

제57회 한국식물분류학회 정기총회 및 국제학술대회

The 57th Annual Meeting and International Symposium of the Korean Society of Plant Taxonomists (KSPT)

- ◆ **일자 Date:** 2026년 2월 5일(목) ~ 6일(금)
- ◆ **장소 Venue:** 한림대학교 캠퍼스라이프센터 비전홀(4층)
Campus Life Center, Vision Hall (4th floor), Hallym University, Chuncheon, Korea

2월 5일(목)

등록 및 총회

10:30~ 학술대회 등록 Registration

11:00~12:00 총회 General Meeting

12:00~13:00 점심식사 Lunch

개회식 및 시상식

13:00~14:00 개회식, 죽파식물분류학상 시상식, 우수논문 시상식

Opening Ceremony, KSPT Jukpa Award and Best Paper Awards Ceremony

I. International Symposium – Plant Taxonomy in a Changing World

Session 1.

Chair: Sangtae Kim (Sungshin Women's Univ, Korea)

14:00~14:40

Daniel Park (Korea University, Korea)

Herbaria and global change

14:40~15:20

Yu-Hsin Tseng (National Chung Hsing Univ., Taiwan)

Past, present, and future of *Orobanche coerulescens* in Taiwan: insights from evolutionary history and population genomics of an altitudinally disjunct species

15:20~16:00

Bin-Bin Liu (Institute of Botany, Chinese Academy of Sciences, China)

Ortho2Web: a new workflow for investigating reticulate evolutionary mechanisms

16:00~16:15 Coffee Break

Session 2.

Chair: Insu Choi (Hannam Univ., Korea)

16:15~16:55

Atzuko Takano (Univ. of Hyogo and Museum of Nature and Human Activities, Hyogo, Japan)

Plant taxonomy and artificial intelligence

16:55~17:35

Martin Lysak (Masaryk Univ., Czech Republic)

Genome evolution in crucifers: patterns and underlying principles

II. 죽파식물분류학상 수상 특별강연

Special talk: 2026 KSPT Jukpa Award Awardee

Chair: Kyungsik Cheon (Sangji Univ.)

17:35~18:05

최혁재 Hyeok-Jae Choi (Changwon National Univ.)

Delimiting species boundaries in *Hosta* section *Capitatae* (Asparagaceae) using MIG-seq and morphological analyses: taxonomic revision with new taxa from Korea and Japan

2월 6일(금)

III. 일반 학술발표 General presentation

Session 1.

VISION HALL, CLV 4th FLOOR

Chair: Kyoungsoo Choi (Kyungpook Nat. Univ.)

09:00~09:15

Sang-jin Han^P(Kangwon Nat. Univ.), Ki-Oug Yoo

O-01. A taxonomic study of Korean *Hylodesmum*

09:15~09:30

Jun-Ho Song (Chungbuk Nat. Univ.)^P, Kyeonghee Kim, Seung Mok Ryu, Inkyu Park

O-02. Integrative taxonomy of the Korean genus *Peucedanum* L.

09:30~09:45

Hyeonjin Kim (Chungnam Nat. Univ.)^P, Bokyung Choi, Tae-Soo Jang

O-03. Species delimitation of *Veratrum* (Melanthiaceae) in Korea and Japan: insights from micromorphological, molecular and cytogenetic analyses

09:45~10:00

Hye One Kim (Gachon Univ.)^P, Joo-Hwan Kim

O-04. Molecular phylogeny and biogeography of subfamily Medeoloideae (Liliaceae): Insights from East Asia-North America disjunct distribution

10:00~10:15

Yu Gyeom Kim (Gachon Univ.)^P, Hee-Young Gil, Joo-Hwan Kim

O-05. The evolutionary origin of *Erythronium* L. based on molecular phylogeny and historical biogeography

Session 2.

CLC 1ST FLOOR LOBBY

10:15~11:00

휴식, 포스터 발표 Coffee break and Poster Session

Session 3.

VISION HALL, 4th FLOOR

Chair: Jung-Hyun Lee (Chonnam Nat. Univ.)

11:00~11:15

Iseon Kim (Sungkyunkwan Univ.)^P, Myong-Suk Cho, Ji-Hyeon Jeon, Yoon-Seul Choi, Gyu Eun Kim, Chae Young Lee, Hyuk-Jin Kim, Hee-Young Gil, Seung-Chul Kim

O-06. Genetic diversity and population structure of *Styrax obassia* (Styracaceae) revealed by genome-wide genetic variations

11:15~11:30

Valner Matheus Milanezi Jordão^P

(Programa de Pós-Graduação em Botânica, Escola Nacional de Botânica Tropical, Instituto de Pesquisa Jardim Botânico do Rio de Janeiro, Brazil)^P

O-07. From “Flora Brasiliensis” to flora and funga of Brazil online: towards fully monographing the species-rich genus *Machaerium*

