinetobacter* adopt a mutualistic lifestyle and utilize host-derived nutrients to robustly mobilize P normally inaccessible to plants. The rhizoplane, but not the surrounding space, served as a hotspot for P acquisition by both plants and bacteria. Our work reveals a mutualistic strategy between bacteria and a non-mycorrhizal plant that promotes P nutrition, providing important support for developing green bio-fertilizers, advancing chemical fertilizer reduction, and enabling the development of eco-friendly agriculture.

ZnO/Nanobiochar-Based Photocatalysis Ameliorates Polyethylene Microplastic Toxicity and Promotes Cucumber (*Cucumis sativus* L.) Growth and Physiology

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The accumulation of polyethylene microplastics (MP) in agroecosystem poses serious threat to plant health. This study evaluated the ameliorative potential of zinc oxide modified nanobiochar (ZnO/NB) through photocatalysis to degrade polyethylene MP and mitigate their phytotoxic effects on cucumber (*Cucumis sativus* L.) seedlings grown under Petri plate conditions. A completely randomized design was used five treatments: control (C), microplastic alone (MP), ZnO/NB alone as photocatalyst (PC), microplastics with ZnO/NB applied at sowing (MP+PC), and microplastics applied at sowing followed by ZnO/NB application after 3-5 days (MP→PC). Seedlings were monitored for 18 days, and germination indices, biomass, photosynthetic pigments, primary and secondary metabolites, and antioxidant enzyme activities were measured. UV-Vis spectrophotometry showed enhanced light absorption capacity of ZnO/NB, while fluorescence microscopy detected MPs residues in plant tissues. MP exposure reduced germination by 73%, impaired biomass accumulation, and increased oxidative damage. In contrast, PC treatment enhanced root length (3-fold), chlorophyll content (2-fold%), carotenoids (2-fold), soluble proteins (70%), and SOD activity (72%) compared with control. Both MP+PC and MP→PC alleviated MP-induced stress, improved the physiological parameters compared to MP alone, with MP→PC showed time-dependent detoxification with intermediate recovery. These preliminary findings showed that ZnO/NB- based photocatalysis can degrade microplastic and partially reverse their adverse effects. Future studies should investigate the photocatalytic potential of ZnO/NB under soil conditions as an eco-compatible strategy to mitigate microplastic toxicity through degradation.

Key Words: Polyethylene microplastics; Zinc oxide modified nanobiochar; Photocatalysis; Phytotoxicity; Cucumber (*Cucumis sativus* L.); Oxidative stress amelioration

Genotypic Variation in Glandular Trichome-Mediated Secondary Metabolism under Drought and Salinity Stress in Borage

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Glandular trichomes play a key role in plant adaptation to abiotic stresses through the production and accumulation of secondary metabolites. This study evaluated the effects of drought and salinity stress on secondary metabolite accumulation in glandular trichomes of Iranian borage (*Echium amoenum*) and European borage (*Borago officinalis*). Different *E. amoenum* genotypes were subjected to drought or salinity stress under controlled conditions, while two *B. officinalis* genotypes were exposed to salinity stress in a soilless culture system. Histochemical staining was used to localize alkaloid and phenolic compounds in glandular trichomes, and spectrophotometric assays were applied to quantify total phenolic and alkaloid contents. Both drought and salinity stress enhanced secondary metabolite accumulation in glandular trichomes in all experiments. Stress responses were strongly genotype-dependent, with the Shiraz genotype of *E. amoenum* and the Pakan genotype of *B. officinalis* showing greater induction of secondary metabolism. These findings demonstrate that glandular trichomes act as active sites of stress-induced metabolic regulation and highlight the importance of genotype selection and stress management for improving stress tolerance and medicinal quality in borage species.

Key Words: Glandular trichomes; Secondary metabolites; Abiotic stress; *Echium amoenum*; Borago officinalis

Evolutionary, structural, and functional insights into plant *URICASE* reveal its central role in allantoin-mediated salt stress tolerance

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Allantoin, an important intermediate in nitrogen metabolism, plays a significant role in enhancing plant tolerance to abiotic stress. URICASE, a key enzyme in the allantoin biosynthesis pathway and overexpression of the *URICASE* gene in Arabidopsis led to improved salt tolerance. An evolutionary study of URICASE in 157 plant species revealed three major phylogenetic groups, reflecting the transition from algae to higher plants. A conserved protein domain (Pfam01014 domain) was identified across all species. Enzyme activity assays showed that ureidic legumes such as *Vigna radiata* and *Glycine max* had the highest URICASE enzyme activity, while *Cucumis sativus* had the lowest. Structural modelling and docking studies showed conserved substrate binding sites, with specific amino acid changes near the active site in legumes that may enhance enzyme efficiency. URICASE from the salt-tolerant wild rice *Oryza coarctata* was cloned and characterized for the first time. Fluorescence spectroscopy confirmed uric acid binding with a dissociation constant of 10.89 micromolar and a Hill coefficient of 1.81, suggesting cooperative binding. Circular dichroism revealed a shift from alpha helix to beta sheet upon ligand binding. Molecular dynamics simulations confirmed the stability of this interaction. These findings reveal both the evolutionary conservation and functional variation of *URICASE* in plants. RNA-Seq and co-expression analysis identified C-repeat/dehydration responsive element binding factor 2 (CBF2) as a transcriptional regulator of *URICASE*, validated through mutant studies and Electrophoretic mobility shift assay confirmed CBF2 binding at both promoter and 3′UTR regions.

Chromium Tolerance in *Alternanthera tenella*: A Shift from Structural Defense to Intracellular Detoxification

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Chromium (Cr) toxicity poses a major environmental challenge due to its persistence, mobility, and capacity to induce severe oxidative and metabolic damage in plants. Although *Alternanthera tenella* exhibits remarkable tolerance to Cr stress, the molecular mechanisms underlying this adaptation remain poorly understood. In the present study, integrated metabolomic, transcriptomic, and qRT-PCR analyses were employed to elucidate the mechanisms governing Cr tolerance in *A. tenella*. Chromium exposure triggered extensive molecular reprogramming, resulting in 1816 differentially expressed genes (DEGs) and 74 differentially accumulated metabolites (DAMs). Transcriptomic evidence indicated that Cr uptake occurred through non-specific metal transport systems, including sulfate transporters, ZIP, NRAMP, HMA, YSL, and ABC transporters. Although cell wall-associated responses were activated, the downregulation of several phenylpropanoid and lignin biosynthetic genes including PAL, 4CL, HCT, and CCoAOMT suggested that structural immobilization contributed only partially to Cr exclusion. Instead, *A. tenella* predominantly relied on intracellular detoxification mechanisms. Enhanced sulfur assimilation and glutathione metabolism, evidenced by the upregulation of ATPS, SAT, GCS, GSS, GST, phytochelatin- and metallothionein-related genes, promoted the formation of Cr-chelate complexes. Upregulation of nicotianamine synthase and enrichment of organic acid metabolites further indicated the participation of multiple ligand systems in Cr complexation. Increased expression of FQR1 suggested cytosolic reduction of Cr(VI) to the less toxic Cr(III), while ABCC transporters, particularly ABCC2, facilitated vacuolar sequestration of Cr-thiol complexes, a mechanism further validated by RT-qPCR. Metabolomic data further revealed enrichment of glucosinolate, flavonoid, amino acid and α-linolenic acid metabolism, with accumulation of flavonoids, organic acids, and phenolic compounds that likely contribute to antioxidant defense and metal complexation. The simultaneous activation of MAPK signaling, calcium signaling, phytohormone networks, and stress-responsive transcription

factors facilitated downstream detoxification processes. Although Cr severely impaired photosynthetic machinery as evidenced by suppression of photosystem-associated genes and accumulation of chlorophyll degradation products, *A. tenella* partially compensated through metabolic reprogramming including enhanced C4-associated carbon fixation pathways. Hence, the study demonstrates that Cr tolerance in *A. tenella* is governed by an integrated detoxification network centered on sulfur-driven chelation, multi-ligand metal complexation, and vacuolar compartmentalization. Beyond providing new mechanistic insights into plant adaptation to metal toxicity, this work identifies key pathways and candidate genes that may serve as valuable targets for phytoremediation improvement and the development of metal-resilient crop species.

Key Words: Phytoremediation, heavy metal, transcriptome, metabolomics, chelation, sequestration.

Title: Distinct Physiological and Molecular Adaptation Strategies of Pigmented Carrot Cultivars to Drought Heat Stress

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Carrot (*Daucus carota L.*) productivity and root quality are increasingly threatened by drought and heat stress under changing climatic conditions. The combined occurrence of drought and heat stress typically exert more sever effects on plant growth than either stress applied individually. However, the physiological and molecular mechanisms under lying tolerance to combined drought heat stress in pigmented carrot germplasm remain largely unexplored. This study investigated cultivars differing in root pigmentation under drought heat and combined drought heat stress conditions. Plants were grown under controlled environmental conditions and exposed to stress treatment at the taproot initiation stage. Growth traits, root developments, oxidative damage indicators antioxidant capacity, phytochemical characteristics and stress responsive gene expression were evaluated to identify key determinants of stress tolerance. Combined drought heat stress imposed the strongest adverse effect on plant performance resulting in substantial reductions in root development water status, and photosynthetic pigments. Significant genotypic variation was observed across physiological, biochemical and molecular traits. Among the evaluated cultivars, cosmic purple exhibited the highest level of stress tolerance. This cultivar maintained 28% higher relative water content and 22%higher chlorophyll retention under stress conditions. Reduced oxidative damage was associated with a 5.2- fold increase in CAT expression under heat stress highlighting the importance cellular integrity under adverse environmental conditions. In contract Atomic Red was the most susceptible cultivar and accumulated 47% higher malondialdehyde (MDA) levels under stress indicating sever membrane lipid peroxidation and oxidative injury. Scarlet Nantes displayed a distinct drought adaptive response characterized by significant upregulation of PDH1(5.4-fold), MAPK (4.3-fold). These expression patterns indicate the activation of osmotic regulation stress signaling and cellular protection pathways that contribute to improved drought resilience. Increased expression of MYB48, ABA, and KDA associated

genes in tolerant cultivars further supported the role of transcriptional regulation and hormone mediated signaling in stress adaptation. The result demonstrates that tolerance to drought and heat stress in carrot is governed by multiple interacting physiological and molecular mechanisms rather than a single protective response. Distinct adaptation strategies were identified among cultivars with antioxidant mediated tolerance predominating in cosmic purple and signaling mediated drought adaptation prevailing in scarlet Nantes as promising donor genotypes for breeding climate resilient carrot cultivars and provide valuable targets for improving adaptation to increasingly variable environmental conditions.

Key Words: Drought Heat Stress, Abiotic Stress, Antioxidant Defense, MAPK Signaling, Climate Resilient

Development of White Button Mushroom (*Agaricus bisporus*) Spread for Food Application

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Ready-to-eat and convenient food products are now becoming the need of the present food market. Change in the lifestyle of the people, including work overload, involvement of women in the workforce, small family system, and time saving, raises the demand for convenient food. Current consumer demands for nutritious food with less cooking effort. Spreads are the convenience snacks that are consumed by spreading them on a base, such as bread or crackers. This research aimed to develop and evaluate a mushroom-based spread that uses *Agaricus bisporus*, a low-fat substitute for regular spreads. Various mushroom spread formulations were made by using different amounts of mushrooms. A proximate analysis was used to evaluate the moisture, protein, fat, fiber, and ash content, together with pH and free fatty acid (FFA) levels, color, and texture. The microbial level and the sensory evaluation were conducted to evaluate acceptability. Increasing the amount of mushrooms in the spread made it nutritious. The highest mushroom treatment resulted in more moisture (66.54%), a rise in protein to 25.42%, dietary fiber at 1.40% and a decrease in fat to 5.01%. Higher mushroom content led to darker color (a decline in L* value from 93.65 to 73.46), yellowness (raising of b* value to 20.27), and red-green shift (raising of a* value to 0.90), showing considerable color changes. Texture analysis of samples showed higher hardness (34.80-69.50), higher adhesiveness (13.70-19.60), and lower cohesiveness (0.86-0.68) with higher mushroom level. Evaluating the sensory showed that the formulation with a moderate addition of protein (T_1 and T_2) received the highest scores for flavor, appearance and overall acceptability. Higher levels of mushroom (T_3 and T_4) resulted in darkness and more intense mushroom flavor, which caused slight decreases in sensory score. FFA analysis showed that FFA levels progressively increase and reach 0.56%, which suggests that improved preservation techniques are needed to inhibit lipid deterioration. The developed mushroom-based spread had the potential to be considered a functional food, meeting people's nutritional and taste needs. Further research should focus on the improvement of formulation, enhancing sensory qualities, and

industrial scalability. Regulatory framework and market acceptance should also be considered in industrial application.

Key Words: Functional food, *Agaricus bisporus*, mushroom spread, low-fat formulation, dietary fiber, plant-based nutrition.

Transcriptomic Analysis of Flowers in the Solanaceae Reveals an Unexpected TCP Expression Pattern Underlying Floral Symmetry Divergence

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Intricate relationships between angiosperms and pollinators are often reflected in the genetic underpinnings of floral symmetry. There are two main types of floral symmetry, radial (actinomorphic, ancestral) and bilateral (zygomorphic, derived), both of which are present in the Solanaceae family. Morphological and phylogenetic analysis suggests that flowers in the Solanaceae follow independent evolutionary trajectories between whorls, contributing to a dynamic evolutionary history of symmetry. *Browallia speciosa* Hook. and *Schizanthus grahamii* Gillies. of the Solanaceae exhibit zygomorphic flowers with unique stamen configurations and intricate petal displays, including aborted stamens and distinct dorsal banner petals which guide pollinator interactions. *B. speciosa* and *S. grahamii* share aspects of the zygomorphic pattern in their androecia derived from a shared ancestral state, whereas the zygomorphy in their corollas is the result of independent evolutionary gains in the two genera. Previous work identifies TCP and MYB transcription factor families as regulators of floral organ development, often working jointly to regulate dorsoventral symmetry. Here, we characterize a novel expression pattern of TCP mechanisms in correlation with the development of corolla and androecium symmetry in *B. speciosa* and *S. grahamii*. Specifically, we have found unexpected expression patterns including divergent expression of *CYCLOIDEA2 (CYC2)*-like genes. RT-qPCR reveals that *CYC2A-1* in *S. grahamii* and *CYC2A* in *B. speciosa* follow a similar expression pattern, with high expression in the dorsal and ventral stamen compared to extremely low levels in the lateral stamen. *CYC2A-2* in *S. grahamii* reveals a complementary expression pattern in the functional lateral stamens, which may indicate genetic divergence among these paralogs. *CYC2B,* on the other hand, is extremely lowly expressed in the stamen of both species, while being primarily expressed in the dorsal sepals of both *B. speciosa* and *S. grahamii.* Preliminary RNA-seq data reflects the results of the RT-qPCR in both presence of *CYC*

paralogs and expression pattern. These patterns suggest that *CYC2* function in the Solanaceae has diverged from that of other families in its role in regulating floral symmetry. Our work on *B. speciosa* and *S. grahamii* provides testable hypotheses on the uncharacterized genetic mechanisms underlying the evolution of zygomorphy in the androecium and corolla within the Solanaceae.

Key Words: Solanaceae, TCP, MYB, CYCLOIDEA, RADIALIS, DIVARICATA, floral symmetry, zygomorphy

Where Does Human Inspiration Come From and Its Revelation on Plant Research

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Why do some nations produce disproportionately more transformative scientific breakthroughs than others? As of 2025, the United States has received 428 Nobel Prizes, representing approximately 34% of all awards globally. This enduring leadership across the sciences prompts a deeper question: where does human inspiration truly come from? Drawing upon Qian Xuesen's theory of "inspirational thinking", the author's previously published three papers on human inspiration, and recent advances in cognitive neuroscience—particularly the role of the Default Mode Network (DMN) in remote association and insight generation—this talk proposes that inspiration is not random chance, but the sudden recognition of hidden order after sustained and honest observation. Insights emerge not when we exert greater effort to think, but when the brain, in a relaxed yet alert state, autonomously connects distantly related information.This recognition of 'order' leads to a profound question: Why is there order at all? The Tao Te Ching declares, "The Dao gives birth to one, one gives birth to two, two gives birth to three, and three gives birth to ten thousand things." The Gospel of John declares, "In the beginning was the Dao (the Word), and the Dao was with God, and the Dao was God" (John 1:1). The order that Chinese civilization has long sought—the order that scientists discover in laboratories and fields—is not accidental. It is created. Recent breakthroughs in plant heat stress research provide a striking scientific illustration of this created order. In December 2025, a landmark study published in Cell by Lin Hongxuan's team decoded a complete signaling cascade in rice: heat stress → membrane lipid remodeling → DGK7 activation → PA generation → MdPDE1 → nuclear cAMP hydrolysis → heat tolerance gene expression. This "stepwise decoding mechanism" reveals how plants sense physical heat signals and convert them into biological instructions. The study, which integrated time-series transcriptomics with lipid metabolomics, demonstrated that single-gene improvement achieved 50-60% yield increase under heat stress, while dual-gene improvement doubled yields, without compromising yield under normal conditions. This is not random evolution; this is

designed order waiting to be discovered. This talk argues that the disparity in scientific breakthroughs between nations reflects, in part, a difference in worldview. A civilization that believes the universe is created, ordered, and knowable—and that human beings are called to "discover" rather than "invent" truth—will produce a different kind of inspiration than one that believes everything is accidental. For plant scientists, the implication is profound: the same "Dao" that orders the cosmos orders the lipid bilayer of a cell membrane. The ultimate source of human inspiration and the ultimate source of plant stress responses converge on the same truth—the Creator who established all order.