11:30~11:45

Young-Jong Jang (Chonnam Nat. Univ.)^P, Eun-Kyeong Han, Jung-Hyun Lee

O-08. Subgenomic composition underlies features of clonal lineage structure in sporophytic apomictic system: new insights from the warm-temperate shrubs *Damnacanthus indicus* and *D. major*

11:45~12:00

Sang Hee Park (Chungbuk Nat. Univ.)^P, Hyoung Tae Kim, Jung Sung Kim

O-09. An Integrative Assessment of the Korean Hymenophyllaceae and Aspleniaceae including their cryptic species

12:00~12:15

Dwiki Prasetya (Daegu Univ.)^P, Kyong-Sook Chung, and Hyosig Won

O-10. Ecological and evolutionary study on the Korean *Siderostictae* group of *Carex* (Cyperaceae)

12:15~12:30

우수논문발표 & 우수포스터 시상식 Best Presentation & Poster Awards

폐회 Closing

포스터 발표 목록

(P1: Floristic study, P2: Taxonomy, P3: Phylogeny and Genomics)

P1-01	Forecasting the suitable habitat and ecological effects of <i>Rheum nanum</i> (Polygonaceae) in Mongolia under climate change	Zagarjav Tsegmed
P1-02	자월도, 승봉도, 대·소이작도(인천광역시 옹진군 자월면)의 식물상	나누리
P1-03	Categorization of alien plants in the Republic of Korea using a biological invasion framework and their characteristics	EunSuKang
P1-04	A checklist for the vascular plants of BANGLADESH	Md. Salah Uddin
P1-05	국내 자생 국화속(<i>Chrysanthemum</i> L.)의 화분 염성 비교	백승훈
P1-06	오대산 일대의 산벚나무(<i>Prunus sargentii</i> Rehder) 분포 특성	김유미
P1-07	희귀식물의 국가적색목록 평가: 송양나무, 낙동나사말, 진주고추나무, 꼬인용담, 좁은잎사위질빵	나혜련
P1-08	춘천시 도시림인 봉의산, 안마산의 식물상 비교	이영철
P1-09	아고산대 전나무속 2종(구상나무, 분비나무)의 고사 현황과 지형적 요인	김진원
P1-10	설악산국립공원 기후변화 민감종(고산식물) 분포정보 구축 및 취약성 평가 연구	박승빈
P1-11	덕유산국립공원 관속식물의 다양성과 보전방안	소순구
P1-12	국립공원 특별보호구역 식물서식지의 지정·관리 현황과 보전 가치	신수경
P1-13	New record of <i>Henckelia mishmiensis</i> (Gesneriaceae) from Kachin State, Northern Myanmar	Eui-Kwon Jung
P2-01	국내 <i>Triglochin maritima</i> L. complex에 대한 형태학적·세포학적 분석 및 <i>Triglochin asiatica</i> (Kitag.) Á.Löve & D.Löve의 분류학적 재평가	Tae-Weon Kim
P2-02	A study of the external morphology and sexual system of <i>Mercurialis leiocarpa</i> (Euphorbiaceae)	Yujin Jeon
P2-03	Comparative leaf micromorphology, palynology, and ITS sequence variation in <i>Arisaema thunbergii</i> subsp. <i>geomundoense</i> and <i>A. thunbergii</i> subsp. <i>thunbergii</i> (Araceae)	Yeonchan Kang
P2-04	AI-powered automated identification of riparian invasive alien plants on the Korean peninsula using citizen science data	Hyeonji Moon
P2-05	한국산 산사나무(<i>Crataegus pinnatifida</i>)의 분류학적 연구	WonGyun Yim
P2-06	Taxonomic revision of Korean <i>Salix</i> section <i>Subalbae</i> evidenced by morphological and plastome phylogenetic analyses	Young Moon Kim
P2-07	New insights into <i>Oxytropis</i> (Fabaceae) diversity in Mongolia: description of a new species	Dariganga Munkhulga
P2-08	Improving the current knowledge of <i>Astragalus</i> species (Fabaceae) in Kazakhstan, central Asia based on phylogenetic relationship and morphological notes	Dariganga Munkhulga
P2-09	우리나라 식물명 검증을 위한 초기 식물문헌 분석: 『조선식물향명집』	장주은
P2-10	자생 꿀풀과 덩굴광대수염(<i>Glechoma grandis</i>) 분포 보고	장주은
P2-11	Report of the introduced plant <i>Angelica pubescens</i> Maxim. in Korea	Eun Su Kang