Key Words: human inspiration, membrane lipid remodeling, heat tolerance, DGK7, multi-omics, order, creation

Metabolomic Mapping Reveals Organ-Specific Bioactivity in *Zygostelma benthamii* Rivaling Diclofenac

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Zygostelma benthamii Baill. (Apocynaceae), known locally as "Op Choei Thao" or "Phaya Rak Hom," is a high-value climbing plant native to Thailand, Laos, Cambodia, and Vietnam, whose roots have long been used in traditional Thai medicine as a heart tonic, carminative, and antispasmodic. Despite this ethnomedicinal reputation and commercial demand, the organ-specific phytochemical basis of its bioactivity has never been systematically characterized using integrated metabolomics platforms. Because secondary metabolite biosynthesis and accumulation typically differ across leaves, stems, and roots, resolving this organ-level variation is essential for guiding the rational, sustainable, and biotechnologically informed development of medicinal plant resources, particularly given that traditional use relies on destructive root harvesting. This study applied an integrated LC–MS/MS and GC–MS metabolomics approach to map the chemical composition of *Z. benthamii* leaf, stem, and root extracts and correlated these profiles with their antioxidant, anti-inflammatory, and cytotoxic activities. Plant material was collected from a conservation forest in Khon Kaen Province, Thailand, separated into leaves, stems, and roots, and extracted in methanol. Untargeted metabolite profiling was performed by UHPLC–ESI–QTOF–MS/MS (positive and negative ionization) and by GC–MS/MS. Total phenolic (TPC), flavonoid (TFC), and saponin (TS) content were quantified colorimetrically, and biological activity was assessed using three complementary antioxidant assays (DPPH, FRAP, and phosphomolybdenum-based TAC), an egg-albumin protein denaturation anti-inflammatory assay benchmarked against diclofenac, and an MTT cytotoxicity assay against human colorectal cancer (Caco-2) cells. Root metabolites were additionally compared between fresh and dried conditions by GC–MS. LC–MS/MS identified 73 metabolites across nine chemical classes, with phenolics (22 compounds) and flavonoids (14 compounds) the most abundant. Twenty-one metabolites were shared across all three organs, while leaves contained the most organ-unique compounds (13), stems seven, and roots only two; the flavonoid vitexin emerged as a dominant leaf-enriched metabolite. GC–MS of roots detected 15 metabolites, dominated by triterpenoids such as lupeol acetate, α-/β-amyrin, and γ-sitosterol that were consistent between fresh and dried

tissue, alongside drying-induced shifts including loss of free fatty acids and gain of cyclic triterpenoid acetates. Quantitatively, leaves had the highest TPC (222.33 ± 3.56 mg AAE/g), TFC (234.07 ± 1.88 mg AAE/g), and TS (53.79 ± 0.55 mg/g), although roots showed the highest predicted saponin percentage (49.43 ± 1.56%). This enrichment translated into the strongest antioxidant performance for leaves, with the lowest DPPH IC_{50} (60.34 ± 1.41 µg/mL) and highest TAC (275.35 ± 13.35 µg AAE/mL), while FRAP values for leaf and root extracts were comparable (49.02 ± 0.43 and 53.97 ± 0.70 µg AAE/mL) and both exceeded stems. The leaf extract was also the most cytotoxic toward Caco-2 cells (IC_{50} = 0.735 ± 0.119 mg/mL), roughly 4.2-fold more potent than the root extract (IC_{50} = 3.108 ± 1.183 mg/mL), an effect attributed to vitexin together with kaempferol, apigenin, and other flavonoids detected exclusively in leaf tissue. In contrast, the root extract showed the strongest anti-inflammatory activity (75.18 ± 1.99% inhibition; IC_{50} = 1.22 ± 0.12 mg/mL), exceeding the potency of the reference drug diclofenac (IC_{50} = 2.07 ± 0.06 mg/mL), an effect linked to its high saponin content and compounds detected in the root extract, including syringic acid, eleutheroside E, canrenone, and procyanidin B2. These findings provide the first comprehensive organ-resolved metabolomic map of *Z. benthamii* and show that its traditional therapeutic use is underpinned by chemically distinct, organ-specific bioactive profiles: leaves as a renewable, repeatedly harvestable source of antioxidant and anticancer compounds, and roots as a potent natural anti-inflammatory resource that rivals a conventional pharmaceutical. Because leaf harvesting does not require destroying the plant, these results also point toward a more sustainable resource strategy than the traditional reliance on roots. By linking high-resolution metabolite profiling with functional bioassay data, this work establishes a foundation for the targeted extraction, valorization, and future biotechnological development including compound isolation and in vivo validation of high value molecules such as vitexin and eleutheroside E from *Z. benthamii*, bridging traditional ethnomedicine with modern plant biotechnology.

Key Words: Phytochemical mapping; Vitexin; LC–MS/MS metabolomics; Ethnomedicine validation; Caco-2 cytotoxicity; Plant bioresource

Genomics meets metabolomics: decoding *Arnebia tschimganica* and the shikonin biosynthesis pathway

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The medicinal herb "Zicao" is sourced primarily from Boraginaceae plants and accumulates the naphthoquinone pigment shikonin and its derivatives, compounds with pronounced anti-inflammatory, antitumor, antiviral, and wound-healing activities and substantial industrial value. However, two long-standing obstacles have impeded progress in both fundamental research and applied exploitation: the unresolved taxonomic status of the vulnerable species *Arnebia tschimganica*, which has undergone repeated genus-level revisions yet remains a subject of international debate; and the incomplete understanding of the shikonin biosynthetic pathway and its transcriptional regulation. In this study, the first chromosome-level genome of *A. tschimganica* for the genus *Arnebia* was sequenced, assembled at 611.54 Mb with quality metrics far surpassing all existing Boraginaceae genomes, providing a robust foundation for phylogenomic and biosynthetic analyses. Comparative genomic and transcriptomic analyses provided robust evidence that Boraginales is the sister order to Lamiales within the Lamiids clade. Crucially, within Boraginaceae, *A. tschimganica* is phylogenetically excluded from the *Arnebia* core clade and instead nested as the sister lineage to *Lithospermum erythrorhizon*. This placement, corroborated by karyotypic evidence, suggests its potential reclassification into *Lithospermum*. *A. tschimganica* has undergone a recent whole-genome duplication event shared with other Boraginaceae species, and this event drove the expansion of shikonin biosynthetic gene families as well as the evolutionary development of shikonin biosynthesis in shikonin-producing species. *A. tschimganica* retains a complete set of shikonin biosynthetic genes in its genome, however, systematic characterization and comparative analysis of the metabolomes of *A. tschimganica* and *L. erythrorhizon* revealed significant differences in root metabolites between the two species. Notably, the types and contents of shikonin derivatives in *A. tschimganica* were markedly distinct from those in

L. erythrorhizon. Cross-species transcriptome comparisons between *A. tschimganica* and its high-yielding relative *L. erythrorhizon* provided the mechanistic explanation that, the transcript levels of core genes, such as *GHQ3''H*, *DSH*, and *SAT*, were nearly undetectable, resulting in far lower shikonin content in its roots compared with *L. erythrorhizon*. The reduced shikonin production in *A. tschimganica* is attributed not to gene loss but to the low transcript levels of key biosynthetic genes following species divergence. Furthermore, AtsDSH1, the enzyme responsible for catalyzing the final hydroxylation step in shikonin biosynthesis in *A. tschimganica*, was identified and functionally characterized through *in vitro* enzyme activity assays. A putative transcriptional regulatory network for shikonin pathway genes was constructed to explore the transcriptional regulatory basis of shikonin biosynthesis, based on tissue-specific transcriptome data and weighted gene co-expression network analysis. Two ERF transcription factors were identified as core positive regulators of multiple enzyme genes in the pathway, including *HMGR*, *GPPS*, *PGT*, *GHQ3''H*, *DSH*, and *SAT*, playing central roles in shikonin biosynthesis, as determined by yeast one-hybrid assays and dual-luciferase reporter systems. Collectively, these findings not only provide a high-quality genomic perspective that clarifies the taxonomy of this controversial species but also offer mechanistic insights and valuable regulatory targets for enhancing shikonin yield. These resources and insights will accelerate the conservation, utilization, and biotechnological exploitation of Boraginaceae medicinal plants and contribute to a broader understanding of the evolution and regulation of specialized metabolites in plants.

Key Words: *Arnebia tschimganica*, shikonin, genome, phylogenetic status, ERF transcription factors

Spatiotemporal Transcriptomics Reveals a Conserved Mechanism Underlying Hollow Stem Formation in Plants

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Hollow stems have independently evolved multiple times across the plant kingdom and play crucial roles in plant development and various environmental adaptations. However, the mechanisms underlying stem hollowness remain poorly understood. Water spinach (*Ipomoea aquatica*) is one of the few hollow-stemmed plants in the *Convolvulaceae* family (eudicot: asterid), and its hollow stems are essential for thriving in aquatic environments. Using histochemical staining and transcriptome analysis, we found that programmed cell death (PCD) is involved in cavity formation at water spinach shoot tips. Single-cell and spatial transcriptome analyses further revealed that ethylene and reactive oxygen species (ROS) likely drive and regulate this process by activating transcription factors *IaNAC074*, *IaNAC087*, *IaNAC029*, *IaNTL9*, and *IaTGA9*, which likely initiate PCD, senescence, and autophagy, collectively leading to pith cell death. These findings were validated through treatments with ethylene and ROS reagents in water spinach, as well as transient expression assays in tobacco. Additionally, transcriptomic data suggest that these mechanisms may also play a role in hollow stem formation in horsetail (fern), moso bamboo (monocot) and broad bean (eudicot: rosid), highlighting the conservation of PCD regulatory mechanisms in hollow stem formation. This study not only fills a major knowledge gap in the adaptive

mechanisms of hollow stem formation but also opens new avenues for agricultural and ecological applications, offering strategies to enhance crop tolerance to flooding and accelerate crop growth.

Key Words: pith cavity, mechanism, evolutionary conservation, *Ipomoea aquatica*, single-cell transcriptome

The Genetic Origin of Boxwood Cultivars (*Buxus spp.*) in North America and Resistance to Box Tree Moth (*Cydalima perspectalis*)

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Boxwood plants from the genus *Buxus* have long been instrumental components of the horticultural industry throughout Europe and North America. These shrubs have been grown as pruned hedges and topiaries in many historical formal gardens in Europe and New England, and today as foundation plantings for residential houses across the United States. Boxwoods are a taxonomically complex group, comprised of species native to Europe (*B. sempervirens* – common boxwood), and different areas of Asia (*Buxus sinica* var. *insularis* – Chinese boxwood; *B. microphylla* – littleleaf boxwood; *B. microphylla* var. *japonica* – Japanese boxwood; and *B. harlandii* – Harland boxwood). Over decades, the taxonomic identity of several commercially available *Buxus* cultivars have reportedly been lost. Due in part to the spread of the box wood moth (*Cydalima perspectalis*) in the mid 2000's from eastern Asia to Europe and more recently to North America, ornamental boxwood plantings have been decimated by larvae, often leading to defoliation and plant death. Damage by this moth is now a growing problem in the Eastern United States, despite continued interest in boxwood in the landscape. To assist boxwood breeders in the development of plants resistant to box tree moth, we sampled historically available cultivars, as well as cultivars commercially sold today or under development, using microsatellite markers and ploidy analysis to genetically confirm their taxonomical identity. We then used a garden experiment to test the resistance of these same cultivars to box tree moth, using replicated arrays at one of the first sites in North America where box tree moth was discovered. We confirmed that cultivars derived from *B. sempervirens* were highly susceptible to box tree moth, and that the most resistant varieties were of Asian origin – as expected due to the coevolutionary history of the Asian *Buxus spp.* with the moth. We identified several cultivars of moderate to high resistance, with a highly resistant cultivar traced back to a historical cultivar grex developed in the 1940's and which is no longer commercially available (but is now under propagation). This project demonstrates the importance of researchers working directly with ornamental plant breeders, as well as the

value of maintaining genetic diversity within the native range of these species.

Key Words: box tree moth, cultivar, ornamental, resistance

Decoding plant chromatin architecture across scales from Arabidopsis to maize

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The three-dimensional (3D) organization of chromatin is fundamental to genome function, yet the mechanisms governing its establishment, maintenance, and environmental responsiveness in plants remain incompletely understood. This study aimed to characterize the multi-scale architecture of plant genomes and determine how environmental cues reshape chromatin organization. We applied an integrated framework combining high-resolution Hi-C, Micro-C-XL, genetic perturbation, and comparative analyses in *Arabidopsis thaliana*, soybean, and maize. We further employed Fiber-seq, a single-molecule long-read sequencing approach that simultaneously profiles chromatin accessibility, nucleosome positioning, and DNA methylation at near-nucleotide resolution. Our analyses revealed multiple hierarchical layers of plant genome organization. We identified widespread long-range chromatin loops anchored at gene clusters, many of which were dependent on H3K27me3 and dynamically remodeled during development and environmental stress. At finer resolution, Micro-C-XL resolved more than 14,000 nucleosome-scale chromatin boundaries and showed that RNA polymerase II activity directly contributes to the formation of local chromatin domains. We further demonstrated that EMBRYONIC FLOWER1 (EMF1) acts as a regulator of 3D genome organization by interacting with cohesin and maintaining compartment-domain boundaries. Fiber-seq revealed locus-specific changes in chromatin accessibility across both regulatory and heterochromatic regions, including 5S rRNA loci and CEN180 repeats. In the complex maize genome, Fiber-seq detected a broader spectrum of accessible chromatin regions than conventional approaches and enabled the identification of fine-scale structural variants and long-range regulatory interactions, including a previously unrecognized enhancer–promoter loop upstream of the UB3 gene. These findings establish a multi-scale framework for plant chromatin organization and reveal its regulation by Polycomb-associated pathways, RNA polymerase II, and chromatin architectural factors such as EMF1 and cohesin. They further demonstrate the utility of Fiber-seq for resolving regulatory

landscapes, chromatin heterogeneity, and structural variation in complex crop genomes. Collectively, this work provides a high-resolution view of how plant chromatin architecture is dynamically reprogrammed during development and in response to environmental signals.

Key Words:3D chromatin organization, Hi-C, Micro-C-XL, Fiber-seq, chromatin accessibility, maize, structural variation

Development of Abiotic Stress Classification and Genome-Wide Association Study in the Kazakhstan Cotton Collection Using Optimal Phenotypic Traits

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Cotton (*Gossypium* L.) is a key fiber crop that contributes greatly to the textile industry and the economies of cotton-producing countries. Abiotic stress has a deleterious effect on cotton at all growth stages and overall, productivity and quality are seriously diminished. *Gossypium hirsutum* genotypes were evaluated under laboratory conditions using NaCl, PEG-6000 treatments, and under field conditions to assess salt and drought tolerance based on nine morphophysiological traits. As a result, five salt and drought-tolerance groups were identified using k-means clustering based on MFVD values. Eight lines, including M-4016-6, M-4031-8, M-4014-6, M-4029-9, M-4016-7, M-4016-8, M-4020-2, and M-4016-4, exhibited high tolerance to salt and drought stresses. 22 accessions were classified as highly drought-tolerant. Principal component analysis revealed an inverse relationship between salt and drought tolerance, suggesting stress-specific adaptation. Axiom Cotton Genotyping Array was used for GWAS analysis. After filtering (call rate> 90%, MAF > 0.05), 5092 polymorphic SNPs were obtained, and 3536 of them were annotated and selected for further analysis. In total, 111 unique SNP markers associated with 21 studied traits were identified using six mrMLM methods. Among them, 46 SNPs were located within candidate genes. This study is the first to report on the development of a classification system for salt and drought tolerance and SNP genotyping in the Kazakhstan Cotton Collection. The results demonstrate the potential for developing salt and drought-tolerant cultivars adapted to saline and drought-affected areas and provide a valuable

foundation for future molecular breeding efforts.

Key Words: *Gossypium hirsutum* L.; drought stress classification, salinity stress classification, single nucleotide polymorphism, genome-wide association study, candidate genes.

The value of long-term historical data for forecasting the future of pollinator floral resources

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Ongoing climate change affects the phenology, distribution, and abundance of plants. At my montane study site at 2,900m in the Colorado Rocky Mountains, phenology of wildflowers that are floral resources for pollinators is driven almost entirely by the timing of snowmelt, which is changing rapidly in response to declines in winter precipitation and warming temperatures. These changes are also influencing the abundance of some flower species, through factors such as soil moisture, frost damage, and temperature. We have a 54-year record from counts made three times a week for the growing season for 120 species growing in 35 2x2m plots in a variety habitats. Record-low snowfall in 2025-26 resulted in record-early snowmelt and flowering phenology in summer 2026. Historical data on snowmelt date, flowering phenology, and flower abundance give us the ability to forecast the future of these floral resources for pollinators, including migratory hummingbirds and resident bee species (>190 species of native bees), flies, butterflies, and moths. Phenological reassortment of flowering species will create new communities of co-flowering species for the pollinators, and changing altitudinal and phenological distributions of pollinator species will create new pollinator communities for the wildflowers, requiring plastic and evolutionary responses for the partners to continue to coevolve.

Key Words: flowering phenology; floral resources; climate change; subalpine; long-term

Drought tolerance of shrubs to low mean annual precipitation

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Shrub species are widely distributed in drylands globally and play a key role in ecological function, yet how woody shrubs adapt to low mean annual precipitation remains unclear. Here, we find that shrubs adapt to low mean annual precipitation through a combination of high leaf hydraulic safety and efficiency, greater stomatal redundancy, lower hydraulic redundancy, and strong root elongation. Moreover, shrubs with rhizobium inoculation exhibit enhanced drought tolerance through novel hydraulic trade-off relationships, achieved by increasing both leaf hydraulic efficiency and safety. Upon drought release, roots recover more rapidly than stems and leaves, thereby contributing to plant recovery from water stress.

Vegetation nutrient limitation and its changes in alpine grasslands on the Tibetan Plateau

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Nitrogen (N) and phosphorus (P) are primary limiting factors for terrestrial vegetation growth. Climate change–induced shifts in soil N and P availability can profoundly modulate carbon (C) –climate feedbacks through their regulation of terrestrial productivity. Therefore, elucidating how vegetation N and P limitation responds to climate change is crucial for robust predictions of terrestrial ecosystem C–climate feedbacks. However, our understanding of these shifts in vegetation nutrient limitation under global change remains limited. To address this knowledge gap, we conducted a comprehensive observational campaign across alpine grasslands on the Tibetan Plateau, incorporating large-scale transect surveys, a whole-ecosystem warming experiment, and thermokarst collapse monitoring platforms. On the basis of these coordinated measurements, we assessed the prevailing N and P limitation patterns and their responses to global change. For N limitation, our work provided large-scale observational and long-term experimental evidence that vegetation N limitation intensifies under climate warming. Our results also revealed that changes in soil N availability regulate key C cycle processes, including plant growth and the priming effect on soil organic C decomposition. Regarding P limitation, we found that both plants and microorganisms were generally P-limited. Permafrost thaw enhanced P availability, which in turn promoted plant growth and microbial C decomposition. Collectively, these findings advance our understanding of C–N–P interactions in alpine grasslands under global change.

Temporal beta diversity and plant community shifts across the U.S. under climate change

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Climate change is predicted to have profound impacts on biodiversity; however, different species and communities have varying levels of vulnerability. Ecological modeling offers limited and sometimes misleading understanding of climate effects on biodiversity as these models do not consider intraspecific trait and genetic variability and mitigating biotic interactions. In contrast, continuous and long-term surveys and monitoring offer more reliable assessments of biodiversity responses to climate change. In this study, we assessed temporal shifts in plant community composition and percent cover in 1105 1 m^2 plots across 20 sites, managed by the U.S. National Ecological Observatory Network (NEON), representing each of the 20 eco-climatic domains across the U.S. and Puerto Rico. We computed alpha, spatial and temporal beta diversity for the plots in both the earliest surveys (T1) and those conducted in 2023 (T2), as well as the gamma diversity.We used permutational analysis of variance (PERMANOVA), permutational multivariate analysis of dispersion (PERMDISP), and associated post-hoc tests to test for significance difference in compositional variance between the two surveys. We tested the hypothesis that diverse communities should have the least temporal shifts and exhibit high ecological resilience. We used generalized linear mixed effect models (GLMM) investigate the effects of T1 alpha diversity, elevation, soil, and climatic variables on temporal beta diversity using, and also checked if temporal beta diversity was structured along geographical gradients and among different vegetation classes. The results showed increases in alpha and gamma diversity T1 and T2 surveys, thus, temporal beta diversity was high for most of the NEON sites, driven mainly by native species turnover and species gains. This finding was corroborated by the PERMANOVA and PERMDISP tests which showed significant community shifts in 16 NEON sites that is explained by compositional variance within or between survey years. We observed latitudinal and longitudinal but not elevational, gradients in temporal beta diversity. Herbaceous vegetation classes experienced the lowest temporal community changes, while forest ecosystems and pasture hay showed the highest shifts. GLMM showed significant effects of three soil (soil pH, silt content, fine organic

carbon) and climatic (monthly Tm standard deviation, monthly Tmean standard deviation, and AET coefficient of variation) variables on temporal beta diversity, while T1 alpha diversity has no effect. This indicates that climatic variability such as extreme weather events, rather than temporal climatic means, drive local community dynamics and biodiversity. Given the land use history in many of the NEON sites, observed temporal beta diversity may indicate post-disturbance succession or climate-induced reshuffling of regional species pool rather than an indicator of ecological resilience and stability.