P2-12	New generic classification for Korean <i>Peucedanum</i> L. (Apiaceae) species based on deep phylogenomic study	Kyeonghee Kim
P2-13	Comparative seed morphology and surface micromorphological characters of ten <i>Rhododendron</i> species	Yeon-Ji Lee
P2-14	<i>Cirsium vlassovianum</i> Fisch. ex DC. (흰잎영경귀)의 실체	김성현
P2-15	등골나물속(<i>Eupatorium</i>)의 외부 형태학적 및 분자계통학적 연구	김영현
P2-16	특성조사요령(TG) 제·개정을 위한 목분류 특성조사: 소나무, 다래, 명석딸기, 밤나무	안세문
P2-17	한국산 자작나무속(<i>Betula</i> L.) 열매 형태에 의한 분류학적 연구	김태웅
P2-18	도서·연안에 분포하는 비름과 17종의 비교해부학적 연구: 적응 형질과 연속형성층을 중심으로	한세희
P2-19	국내 분포 개자리속(<i>Medicago</i> L.) 및 토끼풀속(<i>Trifolium</i> L.) 종자의 형태학적 분류	조민수
P2-20	Comparative seed micromorphology of Euphorbiaceae in Korea and its taxonomic significance	Hyeong Jun Jo
P2-21	Spore morphological study of Korean island and coastal Lycophytes and Pteridophytes (II)	Min-Ju Park
P2-22	Sequence characteristics of Korean chestnut trees (<i>Castanea</i> , Fagaceae)	Hyosig Won
P2-23	미기록종 꼭두선이과 신안백정화(<i>Serissa serissoides</i> (DC.) Druce) 분포 보고	박진희
P3-01	Plastid genome characterization of the African endemic legume <i>Humularia</i>	Valner Jordao
P3-02	Genome skimming provides phylogenetic insights into the taxonomic treatment of a Korean population of <i>Leuzea chinensis</i> (<i>Cardueae</i> : Asteraceae)	Juhyun Park
P3-03	Chloroplast genome sequencing of three <i>Viola</i> species and comparative plastome analysis within <i>Viola</i> subsect. <i>Rostratae</i> (Violaceae)	Ah-reum Go
P3-04	백서향나무 종복합체의 분자계통학적 연구	김윤수
P3-05	Analysis of genetic diversity among populations of <i>Menyanthes trifoliata</i> using SSR markers	Hye-Rin Kim
P3-06	Phylogenetic relationships of the Korean <i>Angelica</i> (Apiaceae) inferred from the complete chloroplast genome	Heewon Ji
P3-07	Phylogenetic incongruence and hybrid origin of <i>Spiraea trichocarpa</i> Nakai (Rosaceae) revealed by transcriptome and plastome data	Jong-Soo Kang
P3-08	Chloroplast genome comparison, phylogeny, and molecular evolution of five endemic <i>Potentilla</i> (Rosaceae) species in Mongolia	Nudkhuu Nyamgerel
P3-09	한국산 진고사리속(개고사리과) 외잎진고사리의 기원 분석	구본석
P3-10	Plastid genome based phylogenetic analysis and identification of molecular markers for cultivated taro (<i>Colocasia esculenta</i>) in Korea	Su-Jang Kim
P3-11	Genetic structure and the potential for cryptic divergence in the Ulleung Island population of <i>Viburnum furcatum</i> (Adoxaceae)	Yun-Gyeong Choi
P3-12	A population genetic study of <i>Lysimachia acroadenia</i> (Primulaceae) from Korea and Japan	Junhyun Hur1
P3-13	Is there <i>Suaeda heteroptera</i> in Korea? A molecular phylogenetic analysis suggests the hybrid origin of Korean <i>S. heteroptera</i> between <i>S. maritima</i> and <i>S. heteroptera</i>	Dohyeon Kwag

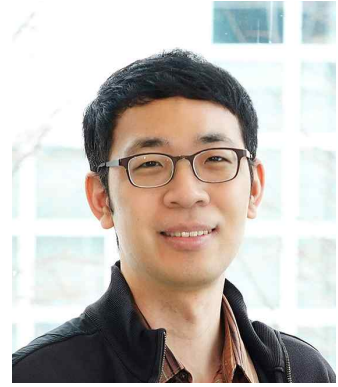
P3-14	Complete chloroplast genome of <i>Solanum carolinense</i> (Solanaceae), an invasive plant in Korea	Hye Been Kim
P3-15	Chloroplast genome assembly and phylogenetic analysis of two Korean endemic plants: <i>Inula minipetala</i> and <i>Semiaquilegia quelpaertensis</i>	Hye Been Kim
P3-16	The complete chloroplast genome of <i>Lamium purpureum</i> var. <i>purpureum</i> (Lamiaceae) and phylogenetic analysis	Yujin Jeon
P3-17	Chloroplast genome assembly and analysis of <i>Richardia brasiliensis</i> (Rubiaceae,tribe Spermacoceae)	Eun Su Kang
P3-18	Genetic diversity patterns of <i>Rhaphiolepis indica</i> var. <i>umbellata</i> in Korea and China: implications for restoration management	Ye-Rim Choi
P3-19	Draft genome assembly and population genetic structure of <i>Euonymus japonicus</i> Thunb.: implications for coastal forest restoration	Tae-Hee Kim
P3-20	Comparative genetic structure of two Korean <i>Sorbus</i> species: <i>S. commixta</i> Hedl. and <i>S. ulleungensis</i> Chin S. Chang	Hee-Joo Choi
P3-21	The complete plastid genome of Korean endemic <i>Aster danyangensis</i> J. Y. Kim & G. Y. Chung (Asteraceae): comparative genomic and phylogenetic analyses	Sun Mi Huh
P3-22	Chloroplast phylogenomics revealed preliminary phylogenetic relationships among Korean species of <i>Anemone</i> (Ranunculaceae)	Gyu-Eun Kim
P3-23	Characterization of the complete mitochondrial genome of <i>Koelreuteria paniculata</i> (Sapindaceae) and comparative analysis within the family	Sung Jin Moon
P3-24	Genetic relationships and conservation strategies of <i>Arisaema takesimense</i> and <i>A. serratum</i> based on 3RAD-Seq analysis	Ji-Eun Lim
P3-25	Population genomics of <i>Silene jensseensis</i> at the southernmost limit in Korea for establishing conservation strategies	Woo-Ho Kim
P3-26	Comparative chloroplast genome analysis of four <i>Juniperus</i> species in Korea (Cupressaceae)	Sung Kyung Han
P3-27	A PacBio HiFi-based draft genome assembly of the Korean endemic species <i>Rubus takesimensis</i>	KyoungSu Choi
P3-28	Fruiting traits and genetic variation in <i>Viburnum sargentii</i> (Adoxaceae)	Hyun-Jun Kang
P3-29	Long-read sequencing resolves complex mitochondrial genome structure of <i>Deutzia paniculata</i> L. (Hydrangeaceae)	Jeongwoo Seo
P3-30	Understanding mitogenome evolution in mycoheterotrophic orchid <i>Chamaegastrodia shikokiana</i> Makino & F.Maek. (Orchidoideae)	Young-Kee Kim
P3-31	Population genetic structure of <i>Persicaria thunbergii</i> in Korea revealed by genotyping-by-sequencing	Kyu Tae Park
P3-32	Genotyping-by-Sequencing 기법을 활용한 해국(<i>Aster spathulifolius</i> Maxim.)의 종자 이동 구역(Seed Zone) 설정 연구	김지은
P3-33	Structural variation and phylogenomics of <i>Adenophora</i> (Campanulaceae) based on complete chloroplast genomes	Yoo-Jung Park
P3-34	The complete chloroplast genome of <i>Orostachys thyrsiflora</i> (Crassulaceae) and its phylogenetic implications	Ji-Eun Park
P3-35	Multiple alternative mitochondrial genome conformations in <i>Cyperus microiria</i> Steud.	Se-Eun Jung
P3-36	Characterization of the chloroplast genome of <i>Tripterospermum japonicum</i> (Gentianaceae)	Hyeyeon Kim
P3-37	Plastid genome sequence of <i>Viola arcuata</i> (Violaceae) from Laos	Hyosig Won
P3-38	스트레스 처리에 따른 개느삼 기내배양체 성분의 함량 변화와 전사체 분석	이화

ABSTRACTS

I. International Symposium Plant Taxonomy in a Changing World

VISION HALL, 4th FLOOR

International Symposium (Feb. 5)
Invited presentation 1.
14:00~14:40, Vision Hall.



Herbaria and global change

Daniel Park

Department of Biology, Korea University, Seoul, Rep. of Korea

Anthropogenic global change is profoundly altering ecosystems. Preventing human-driven biodiversity loss is one of the greatest environmental challenges of our time. Plants form the basis of all terrestrial ecosystems - thus, one of the first steps towards addressing this grand challenge is understanding how plants are responding to global change. Herbarium collections form the foundation of our knowledge of plant diversity and represent irreplaceable snapshots of biological events across space and time, which are critical for global change research. Here we demonstrate how herbarium specimens can be harnessed beyond their original purpose to study the effects of global change on plant phenology, species interactions, and beyond. We used herbarium specimens to elucidate sex-dependent phenological responses to climate change, assess plant-pollinator mismatches, and explore the evolution of plant structural and chemical defenses. We also highlight advances that can facilitate such collections-based research such as the application of artificial intelligence (AI) and discuss potential pitfalls and issues as well. For instance, we demonstrate that large language models (LLM) can effectively georeference historical herbarium specimens based on textual locality descriptions. We argue that herbarium specimens have the power to transform our understanding of plant responses to global climatic change.

International Symposium (Feb. 5)
Invited presentation 2.
14:40~15:20, Vision Hall.



**Past, present, and future of *Orobanche coerulescens* in Taiwan:
insights from evolutionary history and population genomics of
an altitudinally disjunct species**

Yu-Hsin Tseng

Department of Life Sciences, National Chung Hsing University, 40227, Taichung, Taiwan