Key Words: temporal beta diversity, ecological resilience, NEON, United States, alpha diversity, gamma diversity, community ecology, continental scale biology

Heat tolerance is multilayered in *Lemna minor*: eco-evolutionary insights under ongoing climate change

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Climate change is increasing the frequency, intensity and duration of thermal stress events, threatening plant populations worldwide. Heat tolerance is often treated as a fixed property of genotypes or populations, although performance under thermal stress may depend on evolutionary history, phenotypic plasticity and the length of exposure to stressful conditions. Understanding how these interacting sources of variation shape variation in heat tolerance is crucial to predict plant responses to ongoing climate change. Here, we used the clonal aquatic plant *Lemna minor* to examine the eco-evolutionary basis and consequences of heat stress tolerance. Eighteen clonal lines originating from contrasting climatic conditions were grown in a common garden experiment under four constant temperatures spanning benign to stressful conditions: 18, 23, 28 and 33°C. Relative growth rate was measured weekly over five weeks, allowing us to assess genetic differentiation in thermal performance, climate-associated patterns consistent with adaptive differentiation, and time-dependent acclimation responses. Heat stress tolerance varied strongly among *L. minor* clonal lines. Lines from warmer climates initially showed higher growth at 33°C, providing evidence of adaptive differentiation in heat stress tolerance. However, this advantage disappeared under prolonged exposure, showing that heat tolerance is not a static property but depends on the duration of thermal stress. In parallel, acclimation occurred only under sub-optimal temperature conditions: growth increased over time at 18°C, whereas most lines showed a strong performance decline under sustained exposure to 33°C. Finally, we detected substantial variation within clonal lines, indicating that additional sources of potentially epigenetically-mediated novel phenotypic variation may also contribute to thermal performance. Overall, these results show that heat stress tolerance in *L. minor* arises from multiple interacting sources and is dynamically shaped by both

selective history and immediate exposure time, suggesting a more nuanced, multilayered understanding of variation in heat stress tolerance and emphasizing the importance of evaluating such tolerance under ecologically-relevant environmental conditions.

Key Words: Acclimation, adaptive differentiation, climate change, common duckweed (Lemna minor), genetic differentiation, evolutionary ecology, phenotypic plasticity, temperature stress responses

Adaptation of *Mimulus Cardinalis* to Drought Through Changes in Stomata Traits

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Recently, many regions worldwide have been experiencing rising CO_2 levels, increasing temperatures, intensified droughts, more frequent wildfires, and other extreme weather events. These environmental shifts may exert strong selective pressures on plants. Stomata, the critical foliar structures regulating water vapor and carbon dioxide exchange, are highly responsive to such environmental factors. This study aims to understand how plants respond both ecologically and evolutionarily to an extreme, multi-year drought on the West Coast of the United States. We chose the monkeyflower (*Mimulus cardinalis*, Phrymaceae) as our study system and used a resurrection approach to investigate evolutionary changes in its stomatal traits between 2010 and 2017—a period that included a severe drought in the region. By comparing ancestral (2010) and descendant (2017) cohorts before and after the drought, we tested two main questions: (1) Do stomatal traits respond to concurrent changes in drought? and (2) Do populations with higher genetic variance or stronger selection exhibit faster responses? We compare stomatal traits across garden sites, source populations, and cohorts, and further examine the trends and heritability of these traits.

Key Words: Monkeyflower, Stomata, Selection.

Plant hydraulic and thermal adaptations under climate change

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Plant hydraulic and thermal adaptations are crucial to species survival, growth, and distribution. With the increasing frequency and intensity of drought and heatwaves, it is urgent to know the formation of plant hydraulic and thermal traits and their effects on climate niche and biodiversity. Therefore, we conduct research within the framework of "trait-environment-distribution-evolution". Case studies include: 1) Phylogeny and climate shape plant hydro-thermal adaptation strategies; 2) Plant carbon-hydro-thermal trait synergy hypothesis; 3) Coordination between plant thermal tolerance and climatic niche; and 4) Spatiotemporal patterns of plant climatic niches and its relation to biodiversity. Our findings are of great significance for evaluating and predicting plant adaptability under future climate change.

Key Words: plant functional traits, plant hydraulics, plant thermal tolerance, climate niche, species distribution

The invasion processes and ecological impacts of alien plants

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The introduction frequency and invasion extents of alien species keep intensifying under global changes. Current studies mostly focus on local scale or specific taxonomic groups, the global scale patterns and invasion process of alien species invasion and its impacts on biodiversity ecosystem functioning remain poorly understood. Particularly, long term dynamics of forest biodiversity under invasion remain unclear. This talk aims to address a series of topics focusing on large-scale invasion patterns and long-term dynamics. First, we explored the driving factors for successful establishment of alien species. Using naturalized North American species from genera with Eastern Asia North America disjunct distributions and their native sister species, we evaluated niche shifts of alien species during establishment, as well as their phylogenetic distances and niche overlap degrees with native species in both native and invaded ranges. We found that most successfully established alien species underwent niche contraction and failed to occupy novel niches. After naturalization, niche overlap between alien species and their native sister species decreased, and such reduction was positively correlated with phylogenetic distance. These findings reveal that closely related species exert stronger competitive exclusion, and the establishment of alien species is jointly driven by climatic filtering and interspecific competition. We further extended the niche dynamic analysis into global scale and found consistently that niche contraction is more common than niche expansion in global naturalized plants, while plants with island invasion prevalence tend to have larger expansion. Second, based on nearly 30 year plot survey data from eastern U.S. forests, we found that both richness and biomass of alien species in the forest communities increased continuously. Within invaded communities, native species biodiversity continuously declined, whereas uninvaded communities exhibited no significant temporal changes in native species biodiversity, indicating that alien invasions exacerbate native biodiversity loss. By calculating phylogenetic and functional trait distances between native and alien species, we further demonstrated that native species functionally similar and phylogenetically close to alien invaders face higher extinction risks; extinction risks differ markedly between rare and common native species. Interspecific complementarity and divergent responses to disturbance enhance the stability of community productivity.

Finally, we developed an alien species spread model that simulates alien species establishment and spread based on compositional similarity between source range and recipient range species assemblages. The model substantially outperformed alternative models built on environmental similarity (climate, soil, human activity intensity, etc.) between native and recipient regions. Compared with widely used species distribution models, this new model has lower dependence on habitat information of alien species, and its accuracy is insensitive to rapid alien species evolution and sampling biases in occurrence data. It provides a novel tool for early warning and risk assessment of biological invasions. The findings in this study highlighted the growing threat of biological invasion on biodiversity; and revealed the role of biodiversity in sustaining ecosystem functioning and stability under biological invasion.

Mycorrhizae mediate forest biodiversity and ecosystem functioning in the Hengduan Mountains

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Mycorrhizal associations play a pivotal role in sustaining forest biodiversity and ecosystem functioning, yet how they regulate plant species coexistence, community assembly, and ecosystem functioning in mountain forests remains poorly understood. Here, using elevational forest plots in the Hengduan Mountains, we investigated mycorrhiza-mediated patterns of biodiversity and ecosystem functioning along elevational gradients. We found that ericoid mycorrhizal fungi facilitate the coexistence of closely related *Rhododendron* species. We further observed that the dominance of ectomycorrhizal plants and fungi enhances plant and soil carbon storage, plant productivity, and ecosystem multifunctionality. Furthermore, multitrophic biodiversity and biotic associations contribute substantially to maintaining ecosystem multifunctionality. Together, these findings reveal how plant–mycorrhizal associations link biodiversity maintenance with ecosystem functioning in mountain forests and provide new insights into biodiversity conservation and forest ecosystem-service management in the Hengduan Mountains.

Key Words: ericoid mycorrhizal fungi, ectomycorrhizal fungi, biodiversity, elevational gradient, ecosystem multifunctionality

A Multifunctional Seed Coating Promotes Establishment of a Native Grass in Saline-Alkaline Grasslands

Haiyan Ren

Vegetation establishment in saline-alkaline soils is constrained by poor seedling recruitment. Here, we combined physiological assays, transcriptomics, metabolomics, and field validation to evaluate a multifunctional seed coating containing potassium fulvate (FA) and graphene oxide (GO) in the native perennial grass *Agropyron mongolicum*. Under controlled saline-alkaline stress, the combined FA+GO treatment increased shoot and root growth, biomass, and photosynthetic performance, while enhancing antioxidant capacity and reducing oxidative damage. Integrated analyses linked these responses to coordinated regulation of photosynthesis, carbon metabolism, phenylpropanoid and flavonoid biosynthesis, and arginine-related metabolism. Seed priming with the candidate metabolites quercetin and ornithine further promoted seedling growth, providing functional support for pathways identified by the multi-omics analysis. In a one-season field trial, coated seeds produced taller plants and increased vegetation cover, density, and above-ground biomass relative to uncoated seeds. Together, these findings connect seed-interface engineering with physiological and metabolic stress responses and demonstrate the potential of multifunctional seed coating to improve native-grass establishment and support restoration of saline-alkaline grasslands.

Atmospheric nitrogen enrichment decreases grassland multi-scale stability

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Since the Industrial Revolution, anthropogenic activities have led to a marked increase in atmospheric nitrogen deposition. As nitrogen is one of the most critical limiting nutrients for plant growth, the input of biological reactive nitrogen has been shown to reduce both biodiversity and ecosystem stability. By employing nitrogen addition experiments to simulate elevated atmospheric deposition, we similarly observed that nitrogen enrichment simultaneously decreased plant species richness and ecosystem stability. Notably, atmospheric nitrogen deposition does not operate at the scale of a single sampling plot or experimental quadrat; rather, it extends across much larger areas, even at the region. This raises a critical question: can findings from plot-level nitrogen enrichment experiments—specifically regarding the magnitude of stability loss—be reliably extrapolated to broader spatial scales, and what are the underlying mechanisms? To address this, we integrated existing nitrogen addition experiments in grassland ecosystems with metacommunity theory. We found that nitrogen addition consistently reduces ecosystem stability across spatial scales. Ecosystem stability (γ stability) at larger scales was primarily driven by stability at the plot scale (α stability), with spatial asynchrony among local communities further contributing to the maintenance of γ stability. In addition, we found that the seasonality of nitrogen addition modulated the ecosystem stability–area relationship, largely through biodiversity regardless of nitrogen addition. Collectively, these findings suggest that assessing the impacts of atmospheric nitrogen deposition on ecosystem stability requires explicit consideration of both the seasonality of nitrogen deposition and the spatial scale of the target ecosystem.

Demographic rate directional change and its determinants reveal how plant species win in a patchy landscape with frequent droughts

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Relative growth rate (RGR) has been a core demographic performance trait in community ecology because its species-specific divergent responses to light often determine community structure and dynamics. Nevertheless, how divergent responses of plant species in RGR to water stress govern community assembly, alongside the mechanistic basis of inter- and intra-specific variations in functional traits, remain elusive. We propose a theoretical framework for describing how the directional change of RGR across dry and wet patches drives community assembly in a landscape with frequent droughts. The framework was applied to a subtropical understory shrub community where rock fragment content, an important proxy for water stress, shows strong spatial variability. We explored how RGRdir change drives community assembly in a drought-prone landscape and its relationships with plant functional traits. Species with different growth strategies exhibited contrasting response patterns to decreasing soil water availability. Given that species with positive RGRdir change (defined as RGR in dry patches minus RGR in wet patches, divided by their mean) may possess adaptive advantages under spatiotemporally variable soil moisture, we hypothesized that (i) in ecosystems that frequently experience drought, RGRdir change is more sensitive than RGR in detecting interspecific adaptive strategies to water stress, and species with positive RGRdir change will dominate in such patchy landscapes; and (ii) both inter- and intraspecific trait variation are important for plant environmental adaptation, and species with "slow" carbon investment traits coupled with responsive drought-adaptation traits are more likely to exhibit positive RGRdir change. Our findings revealed that: (i) RGRdir change was a better predictor of species dominance than RGR in wet patches, dry patches, or mean RGR; (ii) species that increased RGR as soil water availability decreased were more dominant (higher relative abundance and importance values), and these dominant species generally had acquisitive roots and hydraulically safer stems; and (iii) in response to decreasing water availability, dominant species further enhanced leaf drought tolerance and optimized specific root length, which facilitated faster radial growth and likely released them from light competition. Overall, our study highlights the role of directional RGR change across patches with contrasting

water availability in driving community structure in frequently drought-affected landscapes, and improves our understanding of how drought under global climate change shapes plant community assembly.

Roots enhance the accrual of mineral-associated organic carbon via new carbon formation and microbial conversion of native soil carbon

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The stabilization of plant-derived carbon (C) and the modification of native soil organic matter (SOM) by fresh C input are key processes controlling soil C dynamics, yet the underlying mechanisms are not fully understood, particularly for the subsoil. Here, we conducted a two-year field incubation of 13C-labelled Lolium perenne roots in three grasslands (one alpine and two temperate), to study the incorporation of root-derived C into different SOM fractions and its effect on native SOM dynamics in top- (0–10 cm) versus subsoils (30−40 cm). After two years, the subsoil retained a higher proportion of the initial root C input (19.0 ± 0.8%) than did the topsoil (11.0 ± 1.7%), of which a greater fraction directly sorbed to the mineral-associated organic matter (MAOM) without prior microbial processing. The formation of root-derived MAOM was independent of the decomposition of root-derived light fraction (LF) and particulate organic matter (POM). In contrast, root inputs stimulated the microbial conversion of native POM and LF, leading to their stabilization as microbial-derived MAOM. Our results highlight the critical role of the subsoil in soil C sequestration and reveal that fresh C inputs enhance MAOM accrual via sorption of new C and microbial-mediated transformation of native soil C.

Incorporating Plant Genetic Diversity to Optimize the Conservation Network in the Third Pole

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Climate change poses a significant threat to the survival of many species. Although protected areas can slow down biodiversity loss, they often lack systematic planning and do not integrate genetic diversity. Genetic diversity is a key prerequisite for species survival and the ability to tolerate new conditions. Using population genetic and distribution data from 96 plant species in the Third Pole (encompassing the Tibetan Plateau and adjacent mountains), we mapped patterns of genetic diversity, projected climate-driven range dynamics and future genetic erosion, and designed an optimal conservation framework for the region. We identified several patches of high haplotype diversity (HD), with a relatively high number of haplotypes in southeastern Third Pole. Regression models revealed that climate and topography have interacted to shape patterns of genetic diversity, with latitude and precipitation being the best predictors for HD of cpDNA and nrDNA, respectively. Ecological niche modeling predicted an approximate 43 km northwestward and 86 m upward shift in suitable habitats under future climate scenarios, likely leading to

a significant loss of up to 13.19% and 15.49% of cpDNA and nrDNA genetic diversity, respectively. Alarmingly, 71.20% of the newly identified conservation priority areas fall outside of the existing protected areas and planned National Park Clusters. Therefore, we recommend expanding the network by 2.02×10^5 km² (5.91%) in the Third Pole, increasing the total conserved area to 1.36×10^6 km² (39.93%) to effectively preserve the evolutionary potential of plants. This study represents an innovative attempt to incorporate genetic diversity into biodiversity conservation efforts.

Key Words: conservation network, ecological niche modeling, genetic diversity, genetic erosion, National Park Cluster, systematic conservation planning, Tibetan Plateau

Reading the Future in Deep Time: Cretaceous Amber as an Empirical Lower Bound for Plant Community Reorganization under Extreme Greenhouse Climates

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Under high-emission scenarios, atmospheric CO_2 and global mean temperature will approach mid-Cretaceous super-greenhouse values within one to three centuries. The question this poses to plant science is not how much warming, but what becomes of vegetation under it: does a forest ecosystem collapse, or does it reorganize into a new steady state? The modern observational record contains no climate perturbation of this magnitude, so the reference must be sought in deep time. Yet the Cretaceous world differed in plate configuration, ocean circulation and even in which lineages held the canopy. It is therefore not a mirror of the future greenhouse but its empirical lower bound — the outcome when extreme warmth is imposed slowly, on a world under no other stressor. The obstacle has been that Cretaceous climate is well constrained while Cretaceous ecosystems are not: conventional fossils record discrete species but do not reassemble into a functioning community.What is required is a deep-time archive of an entire ecosystem, and amber is that archive. The deposit we work on had been studied for a century under a mistaken Eocene age until U–Pb dating placed it precisely at the onset of the Cretaceous thermal maximum, at low palaeolatitude. Each piece preserves a three-dimensional microhabitat together with the predation, symbiosis and fire signals running through it; enough pieces compose an ecological snapshot. We assembled a single-deposit, fossil-bearing collection exceeding ten thousand specimens and an integrated reading workflow — large-pixel focus stacking, micro-CT, confocal and electron microscopy — coupled with a taphonomic control protocol that uses amber colour and diagenetic redox state to separate ecological signal from burial noise, and with explicit ethical sourcing standards since adopted by several international groups. This framework also resolved long-standing taxonomic misassignments, supplying a reliable foundation for reconstruction. On that foundation we reconstructed the functional architecture of a tropical forest at the greenhouse peak: vertical stratification from a bryophyte ground layer through wetland-margin and shaded-understorey ferns to a tree-fern subcanopy, a multi-family beetle decomposer chain running

from fresh wood to humus, and direct evidence of ectomycorrhizal symbiosis. Species composition shares almost nothing with modern rainforests, yet network connectivity and functional partitioning overlap closely. This invariance amid change is precisely what licenses the comparison. Forest maturity, however, is measured not by structure alone but by the complexity of life the structure can support, and here the amber is decisive: potter wasp nests preserved with their eggs and matching living relatives in material selection and brood provisioning, archaeid spiders with hyper-elongated chelicerae specialized on spider prey, and termitophilous rove beetles integrating host recognition with chemical signalling. Such behavioural programmes cannot run without a mature, structurally complete forest beneath them. If the architecture was conserved, why were the protagonists replaced? The angiosperm displacement of gymnosperms has long been attributed to intrinsic competitive advantages, which fails to explain why the transition accelerated in step with greenhouse intensification. We identified in amber a complete fire-adaptive syndrome in angiosperm flowers — reduced needle-like leaves, dense indumentum shielding meristems, tightly packed capitate inflorescences, hard woody capsules, and a clumped resprouting habit — closely matching modern Cape Fynbos shrubs and co-preserved with charcoal. Independent confirmation comes from the insect side: an extinct bostrichid subfamily whose living relatives breed exclusively in post-fire deadwood, and buprestids bearing infrared receptors homologous to those of modern fire-seeking taxa. Frequent wildfire under high oxygen and high biomass thus acted as an evolutionary sieve, removing tall gymnosperms and selecting fire-adapted angiosperms into the vacated niches. Three lines now extend this framework forward. Refining the lower bound, systematic analysis of over three thousand amber plant fossils shows angiosperms already occupying nearly every functional niche far earlier at low latitudes than mid-latitude records imply, with the tropical island system serving simultaneously as museum, cradle and corridor. Testing it independently in the present, 59.6% of New Guinean endemics originated within the past five million years, and these young lineages concentrate in the tropical lowlands where climate velocity is now highest. Projecting it forward, seasonal extremes rather than annual means govern growth-form limits, predicting growth-form reorganization across 63.8% of ecoregions by 2060. The Cretaceous constrains the direction of change, not its rate — and rate is where the present departs from the reference. That distance is the quantity worth measuring.

Key Words: greenhouse climate; amber palaeobotany; angiosperm radiation; wildfire regime; deep-time reference frame

Natural variation of AcEGY3 mediates chloroplastic ROS homeostasis to confer kiwifruit thermotolerance

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Climate change pose a severe challenge on global agricultural production including cultivation of fruit tree. The genus of *Actinidia* consists of the popular kiwifruits consuming worldwide. Most kiwifruit species are naturally distributed in warm and moist environments. So, they are vulnerable to high levels of heat stress. Till now, genetic basis of kiwifruit thermotolerance has remained largely unexplored. Here, we uncover a natural variation responsible for thermotolerance in kiwifruit species. We reveal that thermotolerant kiwifruit species have increased expression of *AcEGY3*, a gene encoding a chloroplast-localized protein, which can promote expression of nuclear thermotolerance genes via H_2O_2-dependent retrograde signaling. We show that natural variation in the promoter of *AcEGY3* constitute a binding site for the heat stress-inducible transcription factor AcGATA1. The increased expression of *AcEGY3* is regulated by AcGATA1 and its possible interaction with another transcription factor AcHSFA2-2. This natural variation is absent from the thermosensitive kiwifruit species. The downstream target genes including *AeHSP70* and *AeMPSR1* were identified. Collectively, our results reveal genetic basis of kiwifruit thermotolerance and set the foundation for breeding thermotolerant kiwifruits cultivars.

Harnessing Multimetal-Tolerant Root Associated Fungal Strains from *Alternanthera tenella* Colla for Plant Growth Promotion and Metal Stress Mitigation

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Heavy metal contamination poses a significant challenge to agricultural productivity and environmental sustainability. *Alternanthera tenella* Colla is an invasive plant species widely distributed across degraded and polluted environments, with previous studies demonstrating its ability to tolerate and accumulate various heavy metals. Root-associated fungi can enhance plant adaptation to stressful environments through metal detoxification, nutrient mobilization, and production of growth-promoting compounds, making them promising candidates for sustainable bioremediation strategies. In this study, root-associated fungal strains of *A. tenella* growing in heavy metal-contaminated industrial sites were investigated for their heavy metal tolerance, plant growth-promoting (PGP) traits, and ability to enhance rice seed germination under metal stress. Fungal isolates obtained from bulk soil, rhizosphere, and root compartments were screened for tolerance to Cadmium (Cd), Chromium (Cr), Lead (Pb), and Aluminium (Al) and assessed for PGP attributes including indole-3-acetic acid (IAA) production, phosphate solubilization, ammonia production, and siderophore production. ICP-OES analysis revealed elevated concentrations of Al and Cd in the study area and identified the hyperaccumulation of Cd by *A. tenella*. Most fungal isolates exhibited tolerance to multiple heavy metals, with *Fusarium fujikuroi* showing the highest tolerance. All isolates demonstrated key plant growth-promoting traits, including IAA production, phosphate solubilization, and ammonia production, while siderophore production was absent in *Aspergillus keveii* and *Talaromyces verruculosus*. FTIR analysis of metal-tolerant fungal strains revealed the involvement of hydroxyl, amine, carbonyl, and alkane functional groups in metal binding, suggesting their role in metal sequestration and detoxification. Seed germination assays demonstrated that *F. fujikuroi* and *Sarocladium kiliense* significantly enhanced rice germination under Al, Pb, Cd, and Cr stress. The combination of multi-metal tolerance and plant growth-promoting capabilities highlights the potential of these indigenous fungi as

bioinoculants for improving crop establishment, enhancing stress resilience, and supporting bioremediation of contaminated soils.

Key Words: Rhizosphere, Heavy metals, Tolerance index, FTIR, PGP traits

Structural, Physiological and Photosynthetic Gene Expression responses of *Alternanthera tenella* Colla under Chromium stress

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Chromium (Cr) contamination resulting from industrial activities poses a serious threat to plant productivity and ecosystem sustainability. Understanding the adaptive mechanisms employed by plants under heavy metal stress is crucial for developing resilient green systems in a changing environment. In the present study, *Alternanthera tenella* Colla was investigated to elucidate its responses to chromium stress at morphological, physiological, anatomical, and molecular levels. Plants subjected to 240 µM Cr supplied as potassium dichromate ($K_2Cr_2O_7$) exhibited reductions in plant height, root length, and leaf area, indicating the adverse effects of metal toxicity on plant growth. ICP analysis confirmed chromium uptake and accumulation within plant tissues, indicating the capacity to withstand substantial metal loads. Anatomical examination of leaf cross-sections revealed structural modifications associated with chromium stress, suggesting alterations in tissue organization and photosynthetic architecture. Physiological assessment demonstrated pronounced changes in photosynthetic pigments and metabolic constituents, including chlorophylls, carotenoids, soluble sugars, starch, proteins, amino acids, nitrogen and glutathione. These responses indicate metabolic adjustments and activation of protective mechanisms aimed at mitigating chromium-induced stress. To further understand the molecular basis of adaptation, the expression profiles of key photosynthesis-related genes were analyzed using quantitative real-time PCR. The C3 pathway genes *RBCL* and *RBCS* exhibited reduced expression under chromium stress, whereas the C4-associated genes *PPC, PPDK*, and *CA* were upregulated. This contrasting expression pattern suggests photosynthetic reprogramming that may enhance stress acclimation and carbon utilization under adverse conditions.Taken together, the results demonstrate that A. tenella responds to chromium toxicity through coordinated morphological, anatomical, physiological, and molecular modifications. These findings provide new insights into plant adaptation to heavy metal stress and contribute to the broader understanding of mechanisms supporting plant resilience in environmentally challenged ecosystems.

Microbial Role in Phytoremediation of *Alternanthera tenella* Colla under Heavy Metal Stress

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Heavy metal contamination poses a serious threat to soil fertility and environmental safety. Present study investigates the interaction between *Alternanthera tenella* Colla and rhizosphere microbes isolated from heavy metal contaminated site. A pot study was conducted using Al, Pb, Cr, and Cd with four treatments: (i) plant with heavy metals, (ii) plant with microbes, (iii) plant with microbes and heavy metals, and (iv) control (plant only). Isolated rhizobacteria were characterized for urease activity, fluorescence under UV, and diffusible pigmentation, using *Proteus* sp. as positive control for urease test and *Escherichia coli* as negative control for urease, flourescense and diffusible pigmentation tests. Metal accumulation in plants was quantified using ICP-MS after acid digestion. Remediation efficiency was assessed through translocation factor (TF), bioconcentration factor (BCF), and bioaccumulation factor (BAF). Biochemical stress responses were evaluated by estimating root proline content and malondialdehyde (MDA) levels for lipid peroxidation. *Pseudomonas gessardii* tested positive for urease activity, fluorescence, and diffusible pigmentation, whereas *Bacillus thuringiensis* was negative for all three traits. Microbial inoculation enhanced heavy metal uptake by *A. tenella* compared to uninoculated plants under metal stress, with higher BCF, TF, and BAF values recorded for the plants under microbe with metal treatment. Heavy metal stress increased proline and MDA levels in plants, but inoculation with microbes reduced MDA accumulation and moderated proline levels relative to uninoculated metal-treated plants, indicating alleviation of oxidative stress. This integrated approach implies the role of specific microbial traits in enhancing phytoremediation of *A. tenella* and highlights plant–microbe interactions as an eco-friendly rhizoremediation strategy for remediation of Al, Pb, Cr, and Cd contaminated soils.

Key Words: Phytoremediation, Alternanthera, heavy metal, BCF, TF, BAF, oxidative stress

Merism of Begoniaceae: revisiting an issue of numbers

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Merism is one of the primary features which shape the Bauplan of a whorled flower. Begoniaceae have a high diversity of merisms in the flowers. To compare the floral ontogenetic patterns of different species, and to interpret the evolution of different merisms in Begoniaceae, floral development process of 13 representative species was observed with SEM, and the ancestral state reconstructions were conducted on seven floral characters. While merism is more variable in carpellate flowers, staminate flowers are mainly tetramerous or dimerous. Dimery and tetramery is similar in staminate and carpellate flowers, although the inner tepals shows a slightly asymmetric pattern in carpellate tetramerous flowers. The 2+1-mery and trimery share similarity with tetramery and pentamery, respectively. Tepal initiation follows a 2/5 sequence in most pentamerous flowers, but the subsequent development may follow three distinct patterns. Hexamery is linked to pentamery. Double positions exist in the staminate flowers with a high merism, but the tepal initiation in the carpellate flowers is likely to follow a simple spiral sequence. The most recent common ancestor of *Begonia* is likely to have had bisexual reproductive units; the staminate flower had four tepals and an actinomorphic androecium, while the carpellate flower had five tepals. The evolutionary trends among the states in each floral character are discussed based on the transition rates. The differences between different merisms affecting tepals, stamens, and carpels are explained by divergent pressures and space availability in the floral buds during development. Our study illustrates the process of floral development of a broad range of species of Begoniaceae in detail, illustrating how merism transitions are achieved by the fusion and shift of floral organs and how pressure and spatial limitation influence floral development and patterning. The combination of multiple floral traits may contribute to the pollination in different taxa in Begoniaceae.

Key Words: Begoniaceae, floral ontogeny, morphology, merism, spatial constraints, ancestral state reconstruction

Urban Refugia or Ecological Trap? Regeneration Constraints and Biodiversity Imbalance of Rare Tropical Plants under Global Change: A Case Study from Bogor, Indonesia

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Climate change and rapid urban expansion have accelerated global environmental change, contributing to increasing rates of biodiversity loss, particularly among rare and endemic plant species that are becoming progressively more vulnerable to extinction. Urban green spaces are increasingly recognized as potential refugia for biodiversity conservation; however, their capacity to sustain long-term population viability remains insufficiently understood, especially in tropical regions. Addressing this gap is essential for redefining the role of urban ecosystems in sustainable plant conservation strategies. This study aims to examine the conservation status and regeneration dynamics of rare plant species within a tropical urban landscape at IPB University, Bogor, Indonesia, an area experiencing rapid urbanization. The relevance of this study is further underscored by increasing land demand for housing, which has contributed to biodiversity decline. A field-based ecological survey was conducted, integrating taxonomic identification, quantitative analysis, and conservation assessment. Data were collected through direct field exploration, including species identification, geographic coordinates, abundance, and classification of growth stages (saplings, poles, and mature trees). A random sampling approach was applied to capture representative community variation within the study area. Conservation status was determined based on the IUCN Red List and Indonesia's priority species list, while population structure analysis was used to assess regeneration dynamics. The validity of findings was strengthened through repeated verification with experts in biodiversity and plant taxonomy. The results identified 11 rare and priority plant species spanning multiple conservation categories, including one critically endangered species (9.1%), three endangered species (27.3%), and one vulnerable species (9.1%). *Dipterocarpus retusus* (Critically Endangered) was represented by only three mature individuals, while several endangered *Shorea* species also exhibited low population sizes, indicating a high risk of local extinction despite being located within a managed landscape. Meanwhile, 54.5% of

the species were classified as least concern, endemic, or nationally prioritized taxa, suggesting that conservation value is not solely determined by global threat status but also by ecological significance at the local scale. Observed population structure revealed clear regeneration imbalance, characterized by the dominance of mature individuals and limited recruitment at early growth stages. Several high-risk species were found only at pole and tree stages, indicating regeneration failure and potential long-term population decline. This imbalance is further reflected in the disproportionate ratio among growth stages. The Shannon diversity index (H' = 0.56) indicated low diversity, while the low evenness value (E = 0.23) highlighted uneven species distribution and strong dominance by a single species. These findings suggest structural imbalance within the community, which may affect ecosystem stability and long-term species persistence. Contrary to the common assumption that urban green spaces function effectively as biodiversity refugia, this study indicates that such environments may instead act as ecological traps, where species persist temporarily but face long-term decline due to disrupted regeneration processes. Factors such as climate change, habitat fragmentation, and low ecological connectivity are likely contributing to this condition. This study provides a framework for evaluating the sustainability of rare and endemic plant populations in tropical urban landscapes. It emphasizes the need to shift from passive conservation approaches toward proactive strategies, including assisted regeneration and enrichment planting. The findings contribute to global efforts in biodiversity resilience by highlighting that the future of plant conservation depends significantly on how urban ecosystems are designed, managed, and integrated into broader conservation networks under ongoing environmental change.

Key Words: urban biodiversity, rare and endangered plants, regeneration constraints, conservation strategies, tropical ecosystems.

Prior Carbon Limitation Effects on Stomatal Regulation and Drought Response in *Carya illinoinensis*

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Drought-induced tree mortality has increased considerably across forest biomes worldwide, threatening critical ecosystem services, including carbon storage, water regulation, and climate stabilization. Although hydraulic failure and carbon starvation are both recognized as mechanisms of tree mortality, their interactions and the role of prior C-limitation in drought tolerance remain poorly understood. Disturbances like insect defoliation can deplete the reserves of nonstructural carbohydrates (NSC) in trees before drought even begins. NSC support defense metabolism and facilitate osmotic adjustment to maintain cell turgor under water stress. However, there is currently limited evidence that reduced NSC availability impairs turgor maintenance during drought, and the effects of tree NSC status on stomatal regulation strategies and water conservation capacity remain unclear. Depletion of NSC could limit the availability of soluble sugars for osmotic adjustment in guard cells, which is required for stomatal opening because these sugars act as osmolytes. This mechanism provides a pathway by which C limitation can alter stomatal behavior. As NSC reserves decline, trees may close stomata at higher leaf water potential (Ψ_{Leaf}) or conversely delay stomatal closure to maintain photosynthetic carbon gain despite greater desiccation risk. Such shifts in stomatal regulation can be described along a continuum from isohydric, where stomata close at relatively high (less negative) Ψ_{Leaf} to conserve water, to anisohydric, where stomata remain open at more negative Ψ_{Leaf} to sustain photosynthesis. NSC depletion may also limit osmotic adjustment in other tissues and increase the turgor loss point (Ψ_{TLP}), reducing the ability of cells to maintain turgor as drought intensifies. Even after stomata fully close, residual water loss continues through incompletely sealed stomata and the leaf cuticle, known as minimum leaf conductance (g_{min}). Recent evidence also suggested that defoliation, a primary cause of C-limitation,

can increase g_{min}, which accelerates water depletion during prolonged drought and shortens the time to lethal hydraulic thresholds. Therefore, this study will test how prior C-limitation alters leaf osmotic adjustment, turgor maintenance, stomatal regulation, and residual rates of water loss during drought in one-year-old pecan (*Carya illinoinensis*) saplings, which are sensitive to drought stress. Saplings will receive three C treatments (control, shade to suppress photosynthesis and deplete NSC, and complete defoliation to mimic severe herbivory). Progressive drought will then be imposed via gradual soil dry-down until stomatal closure. During dry-down, we will measure (1) Stomatal conductance (g_s)and Ψ_{Leaf} to characterize stomatal response and identify stomatal closure thresholds, (2) Ψ_{TLP} and osmotic potential at full turgor to quantify osmotic adjustment, (3) g_{min} after full stomatal closure to assess residual water loss, and (4) tissue NSC concentrations to link physiological responses to C status. We hypothesize that prior C-limitation will alter stomatal regulation (either leading to earlier closure at less negative Ψ_{Leaf} if NSC depletion limits osmotic adjustment, or delayed closure if C-limited saplings prioritize photosynthetic recovery), increase Ψ_{TLP} due to a negative correlation between leaf NSC and osmotic potential, and cause C-limited saplings to exhibit higher g_{min}, accelerating water depletion during drought. By experimentally manipulating C status before drought in pecan, this study will track coordinated changes in g_s–Ψ_{Leaf} relationships, Ψ_{TLP}, g_{min}, and NSC pools. These findings will advance mechanistic understanding of how C depletion predisposes trees to hydraulic failure and lethal dehydration under compound climate and biotic disturbances, which will improve forest vulnerability predictions and will inform targeted management interventions.

Key Words: nonstructural carbohydrates, stomatal conductance, turgor loss point, minimum conductance, osmotic adjustment, drought tolerance, *Carya illinoinensis*, carbon starvation, tree mortality

Multi-omics insights into the genomic basis of adaptation and maladaptation to climate change in *Populus* species

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Abstract: Global climate change is rapidly accelerating biodiversity loss. Plants are particularly vulnerable to these shifts, as their sessile nature prevents them from relocating to escape rapidly changing conditions. Investigating the diversity of adaptive strategies in wild plant species not only deepens our understanding of the genomic basis of evolutionary adaptation, but also provides invaluable genetic resources for global breeding programs aimed at enhancing climate resilience. Forest trees, as foundational components and primary carbon sinks of terrestrial ecosystems, play a pivotal role in mitigating the effects of climate change. In this talk, I will present our latest research on the genetic basis of climate adaptation and maladaptation within and across *Populus* species over varying evolutionary timescales—from the past to the future. To achieve this, we integrate species-specific pangenomes and cross-species super-pangenomes with multi-omics data—including transcriptomes, methylomes, and large-scale population genomics—complemented by functional molecular validation. Ultimately, by dissecting the genes and natural variants associated with diverse climatic and environmental variables, we aim to translate these findings directly into tree breeding. Our overarching goal is to leverage these genetic resources to develop new, climate-resilient poplar varieties capable of thriving in diverse environments in the face of global climate change.

Key Words: global climate change, Populus, multi-omics, adaptation, tree breeding

From Adaptation to Transformation: Plant Sciences for Climate-Smart Ecosystems

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Climate change is driving significant shifts in species distributions, ecosystem functioning, and biodiversity dynamics, particularly in mountain ecosystems that are highly sensitive to environmental change. This study investigates the role of plant sciences in facilitating the transition from climate adaptation to ecosystem transformation through an integrated assessment of biodiversity, traditional ecological knowledge (TEK), and emerging digital technologies in selected Himalayan landscapes of northwestern India. The research combines ethnobotanical surveys, vegetation assessments, stakeholder consultations, and geospatial analysis to examine how climate-resilient plant diversity and community-based management practices contribute to ecosystem adaptation. Data were collected from traditional agroforestry systems, community-managed forests, sacred groves, and high-altitude habitats to evaluate changes in species composition, local perceptions of climate variability, and adaptive resource-use strategies. These field observations were complemented with remote sensing datasets and predictive ecological modelling to identify vulnerable habitats, climate refugia, and potential shifts in the distribution of ecologically and culturally important plant species. Results indicate that ecosystems characterized by higher plant functional diversity and strong community stewardship exhibit greater resilience to climatic stress. Traditional agroforestry systems and sacred landscapes were found to serve as important reservoirs of biodiversity, carbon sequestration, and ecosystem services, while local ecological knowledge provided critical insights into long-term environmental change and adaptive management. Geospatial analyses further revealed the potential of climate-refugia mapping and AI-assisted monitoring tools for identifying priority areas for conservation and restoration under future climate scenarios. The study proposes a transformative framework for climate-smart ecosystem management that integrates biodiversity conservation, ecological restoration, digital technologies, and traditional ecological knowledge. The findings demonstrate that climate resilience can be strengthened not only through technological innovation but also through the revitalization of biocultural knowledge systems and community-led stewardship. By positioning plants

as key agents of ecosystem transformation, the research highlights the importance of interdisciplinary and inclusive approaches for achieving nature-positive development, climate resilience, and sustainable landscape management in a rapidly changing world.

Geographical Patterns of Tree Growth in the Qinling Mountains Inferred from Stable Hydrogen Isotopes of Lignin Methoxyl Groups

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The Qinling Mountains are characterized as a distinct transition of bioclimatic zones along the north-south geographic boundary in China. Although ongoing global warming may affect the growth of most tree species across north-south slopes, elevation gradients, and alpine treeline, the effect of modern warming on the stable hydrogen isotopes of lignin methoxy groups (δ^2H_{LM}) in tree-ring wood is still unknown. We developed early- and late-wood δ^2H chronologies of multiple tree species from 1900 to 2018 at 700-m intervals from 1700-3100 m a.s.l. and north-south slopes along the Mt. Taibai gradient, the peak of the Mt.Qinling. The δ^2H_{LM} values of the earlywood were relatively enriched in ^2H compared to the latewood, and an elevation-dependent depleting trend along the altitudinal gradient was observed in *Pinus tabulaeformis*, *Abies fargesii*, and *Larix chinensis* species. The combined new δ^2H_{LM} chronologies, based on the lag-1 autocorrelation and the weighted average of the current year earlywood and previous latewood, could merge the corresponding temperature signals from the middle- and low-elevation sites. In addition, the δ^2H_{LM} values of the evergreen broadleaf (*Rhododendron purdomii*) shrub were enriched by 23.3‰ in ^2H compared with those of the deciduous conifer (*Larch chinensis*) tree. However, the multispecies δ^2H_{LM} composite significantly reflected the temperature and precipitation during the growing season (May to September). Therefore, topographic effects such as elevation and slope differences should be considered in large-scale applications of δ^2H_{LM} values in tree growth studies.