Disjunct geographical distributions in plants typically result from vicariance or long-distance dispersal. Owing to phylogenetic niche conservatism, closely related taxa or conspecific populations generally occupy similar ecological niches. However, the parasitic plant *Orobanche coerulescens* exhibits a unique altitudinal disjunction in Taiwan, occurring in both coastal lowland and montane regions above 2,500 meters. To elucidate the mechanisms driving this pattern, we integrated morphological characters, population genomics (plastome and ddRAD) and ecological niche modeling (ENM) to reconstruct the evolution history and assess the ecological drivers of this endangered species in Taiwan. Our results reveal no significant morphological differentiation among altitudinal groups or between Taiwanese and extra-limital populations, supporting their conspecific status. Plastome phylogenetic analyses suggest that the populations of Taiwan likely originated from two independent eastward dispersal events from Europe, giving rise to two major genetic lineages: one comprised of western coastal and montane regions, and the other restricted to eastern coastal region. Furthermore, ddRAD data reveal a high degree of genetic differentiation among Taiwanese populations, probably resulting from bottleneck effects and predominantly inbreeding mating system, despite evidence of occasional outcrossing. ENM demonstrates that host plant occurrence is the primary determinant of *O. coerulescens* distribution, with the altitudinal disjunction reflecting the distinct ecological requirements of its specific hosts. Under four future climate scenarios, low-altitude populations are predicted to remain relatively stable or slightly contract, while high-altitude populations show a trend toward expansion. Overall, this study clarifies the evolutionary history and potential future habitat dynamics of *O. coerulescens* populations, providing crucial insights for development of effective conservation strategies.

International Symposium (Feb. 5)
Invited presentation 3.
15:20~16:00, Vision Hall.



Ortho2Web: a new workflow for investigating reticulate evolutionary mechanisms

Bin-Bin Liu

State Key Laboratory of Plant Diversity and Specialty Crops, Institute of Botany, Chinese Academy of Sciences, Beijing, China

Reticulate evolution—driven by hybridization, introgression, incomplete lineage sorting (ILS), and polyploidization—routinely generates strong phylogenetic conflict and complicates both evolutionary inference and downstream taxonomic decisions. To address this challenge, we present Ortho2Web, a modular, extensible workflow designed to standardize and integrate multi-source genomic evidence for dissecting reticulate mechanisms. Ortho2Web is compatible with diverse public and newly generated datasets (e.g., WGS, deep genome skimming/DGS, Hyb-Seq, RNA-seq, RAD-seq), enabling flexible, customizable analyses rather than dependence on any single algorithm. By integrating multiple complementary tools and emphasizing cross-method consensus, Ortho2Web improves inference robustness and makes complex evolutionary histories more interpretable and reproducible. We demonstrate the workflow using three empirical case studies that represent common reticulation scenarios: (i) the bellflower tribe (Campanuleae), a ~620-species radiation with pervasive hybridization and polyploidy, where Ortho2Web helps reconstruct a stable backbone and map major reticulate events; (ii) *Pyrus* (pears), characterized by frequent hybridization and substantial ILS, where a step-by-step exclusion (SSE) strategy refines the diagnosis of ILS versus gene flow; and (iii) polyploid lineages in broad *Prunus*, where widespread introgression coincides with repeated polyploidization, and the DGS-tree2GD component supports intuitive detection of polyploidy-associated signals and the presence/strength of interspecific gene flow. Collectively, Ortho2Web provides a practical, scalable framework for translating phylogenomic conflict into mechanism-aware evolutionary conclusions.

International Symposium (Feb. 5)
Invited presentation 4.
16:15~16:55, Vision Hall.



Plant taxonomy and artificial intelligence

Atzuko Takano

Univ. of Hyogo and Museum of Nature and Human Activities, Hyogo, Japan

While the intrinsic value of herbarium specimens is self-evident to plant taxonomists, the digital transformation of these collections and the rapid advancement of generative AI are unlocking unprecedented potential. Currently, numerous studies have demonstrated practical applications, such as the construction of automated species identification systems trained on vast datasets of herbarium images, the development of applications for the automated extraction of morphological traits (e.g., leaf size, floral, and fruit characters), and phenological analyses utilizing these datasets. In the future, further innovations in image classification models and hardware may enable the development of tools for automatically generating taxonomic keys or drafting formal descriptions of new species. This presentation provides an overview of the current integration of AI within the fields of plant taxonomy and biodiversity research, and offers perspectives on how these technologies may fundamentally transform the workflow of taxonomists in the coming years.

International Symposium (Feb. 5)
Invited presentation 5.
16:55~17:35, Vision Hall.



Genome evolution in crucifers: patterns and underlying principles

Martin A. Lysak

CEITEC - Central European Institute of Technology, Masaryk University, Brno, Czech Republic