Key Words: geographical patterns, tree growth, climatic ecology, δ2HLM

IMPACTS OF MANAGEMENT PRACTICES ON PLANT-RHIZOBIA SYMBIOSIS IN AGROECOSYSTEMS OF COASTAL KENYA.

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Beneficial symbiotic associations between plants and soil microbes are important drivers of agroecosystem stability and resilience. Grain legumes such as *Vigna unguiculata* (L.) Walp and *Vigna radiata* (L.) R. Wilczek are key, climate-resilient crops for most coastal Kenyan smallholder farming communities. Despite their importance, production still remains low due to nutrient depletion influenced by conventional farm management practices that derail natural nutrient cycling processes. Protecting native mutualistic microbes is crucial for maintaining natural pathways for plant nutrition. Rhizobia bacteria serve as key partners for these legumes, promoting biological nitrogen fixation (BNF). BNF naturally improves soil fertility reducing the need for synthetic chemical fertilizers. A study was conducted on ten farms in Coastal Kenya to determine the impact of organic and inorganic fertilizer input on plant-rhizobia symbiosis. The functions and species of rhizobia bacteria were assessed for two legume crops (*Vigna unguiculata* (L.) Walp and *Vigna radiata* (L.) R. Wilczek). Field and greenhouse experiments were established under Randomized Complete Block Design (RCBD). The crops were amended with commercial organic input (WonderGro soil conditioner), cattle manure and inorganic fertilizer (Di-ammonium phosphate (DAP)) to evaluate the impact of soil amendments on the symbiosis, using rhizobia nodulation as the measure of function. Analysis of Variance (ANOVA) and Fishers LSD were performed using R software to assess the effects of the treatment inputs on nodule abundance. Significant differences in nodulation were observed with treatments combining WonderGro soil conditioner with cattle manure or DAP having higher nodulation (>20%) as compared to single applications. WonderGro as a single amendment, enhanced nodule abundance performing as good as manure and even better than No input control. Inorganic amendment, DAP as a single amendment was observed to suppress nodule abundance in comparison to the organic amendments. Rhizobia isolates were places

in six groups based on the morphological and biochemical characteristics. Molecular characterization was performed using the 16S rRNA gene sequencing with the universal primers 27F and 1492R. The sequences were analysed using bioinformatics tools on MEGA12 software and BLASTn on the NCBI database. Analysis revealed four distinct genera, Neorhizobium, Rhizobium, Mesorhizobium and Ochrobactrum, all from the order Hyphomicrobiales. Overall, the application of organic amendments was found to enhance plant-rhizobia symbiosis better that inorganic fertilizers. Integrating inorganic fertilizer with organic fertilizer further enhanced the symbiosis, providing additional advantages that help counteract the negative effects associated with the chemical fertilizers. The findings highlight the importance of organic based management practices in conservation of plant-rhizobia symbiosis for ecological conservation and climate resilient agroecosystems.

Key Words: Rhizobia bacteria, Plant-Rhizobia symbiosis, Ecological conservation, Agroecosystem.

Eco-friendly hydrogel technology for climate-resilient plant cultivation

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Aridification driven by climate change, along with droughts that are becoming both longer and more frequent, now ranks among the most pressing problems facing plant science and sustainable agriculture worldwide. Tackling this problem means developing materials that are environmentally friendly and biodegradable, capable of easing water stress and helping plants cope with it, without piling additional ecological costs onto the systems they're meant to protect. This work introduces a new biodegradable hydrogel made from carboxymethyl cellulose (CMC), combined with sodium alginate - a green, circular-economy alternative to the synthetic superabsorbent polymers commonly used today, which often draw environmental criticism because they biodegrade poorly and can harm soil ecosystems over time.The hydrogel's three-dimensional polymer network came together through a two-stage crosslinking process. In the first stage, the material underwent preliminary ionic modification using manganese sulfate and zinc sulfate, which introduced important micronutrients directly into the polymer matrix. The second stage involved primary crosslinking in a calcium chloride solution, which stabilized the alginate-CMC network through ionic gelation. These two steps produced a hydrogel that is mechanically stable while also embedding agronomically valuable trace elements within the material itself meaning water management and plant nutrition are handled by a single sustainable platform rather than two separate interventions. Both laboratory tests and vegetation experiments confirmed that the hydrogel has real potential as a tool for climate-resilient cultivation. At a concentration of 0.5%, the samples retained an additional 45–50 g of water, which translates to roughly 12–30 m^3 ha^{-1} of water conserved in the root zone, water that directly supports plant availability under deficit conditions. At a 1.0% concentration, the hydrogel delayed the onset of critical soil desiccation by 16–18 days compared to untreated controls. The vegetation experiments went further, showing that hydrogel application improved both growth and developmental performance in cereal crops subjected to water-deficit stress, which underscores just how relevant this material could be for crop productivity as environments grow increasingly arid. One of this work's key contributions

to sustainable plant science is its environmental safety assessment specifically, how the hydrogel affects soil biological activity, a fundamental driver of plant-soil interactions and overall ecosystem health. Catalase activity increased from 5.02 to 5.13 mL of 0.1 M $KMnO_4$ per 10 g of soil within 20 minutes; dehydrogenase activity rose from 0.181 to 0.210 mg TPF per 10 g of soil within 24 hours; and urease activity reached 127 mg $N–NH_4$ per 10 g of soil, also within 24 hours, all of these values exceeded what was measured in the controls. This stands in contrast to synthetic hydrogels, which frequently suppress soil enzymatic activity. The biodegradable material we developed instead actively stimulated the microbial and enzymatic processes essential for nutrient cycling and soil fertility, reinforcing the health of the plant-soil system rather than undermining it. These findings demonstrate that the biopolymer hydrogel offers an integrated solution to several agronomic challenges that are typically addressed in isolation. The combination of CMC, sodium alginate, and micronutrient ions (Mn^{2+}, Zn^{2+}), stabilized through a two-stage crosslinking process, enables the material to retain water under deficit conditions, delay the onset of soil desiccation, and stimulate rather than suppress soil microbial and enzymatic activity. This multifunctionality sets the hydrogel apart from conventional synthetic superabsorbent polymers, whose water-retention benefits are frequently offset by adverse effects on soil biology.

Key Words: biodegradable hydrogel, climate change, green technology, soil water retention, drought resistance, sustainable agriculture, eco-friendly biopolymer

How to Conduct the Work of Grass Taxonomy at a Botanical Garden in a Major Metropolis

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Of all plants, grasses (Poaceae) are the most important to man. The taxonomy on grasses are often considered to be difficult because of the tiny and unique floral structures in grasses. In the era of genomics and bioinformatics, and under the current academic evaluation system, conducting grass taxonomy is no easy task. The authors selected the Shanghai Botanical Garden and carried out the following work related to grass taxonomy: 1) Rebuilt and reorganized the existing but previously unmanaged SG herbarium, recruited volunteers to digitize specimens, and prepared for the future collection of grass specimens; 2) Started collecting, identifying and preserving grass specimens from across China; 3) In collaboration with the Kunming Institute of Botany, Chinese Academy of Sciences, the author conducted phylogenetic research on the relationships among *Pseudosorghum* and the Saccharinae subfamily (Poaceae); 4) In collaboration with the South China Botanical Garden, Chinese Academy of Sciences, the author clarified the nomenclatural issues regarding two new species in the genus *Cymbopogon*; 5) In collaboration with The Germplasm Bank of Wild Species at the Kunming Institute of Botany, Chinese Academy of Sciences, the authors is collecting germplasm resources of crop relatives. By sharing the work on grass taxonomy and related research in a small botanical garden, the authors hope to garner further support and encourage all the Chinese colleagues in plant taxonomy never to give up. Plant taxonomy always plays a most fundamental but also vital role in plant science research even under this rapidly developing and changing era.

Key Words: grass, taxonomy, phylogeny, crop relatives

Rapid chromosomal restructuring drives rediploidization and evolutionary innovation post-polyploidy

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Accelerating global environmental change poses a central challenge for future botany, namely understanding how plants reorganize their genomes during climatic instability and habitat shifts. Whole-genome duplication creates evolutionary potential, but duplicated genomes must restore stable inheritance through rediploidization. Its chromosome-scale dynamics and contribution to environmental adaptation remain insufficiently resolved. We integrated chromosome-level genomes, phylogenomics, intergenomic synteny and ancestral karyotype reconstruction across *Trapa*, *Sonneratia*, *Lagerstroemia* and *Punica*, together with tissue-resolved transcriptomes specifically from *Trapa*. These lineages share parts of their polyploid history but differ markedly in chromosome number, genome structure and habitat. This framework enabled us to reconstruct successive polyploidization-rediploidization cycles, assign chromosomal changes to defined evolutionary intervals and connect structural genome evolution with regulatory and phenotypic divergence. *Punica*, which diverged before the shared triplication, provided a closely related reference for the ancestral state. We identified an ancient whole-genome triplication shared by *Trapa*, *Sonneratia* and *Lagerstroemia*. Reconstruction of the ancestral Lythraceae karyotype recovered eight proto-chromosomes containing 18,401 proto-genes, indicating that triplication produced 24 chromosomes. *Lagerstroemia* maintained this number, whereas *Sonneratia* was reduced to 12 chromosomes through end-to-end joining, nested chromosome fusion, reciprocal translocation and fission. Shared syntenic breakpoints and maximum-parsimony reconstruction showed that most of this reorganization did not accumulate gradually along a single terminal branch. Instead, a concentrated burst occurred in the ancestral interval between approximately 41.7 and 29.8 million years ago. This burst comprised eight end-to-end joinings, nine nested chromosome fusions and four fissions, substantially reorganizing the post-polyploid chromosome complement before subsequent lineage divergence. Its timing overlapped with the Eocene-Oligocene Transition and its pronounced global cooling, placing rapid karyotype

reorganization within a major episode of environmental change. This temporal concentration reframes early rediploidization as rapid chromosome-scale change rather than gradual gene loss alone. We further detected a younger Trapa-specific polyploidization event dated to approximately 24.11 million years ago. Genome-wide synteny independently supported this event because each corresponding region in closely related lineages matched two homologous regions in *Trapa*. The later rediploidization phase included one end-to-end joining, two nested chromosome fusions, four reciprocal translocations of chromosomal arms and three fissions. By comparison, only one reciprocal translocation occurred after *Trapa* divergence from *Sonneratia* but before the *Trapa*-specific whole-genome duplication, showing that restructuring was again concentrated after polyploidization. The paired *Trapa* homologous regions generated by this younger event showed extensive but unequal gene loss. Significant differences in orphan-gene abundance revealed that corresponding regions followed distinct evolutionary trajectories rather than undergoing uniform fractionation. *Trapa* transcriptomes revealed homologous-region expression bias, with the strongest divergence between aerial leaves and submerged or hypoxia-associated organs. The same homolog usually retained its expression advantage across tissues, supporting stable regional dominance with tissue-specific regulation. Retained genes were enriched in organ development and hormone signaling and were significantly associated with expression differences between water and soil roots. Oxygen-sensing and stress-response components further connected biased retention and regulatory divergence with organ specialization and hypoxia responses. Together, these results show that rediploidization is a recurrent and structurally dynamic phase of plant genome evolution. Rapid chromosomal restructuring stabilizes duplicated genomes, while uneven gene retention and expression divergence generate new regulatory and phenotypic possibilities. The correspondence between extensive chromosome-scale restructuring and major environmental upheaval positions polyploidization-rediploidization cycles as a key evolutionary mechanism that expands genomic flexibility and supports plant resilience, adaptation and innovation under future global change.

Key Words: polyploidization, rediploidization, chromosomal restructuring, global environmental change, plant genome evolution

How Evolutionarily Labile Are Plant Ecological Niches? Evidence from Comparative and Experimental approaches

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Characterizing a species' niche is often the first step toward understanding where, and under what conditions, a species can live. In turn, determining whether a niche is labile or conserved can help identify a species' potential vulnerability to future ecological change. I will describe indirect approaches that my colleagues and I have used to address the central question of niche lability versus constraint. In the first, we use herbarium specimens collected across the species' range and over multiple years to characterize climate niches. We then integrate these niche estimates with knowledge of the evolutionary history of the relevant clade to test how much niche traits have evolved over time and across diverse geographic distributions. Other approaches we have used involve experimental manipulations of environmental conditions to evaluate plant performance across a range of contexts, including extreme conditions. Ultimately, species' performance measured across a range of habitats and conditions will provide an initial indication of how much we can expect species to cope with rapidly changing environments.

Key Words: niche lability, niche constraint, phylogenetic, ecology, climate change

Host phylogeny overrides environmental filtering in shaping root core microbiomes of desert Chenopodieae plants in Xinjiang, China

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Northern Xinjiang is dominated by arid saline habitats suffering concurrent drought and salt stress, a harsh environment where plant-microbe symbiosis largely sustains host survival. Despite the well-recognized importance of microbial symbionts for extremophile plants, it remains unclear how host phylogenetic relatedness and soil properties jointly determine the assembly of root core endophytic microbiomes in desert Chenopodieae, a key salt-tolerant plant group. This research systematically explored the assembly rules and phylogenetic conservatism of core root endophytes across ten co-occurring Chenopodieae species native to northern Xinjiang desert saline lands.We combined multiple analytical approaches including chloroplast phylogenomics, 16S rRNA high-throughput amplicon sequencing, microbial co-occurrence network construction, Blomberg's K test, variation partitioning analysis (VPA), and functional metabolic profiling to dissect the structural composition and functional traits of root endophytic bacterial communities. In total, 396 core ASVs were screened out. These core taxa merely occupied 8.3% of the total microbial diversity but contributed up to 65.90% of all sequencing reads, indicating their dominant abundance within root internal microbiota. A network built with 999 ASVs displayed typical small-world topological features, whose stability was mainly maintained by 179 core microbial taxa. Blomberg's K value reached 1.95, confirming strong phylogenetic conservatism in core endophyte community structure across host species. Soil ammonium nitrogen was identified as the primary edaphic driver regulating core microbiome variation, with core communities showing stronger sensitivity to this nutrient than the whole endophytic assemblage. VPA results quantified divergent explanatory power: host phylogeny independently accounted for 27.7% of core community variance, almost twice the 15.6% explained by soil environmental factors. Functionally, core endophytes adopted chemoheterotrophic metabolism to adapt to carbon-deficient root microhabitats. Host-specific microbial recruitment patterns were observed: nitrogen-cycling keystone genera *Devosia*, *Methylobacterium* and *Pseudomonas* accumulated abundantly in *Atriplex*, *Chenopodium* and *Oxybasis*. By contrast, *Kraschenninnikovia* recruited limited nitrogen-

transforming microbes and preferred endemic stress-resistant taxa adapted to local saline-arid conditions. Collectively, we proposed a “host-dominant, environment-modulated” assembly paradigm for root core endophytes of desert Chenopodieae. This work solidifies long-term co-evolution between chenopod hosts and their symbiotic microbes, highlighting host genetic filtering as the decisive factor shaping core root microbiomes under extreme arid saline stress.

Key Words: Phylogenetic conservatism; Core microbiome; Chenopodieae; Arid environment; Nitrogen cycling; Community assembly

Indigenous Rhizosphere Fungal Consortium Enhances Phytoremediation of Heavy Metals by *Alternanthera tenella* Colla.

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Alternanthera tenella Colla, an invasive plant species widely distributed in degraded and metal contaminated habitats, has gained attention for its exceptional tolerance to heavy metal stress and its ability to accumulate multiple toxic metals, making it a promising candidate for phytoremediation. This study investigated the potential of an indigenous rhizosphere fungal consortium to enhance the phytoremediation efficiency of *A. tenella* under 9 mM aluminium (Al),170 µM cadmium (Cd), 240 µM chromium (Cr), and 680 µM lead (Pb) stress. Heavy metal-tolerant fungal strains were isolated from the rhizosphere of *A. tenella* and screened for their metal tolerance and plant growth-promoting (PGP) traits. Based on their superior performance, *Aspergillus fumigatus*, *Aspergillus terreus*, and *Fusarium fujikuroi* were selected to formulate a fungal consortium. Hydroponically grown plants were inoculated with the consortium and exposed to individual heavy metals. Plant physiological and biochemical responses were assessed by estimating chlorophyll, carotenoids, total protein, proline, hydrogen peroxide (H_2O_2), malondialdehyde (MDA), and the activities of catalase (CAT), ascorbate peroxidase (APX), guaiacol peroxidase (GPX), and glutathione reductase (GR). Heavy metal accumulation in roots and shoots was quantified using inductively coupled plasma-mass spectrometry (ICP-MS). Consortium inoculation significantly alleviated heavy metal-induced oxidative stress, reducing H_2O_2 content by approximately 79% (8.01 to 1.70) and MDA by 10% (1.121 to 1.005), while also lowering proline accumulation and moderating antioxidant enzyme activities, indicating improved cellular redox homeostasis and reduced stress severity. ICP-MS analysis revealed enhanced uptake and translocation of all four metals, with fold increases of 1.77, 1.32, 1.48, and 4.98 for Al, Cr, Cd, and Pb, respectively, demonstrating a substantial improvement in phytoextraction efficiency. These findings demonstrate that indigenous rhizosphere fungal consortia significantly enhance the phytoremediation potential of *A. tenella* and represent a promising, eco-friendly strategy for the sustainable restoration of heavy metal-contaminated environments.

Key Words: Indigenous rhizosphere fungi, Heavy metal contamination, Phytoextraction, Antioxidant defence, Sustainable remediation

Adaptation and maladaptation to climate change in a California oak: lessons from common garden, landscape genomic, and epigenetic studies

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Oaks (*Quercus*) are among the most evolutionarily successful tree genera, diversifying over more than 50 million years to dominate ecosystems across the Northern Hemisphere. Today, however, California oak populations face mounting threats from land-use change, invasive pests and pathogens, altered fire regimes, and increasingly severe drought. Understanding how these long-lived trees will respond to rapid environmental change requires integrating phenotypic, genomic, and epigenetic perspectives on adaptation. In this talk, I will present findings from three complementary research programs using *Quercus lobata* as a model system: a long-term common garden experiment, landscape genomic analyses, and epigenetic greenhouse studies. Results from the common garden reveal climate-associated variation in morphological traits that predict tree growth and provide evidence that some populations are already becoming maladapted to contemporary climate conditions. Landscape genomic analyses identify regions of the species' distribution that are likely to experience increasing maladaptation under future climates. Epigenetic experiments further demonstrate that individual trees differ in their DNA methylation responses to environmental stress, with associated effects on gene expression. Together, these studies provide new insights into the mechanisms underlying adaptation and maladaptation in California oaks facing rapid climate change. I will conclude by discussing how integrating common garden experiments with landscape genomic and epigenetic approaches can improve predictions of tree responses to climate change and inform conservation strategies for resilient forests.

Key Words: Oaks, adaptation, climate change,

Soil moisture influences nectar robbing and plant fitness in a primrose species

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Low soil moisture, a prominent indicator of a changing climate, has overarching impacts on plant reproduction both directly and indirectly by affecting the visitation rate of pollinators. However, the role of soil moisture in modifying the behaviours of species interacting with plants is less well explored, as are the mechanisms associated with those changes in behaviour. Reduced soil moisture can disrupt mutualistic species interactions, potentially shifting them toward antagonism and negatively impacting plant fitness. We investigated the effects and underlying mechanisms of soil moisture on the intensity of nectar robbing (a common behavioural interaction between plants and pollinators) in natural populations of *Primula florindae* on the southeast Tibetan Plateau. To understand the relationships between soil moisture and nectar robbing and the mechanisms involved, we explored within-population variation in nectar robbing, floral and nectar traits, and the diversity and evenness of the co-flowering plant community in areas with natural variation in soil moisture. We then used an experimental approach to test how nectar robbing affected male and female components of *P. florindae* reproduction. We found that plants growing in low moisture soil experienced higher nectar robbing. Low soil moisture was associated with reduced flower size, nectar production, and diversity of nectariferous neighbour plants. However, only flower size (an estimate of nectar accessibility) had a significant effect on the intensity of nectar robbing, with low soil moisture triggering a morphological mismatch between flowers and the primary bumblebee pollinators,

prompting them to shift to nectar robbing behaviours. Nectar robbing reduced all components of male and female plant reproduction explored by up to 45%. This study provides new insight into how soil moisture influences plant–animal interactions, influencing the behaviour of floral visitors from mutualism to antagonism, and highlights that future soil water availability caused by global climate change may not only directly affect plants but also indirectly affect plants through changes in species interactions.

Key Words: climate changes, exploitation, floral larceny, floral visitor behaviour, plant–animal interactions, Primula, reproductive success, water availability

Leaf heat and cold tolerance show contrasting associations with cellulose and starch across tree species

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Leaf thermal tolerance is central to predicting plant responses to heatwaves and cold spells, yet it remains unclear whether heat and cold tolerance form a shared tolerance axis or distinct functional dimensions. We propose that leaf carbon allocation provides a mechanistic framework for this test because carbon is partitioned between persistent structural compounds and labile storage pools with contrasting physiological roles. We measured heat and cold tolerance thresholds based on PSII, structural and nonstructural carbon compounds in 92 tree species across six forests in China and tested whether carbon allocation explains variation in leaf thermal tolerance. Heat and cold tolerance showed a weak but detectable positive coordination across all species, but this relationship was not significant within either leaf habit. Cellulose concentration was positively associated with heat tolerance, whereas starch concentration was negatively associated with cold tolerance,

and these relationships were strongest in deciduous species. Our results support a carbon allocation framework in which structural carbon compounds, particularly cellulose, are associated with heat tolerance, whereas nonstructural carbon compounds, particularly starch, are linked to cold tolerance. This framework helps explain variation in leaf thermal tolerance and may improve predictions based on traits of forest vulnerability to thermal extremes.

Key words Carbon allocation; cellulose; starch; leaf thermal tolerance; heat tolerance; cold tolerance; nonstructural carbohydrates; structural carbon compounds

Asymmetric day-night warming reshapes evergreen and deciduous forest productivity at global scale

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Climate warming is not uniformly distributed across the diel cycle, yet the ecological consequences of asymmetric daytime and nighttime warming remain poorly understood. Because daytime and nighttime regulate distinct plant physiological processes, diel warming asymmetry may influence vegetation functioning beyond the effects of mean temperature change. Understanding how plants with contrasting functional strategies respond to asymmetric warming is therefore critical for predicting future forest carbon dynamics.Here, we integrated global measurements of plant heat tolerance traits (leaf thermal tolerance thresholds, T_{50}) with satellite-derived land surface temperature (LST) and forest productivity (gross primary productivity, GPP) to investigate how asymmetric warming influences forest carbon uptake. Using 744 global angiosperm forest sites, including 415 evergreen and 329 deciduous forests, we combined daytime and nighttime LST to quantify thermal exposure and calculated thermal safety margins (TSM) by integrating environmental temperature with leaf-level heat tolerance. We further evaluated contrasting productivity responses and thermal strategies between evergreen and deciduous forests.We found pronounced diel asymmetry in warming patterns across forest ecosystems, accompanied by widespread reductions in diurnal thermal range. Deciduous forests exhibited stronger productivity sensitivity to daytime warming, consistent with their rapid resource acquisition strategy. In contrast, evergreen forests maintained relatively stable productivity under increasing thermal exposure but showed narrower thermal safety margins, indicating operation closer to physiological heat limits.These findings reveal distinct thermal strategies of evergreen and deciduous forests under asymmetric warming and highlight that the ecological impacts of climate change depend not only on warming magnitude, but also on when warming occurs within the diel cycle.

Key Words: angiosperms, daytime warming, productivity, nighttime warming, thermal safety margins

Molecular mechanisms underlie the stabilization of gene regulatory networks for adaptive evolution of mangrove plants

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Maintaining the stability of gene regulatory networks (GRNs) is a major challenge for plants facing environmental stresses. This is particularly significant in the context of ongoing global climate change. However, how long-term genetic changes stabilize GRNs during stress adaptation remains largely unexplored. Here, we investigated GRN evolution in mangroves, which originated from inland ancestors and adapted to intertidal zones characterized by fluctuating stressors. We first compared the GRN stability between mangrove and inland plant, and found that the representative mangrove plant *Rhizophora apiculata* exhibited markedly more stable gene expression under salinity changes than its inland relative *Carallia pectinifolia*. Many genes that are salt-induced in *C. pectinifolia* are constitutively highly expressed in *R. apiculata*, whereas genes repressed by salt—mostly involved in growth and development—are constitutively downregulated. The shift from stress-responsive to preactivated expression likely enhances GRN stability at the cost of growth, consistent with the "growth-defense trade-off" hypothesis. These expression alterations were predominantly associated with duplicated genes originating from whole-genome duplications. Because gene expression was dominated by regulatory elements, we then explored mechanisms governing GRN stability by assessing regulatory region accessibility using ATAC-seq (Assay for Transposase-Accessible Chromatin using sequencing). Consistent with stable gene expression, *R. apiculata* exhibited stable chromatin accessibility, with many salt-responsive accessible chromatin regions (ACRs) lost, which are associated with the genome-wide elimination of transposable elements. The removal of salt-responsive regulatory elements on ACRs—typically closed under high salinity—thereby promotes preactivated expression of upstream hub transcription factors and stabilizes the expression of numerous downstream targets. As a biological network, GRN stability could be explained by the May–Wigner theory (MWT), a classical theory for explaining network stability. MWT predicts that reducing system complexity enhances

stability under persistent perturbations. Consistent with this prediction, we found that mangrove plants evolved simplified GRNs compared with inland plants. On the one hand, the extensive loss of ACRs and the regulatory elements associated with them reduced connectivity in mangrove GRNs; on the other hand, a comparative survey across major mangrove clades revealed a convergent reduction in gene numbers, producing smaller GRNs. Together, genic and intergenic reductions reshaped GRNs, producing networks that are both smaller and simpler. Extending MWT to GRNs, computer simulations showed that genome reduction increases network stability. In summary, our findings reveal genomic mechanisms that stabilize GRNs in mangroves adapted to fluctuating environments and provide broader insights into plant GRN evolution under future climate change.

Key Words: gene regulatory network stability; mangrove plants; stress response; adaptive evolution; chromatin accessibility evolution

Year-to-year height-based functional reassembly of herbaceous communities across a montane environmental gradient in Nyingchi, southeastern Tibet

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Herbaceous communities can respond rapidly to short-term environmental variation, yet the extent to which their functional composition undergoes directional year-to-year reassembly along montane gradients remains poorly understood. This question is particularly important in mountain regions, where steep environmental gradients can amplify differences in community sensitivity over short distances. Trait-based repeated surveys are useful because they can detect shifts in ecological strategies even when taxonomic summaries alone do not reveal whether community change is functionally directional. We used two consecutive vegetation surveys in Nyingchi, southeastern Tibet, to test whether herbaceous communities showed non-random functional reassembly across a steep elevational gradient. We resurveyed the same plot network in 2024 and 2025, including 62 paired herbaceous plots spanning 819–4408 m elevation, and compared temporal stability among tree, shrub, and herb layers using repeated community-weighted mean (CWM) plant height. We quantified herb height distribution quantiles, species recorded as lost from or gained into paired plots between surveys, baseline- and survey-date-controlled elevation effects, and spatial synchrony using permutation-based Moran tests. Within the observed annual interval, woody layers showed greater functional stability than the herbaceous layer. Herb CWM height declined by a paired mean of 2.33 cm between 2024 and 2025 across the 62 paired plots. Although the simple paired mean shift was moderate, the direction and magnitude of change were not random: after z-standardizing elevation and controlling for baseline CWM height and survey-date gaps, signed herb CWM-height change became more negative with elevation (elevation coefficient = −3.83 ± 1.24, P = 0.003). Under the same controls, the absolute magnitude of

CWM-height change increased toward lower elevations (elevation coefficient = −2.00 ± 0.96, P = 0.043). These results indicate that interannual reassembly was both directional and elevation dependent. Changes in the herb height distribution further supported a contraction of tall-statured community components. Cover-weighted q75 and q90 declined by 5.91 and 5.32 cm, respectively (P = 0.008 and 0.029). Thus, the year-to-year shift was not limited to the community mean; it also involved collapse of the upper tail of the herb stature distribution. Species-level replacement patterns were consistent with non-random height-based reassembly. Herb species recorded as lost from paired plots were taller than species recorded as gained into those plots. At the plot level, the mean height of lost species exceeded that of gained species by 2.36 cm (P = 0.001), and at the event level, the difference was 3.23 cm (P < 0.001). Interannual herb functional changes also showed regional-scale spatial synchrony: change in herb CWM height had positive spatial autocorrelation under a 100-km distance weighting (Moran's I = 1.14, permutation P = 0.022), suggesting that interannual reassembly contained a regional spatial component. Together, the mean shift, upper-tail contraction, lost-versus-gained trait difference, and spatial synchrony provide convergent evidence for non-random stature filtering. Our results reveal rapid height-based functional reassembly of herbaceous communities over a one-year interval in southeastern Tibet. Our inference is limited to directional functional reorganization; the study does not directly test climate causation, long-term demographic change, or taxonomic compositional turnover. The herbaceous layer appears to be a sensitive early-response component of mountain vegetation, capable of registering short-term ecological change before comparable restructuring is evident in woody layers within the observed annual interval. These findings highlight plant height and related trait-distribution metrics as useful indicators for monitoring regional ecological reassembly in mountain ecosystems under environmental variability.

Key Words: herbaceous layer, functional traits, community-weighted mean, plant height, elevation, functional filtering, spatial synchrony, southeastern Tibet

Conservation genomics of the endangered plant *Meconopsis barbiseta*

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Understanding the process and driving factors of species endangerment is a scientific prerequisite for effective conservation efforts. The Qinghai-Tibet Plateau, one of the most biodiversity-rich and climate-sensitive regions in the world, harbors a large number of endemic plant species that are particularly vulnerable to environmental changes. *Meconopsis barbiseta*, an annual herbaceous species belonging to the family Papaveraceae, is exclusively distributed in the alpine meadows of the eastern Qinghai-Tibet Plateau. Due to its narrow geographical range, specialized habitat requirements, and increasing anthropogenic disturbances, this species has been classified as endangered. However, its genetic background and the underlying mechanisms of its endangerment remain largely unexplored.Traditional research on endangered species has long been constrained by limited research scope and a lack of genomic data, making it difficult to systematically assess genetic diversity and population structure, and failing to reveal cryptic genetic erosion, inbreeding depression, or historical population declines that may critically threaten the long-term viability of species. The scarcity of high-resolution genomic information has thus become a major bottleneck in diagnosing the intrinsic causes of endangerment and in scientifically defining conservation units. In this study, we integrated a high-quality, chromosome-level genome assembly of *M. barbiseta* with whole-genome resequencing data from 29 individuals across seven populations. The reference genome, constructed using a combination of Illumina short-read sequencing, PacBio long-read sequencing, and Hi-C chromosome conformation capture technology, provides a complete and accurate reference sequence for population genomic analyses. The resequencing data, derived from natural populations spanning the known distribution range of the species, enable the systematic detection of genome-wide single nucleotide polymorphisms (SNPs), insertions and deletions (InDels), and structural variants. On this basis, we employed population genetic structure inference, genetic diversity assessment, inbreeding coefficient estimation, and effective population size reconstruction through demographic modeling to systematically elucidate the demographic history and genome-wide genetic distribution

patterns of *M. barbiseta*. In parallel, we complemented these analyses with karyotype characterization and seed germination experiments, integrating cytogenetic and reproductive biology data to investigate the genetic causes of its endangerment from multiple perspectives. Collectively, this study aims to identify the intrinsic drivers of endangerment in *M. barbiseta* and to provide a genomic foundation for the resource conservation and sustainable utilization of this species.

Key Words: *Meconopsis barbiseta*, conservation genomics, population genetics, genetic diversity, global change

Conservation biology of the endangered plant *Sinadoxa corydalifolia*

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Sinadoxa corydalifolia is an endangered long-lived perennial herb endemic to the scree habitats of the Qinghai–Tibet Plateau and is classified as a Plant Species with Extremely Small Populations (PSESP), with fewer than 600 wild individuals remaining. As a typical high-elevation specialist, this species serves as an ideal model to disentangle how intrinsic genetic limitations and extrinsic ecological stressors jointly shape the fate of alpine plants under ongoing climate change. Despite its high conservation priority, the link between genomic vulnerability and population-level demographic dynamics remains poorly characterized for many PSESP species.We generated the first chromosome-level genome assemblies of *S. corydalifolia* and its widespread congener *Adoxa moschatellina* for comparative genomic and conservation genomic analyses. The genome of *S. corydalifolia* is approximately 15.73 Gb in size with a contig N50 of 817.66 Mb, encoding 33,331 annotated protein-coding genes and exhibiting 97.1% BUSCO completeness. Comparative genomic analysis identified a lineage-specific whole-genome duplication event subsequent to the ancient γ duplication (Ks peak = 0.843; 4DTv peak = 0.42). Population resequencing of 25 individuals from three *S. corydalifolia* populations and 48 individuals from nine *A. moschatellina* populations revealed strong genetic differentiation and substantially reduced genetic diversity in the endangered species. Notably, no detectable inter-population gene flow was found in *S. corydalifolia*, demonstrating long-term geographic isolation and severely limited adaptive potential. Gene family expansion and contraction analyses identified 227 expanded and 188 contracted gene families in *S. corydalifolia*. Positively selected genes were significantly enriched in functional pathways related to high-altitude adaptation, including stress tolerance, photosynthetic efficiency, and metabolic homeostasis regulation. Complementing these genomic findings, three consecutive years of field monitoring (2019–2021) revealed severe extrinsic ecological pressures threatening natural populations. Large herbivore trampling and pika herbivory caused up to 70% inflorescence damage in the Nangqian population. Demographic analyses demonstrated that individual plant size is positively correlated with survival rate, flowering probability

and reproductive output, indicating a cascading negative effect of size decline on multiple key life-history traits. Importantly, the lower elevational limit of *S. corydalifolia* has shifted upward by nearly 600 m (from 3,900 m to 4,500 m) in recent decades, with all historical low-elevation populations completely extinct, providing solid evidence of climate-driven range contraction in alpine plant species.Collectively, our study reveals a dual endangerment mechanism for *S. corydalifolia*: intrinsic genomic fragility caused by long-term isolation and low genetic diversity, and intensified extrinsic ecological stresses under climate change. We further proposed an integrated conservation framework incorporating genomics-informed management unit division, assisted gene flow among compatible populations, targeted ex situ conservation, and in situ fencing protection for isolated populations. This work clarifies the comprehensive drivers of population decline in a typical alpine PSESP species and provides a reliable genomic and ecological reference for the conservation and management of climate-vulnerable plants in alpine ecosystems.

Key Words: Plant Species with Extremely Small Populations (PSESP), comparative genomics, population genomics, climate change, elevational range shift, conservation genomics

Chromosome-Level Genomes of Four Seagrasses Reveal Adaptive Mechanisms to the Marine Environment

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Seagrasses are the only fully marine angiosperms, forming one of the three most iconic coastal ecosystems together with mangroves and coral reefs. With a global distribution of approximately 0.6–1.6 million km², seagrass beds account for 10%–15% of the global ocean carbon burial, rendering them highly efficient "blue carbon" ecosystems with irreplaceable roles in climate regulation. Despite their ecological significance, seagrass beds are declining rapidly due to anthropogenic disturbance and climate change. All extant seagrasses belong to the order Alismatales and are derived from multiple independent freshwater-to-marine transitions, representing a classic case of multiple independent origins and convergent evolution. The shift from freshwater to marine habitats entails severe environmental challenges, including high salinity, low carbon availability, and iron limitation, making the adaptive mechanisms of seagrasses a central question in marine evolutionary biology. Although genomic resources for seagrasses have accumulated rapidly in recent years, most studies have focused on gene family dosage changes, with little systematic attention paid to adaptation at the coding sequence level. In this study, we generated high quality chromosome-level, haplotype-resolved genome assemblies for four representative seagrass species distributed along the coast of China: *Cymodocea serrulata*, *Syringodium isoetifolium*, *Phyllospadix iwatensis*, and *Zostera caespitosa*. Comparative genomic analyses revealed substantial changes in gene family copy number associated with marine adaptation. Contracted gene families were mainly related to hormone signaling, defense responses, and stress-response pathways, suggesting a reduction or rewiring of ancestral response systems during adaptation to permanently submerged marine habitats. In contrast, expanded gene families were associated with signal transduction, membrane trafficking, ion homeostasis, and carbon metabolism, indicating coordinated genomic

changes underlying osmotic adjustment, nutrient uptake, and physiological maintenance in seawater. Notably, the expansion of sucrose/trehalose biosynthesis and glycolysis supports osmotic adjustment and energy metabolism under saline conditions, while the expansion of carbonic anhydrases (CAs) and phosphoenolpyruvate carboxylase (PEPC) represents a key innovation in carbon-concentrating mechanisms (CCMs) for utilizing marine inorganic carbon. CAs catalyze the reversible interconversion of CO_2 and $HCO_3^-$and are essential for carbon utilization in seagrasses. Higher plants possess three evolutionarily independent yet functionally complementary CA families (α, β, γ) that differ markedly in sequence, structure, metal coordination, and oligomeric state. Here we found that the *α-CA* family has undergone lineage-specific expansion in seagrasses, and all three families showed convergent amino acid substitutions in their catalytic domains, potentially affecting active-site conformation or substrate channels. Thus, seagrass CAs adapted to low-carbon marine environments through both increased gene dosage and amino acid sequence optimization. Our study provides high-quality genomic resources for four indigenous seagrass species and reveals molecular strategies underlying their resilience to ocean environments. These findings not only advance our understanding of plant adaptation in a changing world, but also offer a scientific foundation for seagrass restoration and blue carbon conservation.

Key Words: seagrass, marine adaptation, convergent evolution, carbonic anhydrase

Environmental DNA-Based Monitoring of Invasive Alien Plant Species in Hebei Province, China

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The spread and proliferation of invasive alien plants have become critical challenges threatening ecological security, constraining socioeconomic development, and endangering human health. Currently, traditional methods for surveying and monitoring invasive alien plants face numerous limitations. The use of environmental DNA (eDNA) metabarcoding technology in surveys of invasive alien plants offers advantages such as high efficiency, stable identification results, and low cost. This study focused on invasive alien plants in Hebei Province, China, integrating field surveys with eDNA data analysis. Across two years field campaigns, 167 sampling sites were surveyed across Hebei, followed by molecular experiments and bioinformatics analyses. Results showed that 38 invasive plant species were recorded through field quadrat surveys, while soil eDNA analysis detected 113 invasive species from the corresponding plots. Moreover, significant differences were observed in eDNA detection results across different soil depths, although no significant differences were found between years. The study preliminarily confirmed that soil eDNA technology can effectively reflect the composition of most invasive plant species in the environment, though its detection performance is significantly influenced by the biological characteristics of different invasive species and the quality of the DNA barcode reference database used. Although many challenges remain, soil eDNA technology holds great potential for dynamic monitoring and effective control of invasive plants.