Thanks to Thale cress (*Arabidopsis thaliana*/*Arabidopsis*), the mustard family (Brassicaceae) has become a prominent model group in every aspect of plant biology. It has been 25 years since the *Arabidopsis* genome sequence was published. Over the past quarter-century, we have seen remarkable advancements in phylogenetics, phylogenomics, systematics, and the study of genome evolution within the Brassicaceae (~4,000 species in ~350 genera). As next- and third-generation sequencing technologies become more affordable, the number of family-wide comparative and evolutionary analyses in the Brassicaceae continues to increase. This has led to unprecedented advances in systematics, phylogenomics, and comparative genomics within the family. The ever-increasing amount of sequence data and the number of crucifer genomes sequenced provide new opportunities for previously unimaginable comparative studies. The recently established Brassicaceae Tree of Life has enabled even deeper and more sophisticated evolutionary analyses. The Brassicaceae originated some 38 million years ago after a family-specific whole-genome duplication (WGD) event - At- α (alpha). This important paleopolyploid event, along with several more recent (mesopolyploid) WGDs, all followed by genome-wide diploidization, represents an overarching principle in the evolution of crucifer genomes. Diploidization gradually transforms polyploid genomes into functionally diploid-like structures through chromosomal rearrangements, which often result in dysploid changes, i.e., reduction of chromosome number. These dysploids can lead to reproductive isolation among diploidized offspring, significantly contributing to speciation and cladogenetic events. Dysploid chromosomal rearrangements come in various forms, and their breakpoints can now be characterized with single-nucleotide precision, thanks to the availability of telomere-to-telomere genome assemblies.

II. 죽파식물분류학상 수상 특별강연

Special talk: 2026 KSPT Jukpa Award Awardee

VISION HALL, 4th FLOOR

죽파식물분류학상 수상 특별세미나 (2월 5일)

Special talk: 2026 KSPT Jukpa Award Awardee
17:35~18:05, Vision Hall.



Delimiting species boundaries in *Hosta* section *Capitatae* (Asparagaceae) using MIG-seq and morphological analyses: taxonomic revision with new taxa from Korea and Japan

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The genus *Hosta* Tratt. (Asparagaceae), with approximately 22-45 species reported to date, is native to Korea, Japan, China, and the Russian Far East. The present study provides a complete taxonomic revision of the section *Capitatae* in Korea and Japan based on extensive morphological observations and multiplexed inter-simple sequence repeats genotyping by sequencing (MIG-seq) analysis. We identified three species and two varieties in this section. In particular, we described two new taxa, *H. pseudonakaiana* sp. nov. and *H. nakaiana* var. *wandoensis* var. nov., from Japan (Shikoku) and Korea (southern Jeollanam-do), respectively. The new species is morphologically similar to *H. capitata* in that it has compact spike-like racemes and a ridged scape, but is readily distinguished from it by a narrower leaf, fewer flowers, and lanceolate perianth lobes. The new variety is morphologically similar to *H. nakaiana* var. *nakaiana* in most traits, but differs from it by a longer, looser, spike-like inflorescence, more flowers, and earlier flowering. Phylogenetic and population structure analyses based on MIG-seq supported the establishment of two new taxa in the section *Capitatae*.

III. 일반 학술발표

General presentation

1) 구두발표

Oral presentation

VISION HALL, 4th FLOOR

A taxonomic study of Korean *Hylodesmum*

Sang-jin Han^P, Ki-Oug Yoo

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한국산 도독놈의갈고리속(*Hylodesmum*) 식물의 유연관계를 파악하기 위해 외부형태와 잎 표피 미세형태 관찰, 화분학적, 분자계통학적인 연구를 수행하였다. 그 결과, 정량형질로는 종류 간 구별이 어려웠지만, 생육형, 잎이 달리는 위치, 소엽의 개수, 정소엽의 형태, 소탁엽의 유무, 꽃의 색, 열매의 색 등의 정성형질은 주된 식별형질로 유용하였다. 주성분분석 결과 주성분 1에 의해 큰도독놈의갈고리가 구별되었지만 나머지 분류군들은 중첩되어 구별이 어려웠다. 선형판별분석 결과 큰도독놈의갈고리와 영주갈고리는 뚜렷하게 구별되었고, 개도독놈의갈고리와 긴도독놈의갈고리는 일부 유집되었지만, 도독놈의갈고리와 애기도독놈의갈고리는 혼재되어 있었다. 유집분석 결과 큰도독놈의갈고리와 영주갈고리, 개도독놈의갈고리, 긴도독놈의갈고리는 각각의 그룹을 형성하였지만, 도독놈의갈고리와 애기도독놈의갈고리는 혼재되어 있었다. 잎 표피 관찰 결과 모든 분류군에서 표피세포는 파상형이었고, 큰도독놈의갈고리와 영주갈고리, 개도독놈의갈고리, 긴도독놈의갈고리는 비선모와 선모가 관찰되었으며, 도독놈의갈고리와 애기도독놈의갈고리는 비선모만 관찰되었다. 화분학적 연구 결과 화분은 단립이고, 발아구는 삼공구형이었다. 화분의 형태 및 크기는 모두 비슷하였지만, 표면무늬는 큰도독놈의갈고리와 영주갈고리가 망상, 개도독놈의갈고리와 도독놈의갈고리, 애기도독놈의갈고리는 난선상 그리고 긴도독놈의갈고리는 과립상으로 나타나 구별되었다. 분자계통학적 연구 결과 cpDNA 서열을 토대로 그린 계통수에서는 일부 분류군들이 polytomy를 형성하였지만, ITS와 cpDNA 지역을 합친 계통수는 모든 분류군이 구별되었다. 이상의 결과를 종합하여 한국산 도독놈의갈고리속을 5종 1변종으로 정리하였다.