Key Words: eDNA, metabarcoding, DNA barcoding, invasive species, biodiversity

Hindcasting and forecasting phenology and demography in an era of climate change

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Phenology provides unique insights into how climate change affects seasonal timing of important life history events for both plants and animals. A downside of such studies is that data are only recorded at the rate of one observation per year (e.g., date of emergence from hibernation, first flowering date), thus requiring many years of study before trends can be confirmed, especially in environments with high inter-annual variability. If suitable proxies for phenological drivers (e.g., timing of snowmelt) can be found, it may be possible to hindcast phenology, and once environmental drivers are identified it may be possible to use models of future climate change to forecast phenology. At the Rocky Mountain Biological Laboratory in Colorado (2,900m), we have >50 years of data on flowering phenology and abundance for 150 species of wildflowers, and multi-decade records of flowering abundance for three others. We have used these data to elucidate the precipitation and temperature variables affecting flowering phenology and abundance, and can then use historical stream gage and weather records to hindcast phenology and abundance, and use forecast climate data to predict future phenology and abundance. This provides insights into the past, present, and future for plants, pollinators, and herbivores in montane meadows.

Key Words: long-term data; flowering phenology; demography; climate change

Flower-visiting flies: Their global diversity and importance as pollinators.

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Flies are important flower visitors and pollinators, are much less studied than bees, but may include as many flower-visiting species as bees. They can be as important as bees for pollination of some plants visited by both groups, including at least 100 crop species, although they may be less efficient at pollen acquisition or deposition. Since 1990 I have collected records from published studies of flies visiting flowers, in a database that now has almost 50,000 entries, gleaned from >1,100 papers and websites published since 1848. Records are available from 106 countries. 245 reports are of a single fly species, with a mean of 34 and maximum of 2,039 fly species per source. 264 (57%) plant families are reported as being visited by flies (85% of families with animal-pollinated plant species), but only 2% of all plant species. The top two plant families reported for visits are Asteraceae and Rosaceae. 107 fly families (57%) are reported as flower visitors, including 6% of all genera and 3.7% of all species. Syrphidae and Muscidae are the most commonly reported fly families. A surprising diversity of flies can visit one plant species: *Daucus carota* (Apiaceae) is visited by 94 species of flies from 81 genera and 29 families (628 observations). A single fly species (*Episyrphus balteatus*; Syrphidae) is recorded visiting 1.613 species of flowers in 747 genera from 142 families (2.834 observations). I suspect that published reports are still a fraction of the actual use of flowers by flies. For example, although there are about 6,200 species of Syrphidae, the family with the most published records, only about 1,600 species are reported so far as flower visitors. Similarly, for Asteraceae, the most commonly reported plant family visited by flies, only about 8,900 of 32,000 total species are reported so far in the literature as being visited by flies. Almost nothing is known about the conservation status of fly pollinators, or their life cycles. There are very few data on proboscis length of Dipteran pollinators, their phenology or abundance, or corolla tube lengths of flowers they visit, and most studies do not report the sex of the fly visitors. More data are needed!

Key Words: fly; pollinators; pollination; Diptera

Harnessing Synthetic Biology and Robotics to Engineer High-Yield and Resilient Crops

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Synthetic biology has been widely applied in microbiology and pharmaceuticals but remains an emerging field in plant science. The integration of synthetic biology with robotics is particularly novel for plant researchers and has become a powerful tool to tackle major agricultural challenges. In this presentation, I will demonstrate how robotics accelerates the design-build-test-learn (DBTL) cycle in synthetic biology and enables solutions to improve crop yield and disease resistance. To address yield limitations, automated platforms can significantly enhance oil production in cells, callus tissues, and whole plants. To combat plant diseases, they can rapidly identify effector proteins and validate interactions between effectors and resistance genes at high throughput. Overall, integrating synthetic biology with robotics will open new avenues for boosting crop productivity and combating global hunger.

Cucumber flower and fruit development & genetic improvement

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Flowers and fruits are the reproductive organs that directly affect the yield and product quality in cucumber. Auxin is another hormone besides ethylene that was found to promote female flower production in cucurbits over half century, but how auxin regulates sex determination remains mysterious. Here, we identified the auxin response factor 3 (CsARF3) promotes femaleness by directly stimulating the expression of meristem maintenance gene CsSTM, and repressing the activity of gynoecious gene CsWIP1. We further showed that auxin and ethylene exhibit a reciprocal relationship during sex determination, in which ethylene promotes carpel formation through auxin at the early stage of flower development, and then the auxin signaling in carpel enhances ethylene biosynthesis to inhibit stamen development. In addition, we found that the *Cucumis sativus* CLV3 (CsCLV3) promotes the nuclear translocation of the CLV receptor-associated Gα protein CsGPA1. CsGPA1 directly interacts with the nuclear-localized protein kinase Casein Kinase II α subunit (CK2α). CK2α negatively regulates the SAM size in a kinase-dependent manner and CsGPA1 promotes the kinase activity of CsCK2α2. CsGPA1 and CsCK2α2 act in the same pathway to regulate SAM size by inhibiting the expression of WUS. Therefore, our results provide important new insights into the nature of the CLV3 signaling pathway that leads to WUS repression in plants and promising target genes for crop breeding with high yield. Moreover, I will present the gene regulatory network contributing to the fruit length, fruit neck length and fruit length/diameter variations, and share the recent advance in genetic improvement in fruit appearance, functional components as well as shoot architecture in cucumber.

Fixing hybrid vigor in rice: achieving near-100% clonal seed production with normal seed set

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Apomixis—clonal reproduction through seeds—offers a transformative approach to agriculture by enabling the stable fixation of hybrid vigor and elite heterozygosity across generations. However, the practical implementation of synthetic apomixis has been constrained by the daunting challenge of achieving near-complete penetrance while preserving normal yield potential. In this study, through integrated transcriptomic analyses, we identified a rice sperm-specific transcription factor whose ectopic expression in egg cells effectively induces parthenogenesis and produces haploid progeny. When combined with clonal gametogenesis, this system achieves broadly deployable synthetic apomixis with near-100% penetrance: clonal seed production rates exceeding 99% across all tested hybrid rice cultivars, derived lines, and successive generations. Moreover, through screening a novel promoter with attenuated expression in egg cells, this strategy enables the efficient generation of apomictic hybrid lines that not only sustain near-100% clonal efficiency but also maintain seed yields comparable to conventional F1 hybrids. These findings establish a broadly applicable platform with universal near-complete penetrance for synthetic apomixis, achieving stable fixation of heterosis through clonal seeds and paving the way for the commercial deployment of self-perpetuating hybrid crops.

Key Words: Apomixis; Clonal seed; Parthenogenesis; Haploid; Heterosis; Rice

Establishment and application of plant circadian gene regulatory network reconstitution system

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Circadian rhythms are mainly generated by a gene regulatory network (GRN) constituted by transcription factors (TFs). Comparisons between plant and mammalian circadian clock GRNs suggest conservation of the network architecture rather than its components. Therefore, a rhythm-generating capacity is not restricted to canonical circadian clock GRNs. We found that although the circadian clock GRN was arrhythmic, circadian rhythms were maintained in refrigerated postharvest strawberries. Through systematic dual-luciferase assays and graph-theory-based network analysis, we discovered a noncanonical GRN pillared by five uncharacterized TFs. We developed a “three-module” heterologous reconstitution system and demonstrated the rhythm-generating ability of this GRN. Fruit-specific perturbation of this GRN led to enhanced susceptibility to *Botrytis cinerea*. Collectively, our study identified a noncanonical quasi-circadian GRN, realized the heterologous reconstitution of eukaryotic circadian GRNs for the first time, and demonstrated its function in immune regulation.

植物过氧化物酶体代谢工程和蛋白组成研究

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植物过氧化物酶体是承担脂肪酸β-氧化、光呼吸、ROS代谢及多种激素与次生代谢物合成的多功能细胞器，其蛋白全部经PTS1/PTS2靶向信号导入，是植物合成生物学的重要亚细胞底盘。本报告重点介绍过氧化物酶体蛋白组成研究：利用质谱蛋白组学编目拟南芥过氧化物酶体蛋白组，系统解码PTS1三肽及其上游辅助靶向信号，并开发深度学习预测工具DeepPTS1，实验验证了197个新的水稻过氧化物酶体蛋白，为蛋白预测与工程靶向提供"零件库"与"组装规则"；进而完整解析苯丙氨酸来源水杨酸（SA）生物合成新通路（Nature, 2025），揭示以过氧化物酶体CNL-BEBT为核心的跨区室合成机制，为作物抗病育种提供精准靶点。此外简要介绍过氧化物酶体代谢工程（重构β-氧化、光呼吸与ROS代谢，合成高值化合物）的进展与展望。

Rice root system architecture and drought response

Guoqiang Huang

In rice, the developmental plasticity of root ground tissue, characterized by multiple cortical cell layers, is a key adaptation to water scarcity. While auxin has been implicated in this process, the specific molecular players connecting this environmental cue to cortical patterning remained elusive. We demonstrate that auxin signaling directly activates the expression of SHORT-ROOT (OsSHR) genes via the key transcription factor OsARF5, to drive cortical cell layer formation under mild drought stress. This OsARF5-OsSHRs module directly translates fluctuating water availability into a programmed expansion of the root cortex. Our findings uncover a fundamental mechanistic framework for drought acclimation in a major cereal crop, highlighting how a single hormonal pathway orchestrates tissue-level architectural changes in response to environmental stress

Dissecting Metabolic Networks of Horticultural Plant Chassis for High-Value Secondary Metabolite Production

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Employing high-yielding plants as chassis for the biosynthesis of high-value metabolites represents one of the most prevalent research strategies in synthetic biology. Over the past two decades, our team and collaborators have utilized the globally renowned horticultural crop tomato as a plant chassis to successfully synthesize a wide spectrum of compounds in its fruits. Driven by the rapid advancement of vertical farming technologies, leafy vegetables have recently emerged as novel chassis candidates for plant synthetic biology. In this talk, I will present our latest advances in dissecting the metabolic pathways and regulatory networks of lettuce. Furthermore, I will discuss the advantages as well as the current challenges associated with employing lettuce as a chassis for synthetic biology applications in plants.

Key Words: Synthetic Biology, Plant Chassis, Lettuce, Metabolic Regulation

Biosynthetic pathways of bioactive compounds and evolutionary history of Apiaceous medicinal plants（伞形科药用植物中活性化合物的生物合成途径）

Li Wang

Evolution plays a magic role in driving plant biodiversity, which produces a profound chemical diversity when interacting with variable environments. Our lab focused on questions regarding DNA and chemical languages of medicinal plants. Specifically, we are fascinated with the following questions: 1) What is the origin and evolutionary path of medicinal plants? 2) How are bioactive compounds synthesized in plants? 3) Why do some plants produce one type (or high content) of secondary metabolites, while others not? Taking Apiaceae medicinal plants as study organisms, 1) we have revealed the homoploid hybrid speciation of Ligusticum chuanxiong and identified enzymes catalyzing the interconversion of phthalide compounds, one of which (butylphthalide; NBP) is the first line drug curing ischemic stroke; 2) we have dissected the complete biosynthetic pathway of furochromones in Saposhnikovia divaricate and traced the evolutionary history of two key enzymes involved in the pathway in Apiaceae, which explains the specifically high content of furochromones in S. divaricate; 3) we have explored the genetic and evolutionary underpinnings of furanocoumarin biosynthesis in Angelica.

A synthetic toxin–antidote gene drive overrides Mendelian inheritance in Arabidopsis

Wenfeng Qian

Synthetic gene drives, inspired by natural selfish genetic elements and transmitted to progeny at super-Mendelian (>50%) frequencies, present transformative potential for disseminating traits that benefit humans throughout wild populations, even facing potential fitness costs. Here we constructed a gene drive system in plants called CRISPR-Assisted Inheritance utilizing *NPG1* (*CAIN*), which uses a toxin–antidote mechanism in the male germline to override Mendelian inheritance. Specifically, a guide RNA–Cas9 cassette targets the essential *No Pollen Germination 1* (*NPG1*) gene, serving as the toxin to block pollen germination. A recoded, CRISPR-resistant copy of *NPG1* serves as the antidote, providing rescue only in pollen cells that carry the drive. To limit potential consequences of inadvertent release, we used self-pollinating *Arabidopsis thaliana* as a model. The drive demonstrated a robust 88–99% transmission rate over two successive generations, producing minimal resistance alleles that are unlikely to inhibit drive spread. Our study provides a strong basis for rapid genetic modification or suppression of outcrossing plant populations.

Biochar loaded *Bacillus paranthracis* YB-11 enhances cadmium detoxification effect in tobacco

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Owing to their exceptional growth-promoting effects, strong rhizosphere colonization ability, and environmental adaptability, Bacillus strains are the most commonly used growth-promoting bacteria to enhance soil fertility. However, the habitat of Bacillus in soil ecosystems is seriously threatened by heavy metal contamination. Biochar serves as an environmentally friendly carrier, providing a survival-facilitating microenvironment for bacteria. Specifically, biochar application is regarded as a promising eco-friendly strategy for improving the colonization efficiency of growth-promoting bacteria. Nevertheless, the roles and mechanisms by which biochar-immobilized Bacillus alleviate cadmium toxicity and promote crop growth have yet to be elucidated in depth. To address these gaps, in this study, *Bacillus paranthracis* strain YB-11 was screened as from the tobacco plant rhizosphere as a functional strain and then subject to 40 mg/kg cadmium stress with and without biochar co-application. The strain was inactivated under cadmium stress, whereas its survival rate was effectively improved by biochar addition. The detoxification mechanism of the combined biochar and Bacillus treatment was further verified by pot experiments. Compared with single treatments, the antioxidant capacity and photosynthetic performance of tobacco were significantly enhanced by the combined treatment, and cadmium accumulation in the tobacco leaves and roots was reduced by 49.26% and 48.76%, respectively. Moreover, the combined treatment improved soil available nutrients and enzyme activities to accelerate soil nutrient transformation. Furthermore, the rhizosphere microbial community was reshaped by the combined treatment, characterized by enrichment of cadmium-tolerant and nutrient-optimizing taxa, including Acidobacteriota, Pseudomonadota, Sphingomonas, and Acrophialophora. Metabolomic analysis demonstrated that the combined treatment regulated purine metabolism, lysine degradation, and flavonoid synthesis pathways, which in turn influenced the antioxidant system, photosynthesis, and soil microecology to inhibit cadmium uptake. These findings provide mechanistic insights into the regulation of tobacco cadmium stress responses and the synergistic interaction between biochar and Bacillus for enhancing contaminated farmland remediation efficiency.

Integrated microbiome, metabolome and physiological analysis of NaOH-modified reed carbon mitigates cadmium growth stress in tobacco by recruiting beneficial microorganisms and regulating flavonoid metabolism

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Soil Cd immobilization through biochar (BC) and modified biochar is an environmentally friendly and cost-effective strategy. The main objective of this study was to investigate the effect of NaOH-modified biochar (BC-OH) on tobacco under Cd stress compared with BC, and to systematically investigate its effect on tobacco growth and its mechanism of action in Cd-contaminated soil. The results showed that biochar alleviated tobacco Cd stress and modified biochar was the most effective compared to BC, and BC and BC-OH treatments improved the physiological indexes compared to Cd treatments. Meanwhile, Cd accumulation in leaves and roots was reduced by 66.67% and 60.71%, respectively. BC-OH was more effective in promoting plant growth and root development compared to BC, increasing plant height, stem diameter, leaf length, leaf width, leaf weight and root weight by 11.82%, 25.69%, 30.33%, 24.76%, 40.11% and 30.44%, respectively, compared to Cd. Additionally, photosynthesis was enhanced and antioxidant defenses were activated by BC and BC-OH, resulting in effective counteraction of Cd-induced oxidative stress. Microbial community analysis revealed that BC and BC-OH enriched beneficial soil microbes, including *Crenarchaeota*, *Acidobacteriota*, *Actinobacteria*, and *Chloroflexi*, while boosting nutrient availability. Metabolomic profiling further uncovered that BC-OH modulated critical pathways like phenylpropanoid and flavonoid biosynthesis, strengthening plant-microbe-soil interactions and improving Cd resistance. This study revealed that Cd phytotoxicity was synergistically mitigated through improved soil physicochemical properties, restructured microbial communities, and regulated key metabolic pathways by BC-OH, providing both theoretical foundations and technical support for heavy metal-contaminated soil remediation and fertilizer production.

Progress and Perspectives in Maize Breeding Technology

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To accelerate maize breeding efficiency and promote germplasm innovation, this study systematically reviews the latest progress of doubled haploid (DH) technology, haploid induction, gene editing and multi-technology coupled breeding in maize, and clarifies technical bottlenecks and development directions. With DH technology as the core, the whole process of haploid induction, identification, chromosome doubling and pure line application was integrated. The functions of key genes such as MTL, DMP and CenH3 were analyzed, the induction methods including anther culture, in planta inducer lines and interspecific crosses were compared, and the synergistic applications of DH with genomic selection (GS), haploid-inducer mediated genome editing (HI-Edit) and one-step cytoplasmic male sterility (One-step CMS) were discussed. Conventional breeding requires 6–8 generations for homozygosity, while DH technology can obtain 100% homozygous DH lines in only 2 generations, greatly shortening the breeding cycle. The haploid induction rate in maize has increased from 0.1%–0.3% to over 6.7%, and key gene editing significantly improves induction efficiency. The haploid identification and doubling systems are increasingly engineered, DH+GS synergistically improves genetic gain, HI-Edit achieves rapid directional improvement of traits, and apomixis provides a new pathway for clonal fixation of hybrids. At present, there are still problems such as the trade-off between induction efficiency and seed setting rate, incomplete induction mechanism, and high cost of large-scale application. Breeding technology has become the core technology of modern maize breeding. The dissection and editing of key genes promote the continuous breakthrough of induction efficiency. The coupling of multiple technologies will realize precise and efficient maize breeding, providing important support for maize germplasm innovation and variety upgrading.

Key Words: maize, doubled haploid, breeding technology, genome editing

Chromatin-based regulation mediates trade-off between tiller outgrowth and drought responses in wheat（小麦染色质平衡分蘖发育和干旱抗性的机制）

Ning Zhang

Tillering is a fundamental trait of wheat plant architecture that determines population structure and, consequently grain yield. Reductions in tiller number caused by drought have a significant impact on wheat productivity and represent a major factor contributing to yield loss. However, due to the large and complex AABBDD hexaploid genome of wheat, the molecular mechanisms that coordinate tiller development with drought responses remain largely unclear. To uncover the regulatory pathways underlying this coordination and to identify key genes that balance tiller growth and drought resistance, we performed integrated ATAC-seq and RNA-seq analyses on wheat tiller buds subjected to drought stress. Our results show that drought induces a global increase in chromatin accessibility in tiller buds, with particularly changes in intergenic and distal chromatin regions. These distal accessible chromatin regions likely function as potential enhancers and play critical roles in mediating drought-induced transcriptional regulation. Further motif enrichment and TF–GO network analyses identified a subgenome-diverged MYB-related transcription factor that represses tiller outgrowth while promoting drought tolerance, which we named DROUGHT RESPONSIVE GENE 7 (DRG7). This discovery provides important insights into the molecular regulatory network regulating wheat tiller bud responses under drought stress. Overall, this study systematically elucidates the chromatin-based regulatory mechanisms governing wheat tiller under drought, identifies key drought-responsive genes and regulatory elements, and offers a molecular foundation for improving both tiller development and drought resilience in wheat.

What defines a plant's nose? Volatile perception and plant-plant interactions in maize（玉米中的挥发性物质感知与植物间相互作用）

Lei Wang

王磊

Plants respond to herbivore-induced volatiles from attacked neighbors by upregulating their defenses. How plants perceive these volatiles is unclear. Here, we identify two G-type lectin receptor kinases that function as green leaf volatile receptors. Using transcriptional screens and gene editing, we identify the maize “Hexenyl acetate insensitive 1” (Haci1) mutant, which shows reduced responsiveness specifically to herbivore-induced green leaf volatiles. HACI1 localizes to the plasma membrane. Its extracellular domain shows strong, specific binding to (Z)-3-hexenyl acetate and (Z)-3-hexen-1-ol. Genomic analyses uncover a functional paralogue, Haci2, which is conserved across different grasses. Importantly, haci1/2 double mutants are insensitive to green leaf volatiles and are no longer able to mount defenses in response to volatiles from herbivore-attacked neighbors. Thus, extracellular receptors mediate plant stress volatile perception.

Integrated Phytochemical and Biological Evaluation of *Abies webbiana* Lindl. for Potential Applications in Type 2 Diabetes Mellitus and Infectious Diseases

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Abies webbiana Lindl. (Pinaceae), commonly known as Talispatra, is an alpine medicinal plant extensively used in traditional healthcare systems for managing respiratory, infectious, and metabolic disorders. The present study investigated the phytochemical composition and evaluated the antioxidant, antimicrobial, anti-biofilm, and potential antidiabetic properties of the methanolic extract of *A. webbiana* using phytochemical screening, Fourier Transform Infrared Spectroscopy (FTIR), and Gas Chromatography-Mass Spectrometry (GC-MS) analyses. Preliminary phytochemical screening revealed the presence of phenolics, terpenoids, alkaloids, tannins, steroids, and saponins. FTIR analysis demonstrated characteristic absorption bands at 3433.29 cm^{-1} (O–H stretching of phenols and alcohols), 2997.38 and 2914.44 cm^{-1} (aliphatic C–H stretching), 1660.71 cm^{-1} (C=O stretching), 1429.25 cm^{-1} (aromatic C=C vibration), and 1024.20 cm^{-1} (C–O stretching), indicating the presence of diverse bioactive functional groups in the extracts. GC-MS profiling identified several bioactive phytoconstituents, including Maltol, Catechol, Methyl salicylate, Bornyl acetate, α-Bisabolol, Neophytadiene, Phytol, n-Hexadecanoic acid, Octadecanoic acid, and Vitamin E. The methanolic extract exhibited concentration-dependent antioxidant activity, achieving 36.8% DPPH radical scavenging at 50 µL concentration. Antimicrobial evaluation demonstrated broad-spectrum antibacterial activity, with inhibition zones of 20 mm against *Escherichia coli* and 19 mm against *Proteus mirabilis*. Furthermore, the extract exhibited significant antibiofilm activity, with a maximum inhibition of 57.0% against *Enterobacter aerogenes*. Several identified phytocompounds, particularly phenolic and terpenoid constituents such as Catechol, Phytol, α-bisabolol, and Vitamin E, have been reported to possess antioxidant and glucose-regulating properties that may contribute to the prevention and management of Type 2 Diabetes Mellitus (T2DM) through the reduction of oxidative stress and improvement of insulin sensitivity. The combined FTIR and GC-MS findings suggest that these bioactive

metabolites may be responsible for the observed activities. Overall, this study highlights the therapeutic potential of *A. webbiana* as a natural source of antioxidants, antimicrobials, anti-biofilm agents, and promising antidiabetic compounds, providing scientific support for its traditional medicinal applications and future development as a phytotherapeutic candidate for T2DM management.

Key Words: *Abies webbiana*, FTIR, GC–MS, phytochemicals, antioxidant activity, antimicrobial activity, anti-biofilm activity, phenolic compounds, terpenoids.

Therapeutic Potential of Nicotinamide and ABT263 in Alcohol-Associated Liver Disease through Targeting Cellular Senescence

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Alcohol-associated liver disease (ALD) is a major cause of liver-related morbidity and mortality, yet clinically effective therapies for ALD remain lacking. Here, we demonstrate that alcohol intake and its metabolite, acetaldehyde (ACH), induce senescence in the liver and liver cells, respectively. To assess the therapeutic potential of targeting liver senescence in ALD, we treated ALD-affected mice with the senolytic compound ABT263 and the senomorphic NAD^+ precursor, nicotinamide (NAM). The results show that ABT263 effectively clears senescent hepatocytes and stellate cells, reduces liver triglyceride (TG), but increases plasma alanine aminotransferase (ALT) and TG levels. Conversely, NAM efficiently suppresses senescence and the senescence-associated secretory phenotype (SASP), protecting the liver from alcohol-induced injury in ALD mice. RNA-sequencing analysis revealed that ABT263 treatment downregulated genes involved in adipogenesis while activating the complement pathway. In contrast, NAM upregulated metabolism-related genes, such as *Sirt1*, and downregulated DNA damage marker genes, including *Rec8* and *E2f1*, in the liver. These findings suggest that cellular senescence plays a critical role in alcohol-induced liver injury. Compared to senescent cell clearance by ABT263, suppressing senescence and SASP by NAM may provide a safer and more effective therapeutic approach for ALD.

Key Words: acetaldehyde; alcohol-associated liver disease; cellular senescence; senolytic; senomorphic

Transkingdom Genetic Circuits for Sensing and Programming Root Exudation

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Root exudation delivers plant metabolites into soil, where they shape microbial communities and carbon cycling. Standard exudate analyses quantify bulk carbon release from roots, but obscure the spatial origin and rhizosphere influence of individual compounds. We addressed this gap with a transkingdom engineering strategy that pairs bacterial biosensors with plant synthetic circuits, using both to sense and to program exudation with spatial resolution. On the sensing side, we engineered sfGFP-based, sucrose-responsive gene circuits in the root-associating bacterium *Pseudomonas putida* KT2440 for live imaging of exudate concentrations directly on the colonized root surface. This revealed spatially patterned sucrose release that tracked source–sink physiology across diverse plant species. On the programming side, we built synthetic gene circuits in *Arabidopsis thaliana* that tune sucrose export from root tissue. Using the bacterial sensors to phenotype these engineered lines, we uncovered design rules for graded exudate release and showed how exudate levels reshape microbial community assembly in the rhizosphere. Together, this work establishes transkingdom genetic circuit design as a general strategy for reading and rewriting plant–environment carbon exchange, with broad applicability beyond sucrose to other exudate compounds and plant–microbe systems.

Key Words: root exudate, biosensor, sink–source physiology, synthetic biology

CRISPR/Cas9 Editing of cis-Regulatory Elements Reveals the Regulatory Architecture of Wheat *Ppd-1* and Accelerates Heading Time

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Precise modification of cis-regulatory elements has emerged as a promising strategy for crop improvement because it enables fine-tuning of gene expression without disrupting gene function. In bread wheat, heading time is primarily controlled by the Photoperiod-1 (Ppd-1) genes, whose known photoperiod-insensitive alleles carry large promoter rearrangements associated with altered expression patterns and accelerated flowering. However, the contribution of individual promoter elements to Ppd-1 regulation remains poorly understood. In this study, we used CRISPR/Cas9-mediated promoter editing to accelerate heading in the late-flowering spring common wheat line Velut and to investigate the regulatory role of putative transcription factor binding sites in the Ppd-D1 and Ppd-B1 promoters. Two guide RNAs were designed to target the promoter region containing two predicted binding sites for the transcriptional repressor CCA1 HIKING EXPEDITION (CHE). Following biolistic transformation of immature embryo-derived callus, 133 T0 plants were regenerated. Targeted mutations were identified in 46 plants and included single-nucleotide substitutions, small insertions and deletions, and large deletions of 219–266 bp spanning the core regulatory region and removed the core promoter region containing both CHE binding sites. Twenty edited T0 plants lacked detectable vector integration, indicating that targeted mutations could be generated through transient plasmid expression. Diurnal expression analysis of T2 homozygous lines under short-day conditions showed that promoter mutations altered the expression patterns of both Ppd-D1 and Ppd-B1. Large deletions encompassing CHE binding sites shifted expression towards dawn and nighttime, whereas smaller insertions or deletions adjacent to predicted cis-regulatory motifs also altered the timing of transcription. The diversity of expression profiles observed among different promoter alleles indicates that Ppd-1 transcription is controlled by the coordinated action of multiple cis-elements rather than by a single regulatory motif. Plants carrying promoter mutations headed significantly earlier than

wild-type Velut. Under experimental field conditions with long day, homozygous T2 lines headed 2.5–4.5 days earlier than the control. The strongest effects were generally associated with mutations affecting the core promoter region containing CHE binding sites. Most edited lines showed no reduction in agronomical important traits, indicating that earlier heading could be achieved without an obvious penalty for productivity. Our results demonstrate that promoter editing represents an effective strategy for fine-tuning flowering-time genes wheat. Beyond generating valuable breeding material adapted to regions with short growing seasons, the collection of promoter-edited Ppd-1 alleles provides a unique experimental resource for dissecting the cis-regulatory mechanisms controlling photoperiod response in wheat. This work highlights the potential of regulatory genome editing as both a functional genomics approach and a practical tool for crop improvement.

Key Words: common wheat, heading time, genome editing, promoter editing, photoperiod sensitivity, Ppd-1

Growth regulator genes TaGRF4-GIF1 enhances transformation and genome editing efficiency in recalcitrant barley cultivars

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Barley (*Hordeum vulgare* L.) is one of the most important cereal crops worldwide, yet genetic improvement of elite cultivars by biotechnological approaches remains hindered by their recalcitrance to genetic transformation and regeneration *in viro*. The *TaGRF4-GIF1* morphogenic regulator, a chimeric protein combining the GROWTH-REGULATING FACTOR 4 and GRF-INTERACTING FACTOR 1 domains, has been shown to enhance transformation efficiency in wheat and other plants. However, its application to biolistic transformation of non-model recalcitrant barley cultivars has not been systematically evaluated. The present study aimed to assess the capacity of the wheat *TaGRF4–GIF1* morphogenic chimera to improve regeneration and transformation outcomes in three non-model, poorly responsive barley cultivars when delivered by biolistics, and to test whether this system can be coupled with CRISPR/Cas9-mediated genome editing. As a target, we edited the breeding-relevant barley *NUD* gene, which controls the naked/hulled grain phenotype and has previously been modified only in the model cultivar Golden Promise. In addition, the hull-less character carries practical agricultural value, as it improves feed quality and reduces processing costs. Immature embryo-derived calli of three recalcitrant to *Agrobacterium*-mediated transformation barley cultivars (Tselinny 5, Aley, G-23055) were bombarded with the JD633 binary vector carrying *TaGRF4-GIF1* under the maize UBIQUITIN promoter and the *hptII* selectable marker, together with a CRISPR/Cas9 construct targeting the *NUD* locus. A control construct (L2) lacking morphogenic regulators was used in parallel. Using vectors JD633 and L2, we obtained two populations of 27 and 62 T_0 plants, respectively. Notably, stable independent transformants (14 T_0) were exclusively generated in experiments utilizing the JD633 vector in all three cultivars with transformation efficiencies of 2.5–5.0%, whereas no confirmed transformation events were obtained in the experiment with the control construct. Sequencing analysis identified 5 plants of the Aley, 3 plants of the Tselinny 5

and 6 plants of the G-23035 cultivars exhibiting various mono- and biallelic mutations of *NUD* gene. Molecular screening revealed the presence of transgene-free but carrying edited *NUD* alleles plants in the T_0 generation, likely arising from transient *Cas9* expression. The edited alleles were stably transmitted to the T_1 generation, and the hull-less phenotype cosegregated with the editing genotype. T_1 mutants lacking detectable vector were recovered from all three cultivars. Thus, the *TaGRF4-GIF1* morphogenic regulator enables biolistic transformation of recalcitrant barley cultivars that are otherwise unresponsive to standard protocols. In conclusion, this study demonstrates a practical transformation and editing platform for non-model barley germplasm and contributes to the broader implementation of morphogenic regulator-assisted genome editing in recalcitrant cereals.
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Key Words: barley, biolistic transformation, TaGRF4-GIF1, morphogenic regulator, CRISPR/Cas9, genome editing

Harnessing the power of herbaria and low coverage whole genome sequencing to reconstruct the invasion history of a damaging invasive grass

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Reconstructing invasion histories is critical for understanding the genetic and ecological factors that determine the success or failure of biological invasions and for designing effective management strategies. In the invasive range, processes such as founder effects, admixture, range expansion, and natural selection often interact, complicating the reconstruction of these complex scenarios from modern genomes. However, these

dynamics can be reconstructed more precisely through direct observation of historical samples collected throughout the invasion process. Here, we studied the invasion history of Japanese stiltgrass (*Microstegium vimineum*) in the eastern United States. To this end, we analyzed 431 low-coverage whole-genome sequences from contemporary and historical samples in the invasive range of the eastern United States, as well as from the native range across eastern Asia. We observed three main genetic clusters in the invasive range, one in the south (latitude < 38.5°) and two in the north (latitude > 38.5°), matching the distribution of an important trait: presence/absence of awns. Pairwise F_{ST} between invasive and native populations and *locator* (a machine-learning approach) both suggest that genetic divergence in the invasive range is due to multiple introductions, though the geographic source of these introductions remains unclear. Within groups, we observed little to no differentiation over time (all temporal $F_{ST} < 0.02$), indicating both genetic continuity after initial introductions and limited gene flow between groups. On the other hand, genetic divergence between north and south groups increased over time ($F_{ST} = 0.16$, 0.23, and 0.35 for comparisons before 1960, after 1960, and contemporary, respectively), suggesting that natural selection and/or genetic drift post-introduction contributed to current genetic divergence between invasive groups. We then scanned the genome for temporal selective sweeps (observed as extreme reductions in genetic diversity over time) in the south and north groups separately. Genes within temporal selective sweeps significantly overlap between groups, suggesting that natural selection contributed to rapid evolution in the invasive range. Our results highlight the importance of incorporating historical samples to reconstruct invasion histories and elucidate the genetic mechanisms underlying successful biological invasions.

Rewriting wheat karyotypes through centromere-targeted chromosome engineering

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Engineering karyotypes could expand the genetic and breeding potential of crops, but restructuring gigabase-scale polyploid genomes remains challenging. Here, we developed centromere editing–mediated chromosomal variation (CECV), a strategy employing CRISPR-Cas9 to target abundant centromeric retrotransposons in hexaploid wheat. CECV efficiently induces simultaneous chromosome cleavage across the genome, generating diverse karyotypic variants and reconfiguring up to 11 chromosomes in one generation. Notably, it produced widespread reciprocal translocations, with one line carrying six events involving seven chromosomes. Newly formed translocation chromosomes undergo centromere remodeling, enabling their relatively stable maintenance and heritable transmission. Moreover, balanced translocations impose minimal transcriptional perturbation and maintaining normal growth. These results establish centromeres as effective sites for chromosome engineering breeding and provide a scalable framework for karyotype redesign in polyploid crops.

对核型进行工程化改造，有望释放作物的遗传与育种潜力，但要在 Gb 级多倍体基因组中实现重构仍非易事。为此，我们建立了着丝粒编辑介导的染色体变异（CECV）策略：利用 CRISPR-Cas9 靶向六倍体小麦中大量存在的着丝粒反转录转座子。CECV 可在全基因组范围内高效诱导染色体同步切割，产生丰富的核型变异，并在一个世代内重构多达 11 条染色体。尤其值得注意的是，该策略诱导了广泛的相互易位，其中有一个株系发生了 6 次易位事件，涉及 7 条染色体。新形成的易位染色体会经历着丝粒重塑，因而能够相对稳定地保留下来并传递给后代。同时，平衡易位对基因转录的干扰很小，植株也能保持正常生长。这些结果表明，着丝粒可作为染色体工程育种的有效靶点，也为多倍体作物的核型重新设计提供了可扩展的技术框架。

Deciphering the functions of the RPK2 receptor-like kinase family in maize meristem regulation and immunity for crop improvement

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Optimizing developmental traits, including maize ear and plant architecture, while enhancing disease resistance are pivotal for increasing maize yield. Cell-surface receptor kinases are key switches for development clue and immune signal recognition. However, receptor kinases that coordinate these processes remain poorly understood in maize. Here, we characterize three members of the maize RECEPTOR-LIKE PROTEIN KINASE 2 (RPK2) family: RPK2a, RPK2b and RPK2c, and identified them as candidate regulators of both development and immunity. The *rpk2a* single mutant showed reduced the plant height, enlarged meristems, and increased kernel row number. These phenotypes were further enhanced in the *rpk2a; rpk2b* double mutants, indicating that they redundantly regulate shoot and inflorescence architecture. The *rpk2a; rpk2b; rpk2c* triple mutants, however, showed severe embryo lethality. We further show that ZmRPK2a is required for ZmCLE7 and ZmFCP1 peptide signaling and interacts genetically with the maize CLV–WUS network. In addition, *Zmrpk2a; Zmrpk2b* double mutants showed increased expression of pathogenesis-related genes and elevated levels of defense hormones such as salicylic acid and jasmonic acid, suggesting that they also play a role in immunity. Proteomic analyses of ZmRPK2a-GFP complexes identified several immune related proteins including the flagellin receptor FLS2 and Gβ subunit proteins (ZmGB1). Protein interaction assays and genetic analysis further support that ZmRPK2a might function with ZmGB1 to regulate immune response. Together, these findings identify ZmRPK2 family members play a dual role in meristem homeostasis and immune signaling and provides new genetic resources for breeding high-yielding and disease resistant maize.

优化玉米株型和穗部构型并增强抗病性，是提高玉米产量的重要途径。细胞表面受体激酶是调控植物发育和免疫信号的关键因子。然而，在玉米中，能够协调这两个过程的受体激酶仍缺乏深入研究。本研究对玉米受体样蛋白激酶 2（RECEPTOR-LIKE PROTEIN KINASE 2，RPK2）家族的三个成员 ZmRPK2a、ZmRPK2b 和 ZmRPK2c 进行了功能鉴定，并将其确定为可能同时调控发育和免疫的候选因子。*Zmrpk2a* 单突变体表现为株高降低、分生组织增大和穗行数增加；这些表型在 *Zmrpk2a;Zmrpk2b* 双突变体中进一步增强，表明两个基因在调控茎部和花序构型方

面具有功能冗余。相比之下，Zm*rpk2a; Zmrpk2b; Zmrpk2c* 三突变体表现出胚胎致死。进一步研究表明，ZmRPK2a 是 ZmCLE7 和 ZmFCP1 小肽信号传导所必需的，并与玉米 CLV–WUS 调控网络存在遗传互作。此外，Zm*rpk2a; Zmrpk2b* 双突变体中抗病相关基因的表达升高，防御激素水杨酸和茉莉酸的含量增加，表明 ZmRPK2 家族也参与免疫调控。对 ZmRPK2a–GFP 复合物的蛋白质组学分析鉴定出多种免疫相关蛋白，包括鞭毛蛋白受体 FLS2 和 Gβ 亚基 ZmGB1。蛋白互作实验和遗传分析进一步支持 ZmRPK2a 与 ZmGB1 共同调控免疫反应。综上，本研究表明 ZmRPK2 家族协同调控了分生组织发育与免疫反应，并为培育高产、抗病玉米提供了新的新视角和新候选位点。