Integrative taxonomy of the Korean genus *Peucedanum* L. (Apiaceae)

Jun-Ho Song^{1P}, Kyeonghee Kim², Seung Mok Ryu², Inkyu Park³

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Peucedanum L. (Apiaceae) is a taxonomically complex genus characterized by extensive morphological, chemical, and genetic diversity, which has long obscured species boundaries and generic circumscription. In this study, we applied an integrative taxonomic approach combining macromorphology, micromorphology, chemotaxonomy, and plastome phylogenomics to reassess the taxonomy of Korean *Peucedanum*. *P. miroense* and *P. tongkangense* were newly described from Gangwon Province based on diagnostic morphological characters, ecological preferences, and mericarp features. Both species are morphologically similar to the related species with linear ultimate leaf segments but are clearly distinguished by ovary indumentum, anther color, mericarp shape, and the number and arrangement of vittae. Leaf and petal epidermal micromorphologies of 12 *Peucedanum* from Korea were investigated using light microscopy and large-area, multiscale field-emission scanning electron microscopy combined with a modular automated processing system. We identified consistent micromorphological traits distinguishing the genus *Peucedanum* from the close genera and fine-scale epidermal characters proved helpful in discriminating each taxa. Chemotaxonomic analyses using UHPLC-Q/TOF-MS of 24 accessions representing eight Korean species revealed three distinct chemical groups, supporting recent taxonomic classifications. *P. japonicum* exhibited unique pyranocoumarin derivatives and dense epicuticular waxes, supporting its reassignment to *Sinopeucedanum*, whereas most Korean taxa shared coumarin glucoside profiles consistent with *Kitagawia*. Phylogenomic analyses based on complete plastome sequences confirmed the polyphyly of *Peucedanum* sensu lato and resolved three major clades. Ten Korean taxa formed a well-supported monophyletic group corresponding to *Kitagawia*, while *P. japonicum* clustered with *Sinopeucedanum*. Mericarp anatomical characters further corroborated these phylogenetic relationships. Overall, this integrative study provides a comprehensive taxonomic reassessment of Korean *Peucedanum*, supports the transfer of ten Korean taxa to *Kitagawia* and the reassignment of *P. japonicum* to *Sinopeucedanum*, and highlights the importance of combining morphological, chemical, and genomic data to resolve taxonomic complexity within Apiaceae.

Species delimitation of *Veratrum* (Melanthiaceae) in Korea and Japan: insights from micromorphological, molecular and cytogenetic analyses

Hyeonjin Kim^P, Bokyung Choi, Tae-Soo Jang

Department of Biological Science, Chungnam National University, Daejeon, Korea

The genus *Veratrum* L. (Melanthiaceae), consisting of sections *Veratrum* and *Fuscoveratrum*, is widely distributed across the Northern Hemisphere. Reflecting different taxonomic perspectives, the genus includes between 16 and 48 taxa, as continuous morphological variation complicates interspecific delimitation. This study examined 11 *Veratrum* taxa native to Korea and Japan using scanning electron microscopy for micromorphological analyses, molecular phylogenetic analyses based on ITS, *matK*, *trnL-F*, and *psbA-trnH*, karyotype and genome size estimation, and fluorescence *in situ* hybridisation, with the aim of identifying informative diagnostic characters and reassessing taxonomic boundaries. As a result of microscopic investigation and molecular phylogenetics, leaf micromorphological characters (trichomes and calcium oxalate crystal) and molecular phylogenetics analyses supported the current sectional classification, although interspecific resolution remained limited. In contrast, pollen and orbicule micromorphology showed limited variation and low taxonomic resolution. Cytogenetic analysis reveals that section *Veratrum* is tetraploid ($2n = 4x = 32$; 3.58 ± 0.12 pg/1C), while section *Fuscoveratrum* is diploid ($2n = 2x = 16$; 2.21 ± 0.38 pg/1C). These differences are mirrored in stomatal and pollen sizes, which serve as reliable micromorphological markers for ploidy levels. Notably, *V. nigrum* (section *Fuscoveratrum*) is distinguished by its broadly elliptical leaves, short pedicels, and a unique cytogenetics traits (2.95 ± 0.12 pg/1C; haploid karyotype length $41.95 \mu\text{m}$), confirming these as diagnostic characters. This integrative study highlights the necessity of molecular cytogenetic data for clarifying the evolutionary and taxonomic framework of the genus.

**Molecular phylogeny and biogeography of subfamily Medeoloideae (Liliaceae):
Insights from East Asia-North America disjunct distribution.**

Hye One Kim^P, Joo-Hwan Kim

Department of Life Sciences, Gachon University, Seongnam-si, Gyeonggi-do, Korea

The East Asia-North America disjunction is a well-known biogeographic pattern that provides important insights into plant origins, dispersal, and evolutionary history. The subfamily Medeoloideae (Liliaceae Juss.), comprising the two genera *Clintonia* Raf. and *Medeola* Gronov. ex L., represents a classic example of this intercontinental disjunction. In this study, we investigated the phylogenetic relationships and evolutionary history of Medeoloideae using plastid and nuclear genomic data based on 78 plastid protein-coding genes and the Angiosperms353 loci dataset. Phylogenetic analyses strongly supported the monophyly of Medeoloideae and recovered *Clintonia* and *Medeola* as well-supported sister genera, with western North American, eastern North American, and East Asian *Clintonia* forming distinct clades. Divergence-time analyses estimated the origin of Medeoloideae in the Eocene (ca. 37-40 Mya) and the diversification of *Clintonia* in the late Miocene (ca. 5-8 Mya). This temporal framework coincides with periods of repeated connectivity between North America and East Asia via the Bering Land Bridge, highlighting its potential role in shaping the intercontinental distribution of *Clintonia*. Subsequent lineage diversification on the two continents was likely shaped by contrasting paleoclimatic and geomorphological histories, as well as by Quaternary climatic fluctuations. By integrating plastid and nuclear genomic data, this study clarifies the phylogenetic placement and evolutionary trajectory of Medeoloideae and provides new insights into the origin and evolutionary history of East Asia-North America disjunct lineages within Liliaceae.

**The evolutionary origin of *Erythronium* L.
based on molecular phylogeny and historical biogeography**

Yu Gyeom Kim^{1,2P}, Hee-Young Gil², Joo-Hwan Kim¹

¹Department of Life Science, Gachon University, Seongnam-si, Korea; ²Division of Forest Biodiversity, Korea National Arboretum, Pocheon, Korea

The genus *Erythronium* L. (Liliaceae) comprises approximately 30 species of spring-flowering perennial herbs distributed across Northern Hemisphere temperate regions. Characterized by elegant flowers with six recurved tepals and starch-rich bulbs historically utilized in East Asia, the genus faces taxonomic challenges due to limited diagnostic morphological variation. This study presents a phylogenomic and historical biogeographic analysis using ten newly sequenced plastid genomes via the Illumina MiSeq platform. Assembled plastomes (150,647–151,827 bp) exhibited a typical quadripartite structure, with the *infA* gene consistently pseudogenized. Phylogenomic analysis based on 78 protein-coding sequences from 48 taxa resolved *Erythronium* into three well-supported, geographically disjunct clades: Eurasia, Eastern North America, and Western North America, with *Amana* confirmed as the sister lineage. Molecular dating estimated the crown age at 16.7 Mya, and major clade divergences initiated during the Late Miocene, yielding Eurasian (8.71 Mya), Eastern North American (5.80 Mya), and Western North American (3.35 Mya) lineages. East Asia was identified as the likely biogeographic origin. The disjunct distribution is hypothesized to have potentially resulted from Miocene dispersal via the Bering land bridge, global cooling, and geographic isolation by the Rocky Mountains. These findings suggest that *Erythronium* represents a useful model for understanding the evolutionary and biogeographic histories of temperate-adapted monocots.

O-06. 구두 발표 2월 6일 11:00~11:15

**Genetic diversity and population structure of *Styrax obassia* (Styracaceae)
revealed by genome-wide genetic variations**

Iseon Kim^{1P}, Myong-Suk Cho¹, Ji-Hyeon Jeon¹, Yoon-Seul Choi¹, Gyu Eun Kim¹, Chae Young Lee¹, Hyuk-Jin Kim², Hee-Young Gil², Seung-Chul Kim¹

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Despite increasing concerns regarding ecological disturbances caused by imported seeds in forest restoration, genetic information on native species remains insufficient. *Styrax obassia* Siebold & Zucc. (Styracaceae) is a deciduous tree native to East Asia, distributed across Korea, Japan, and eastern China. However, previous population genetic studies of this species have been limited by restricted geographic sampling and small sample sizes. In this study, population genetic analyses of *S. obassia* across its East Asian range were conducted using 3RAD-seq (triple-enzyme restriction site-associated DNA sequencing). While overall genetic diversity and differentiation among populations were low, significant regional genetic structuring was observed. Notably, Japanese and Chinese populations showed distinct genetic clusters differentiated from majority of Korean populations. These results suggest that the genetic structure reflects the coexistence of regional differentiation and limited gene flow, rather than complete isolation among populations. The genetic data generated herein provide a scientific foundation for the genetic characterization of native Korean populations and are expected to be applicable to forest restoration.

O-07. 구두 발표 2월 6일 11:15~11:30

From “Flora Brasiliensis” to flora and funga of Brazil online: towards fully monographing the species-rich genus *Machaerium*

Valner Jordao^P, Fabiana Filardi, Domingos Cardoso

Research Institute of the Rio de Janeiro Botanical Garden, Rio de Janeiro, Brazil

The taxonomic study of the Brazilian flora began in the XIX century with extensive collections made by European and Brazilian botanists, culminating in the publication of *Flora brasiliensis* (FB). This monumental work documented over 22,000 plant species and established the first comprehensive taxonomic framework for Brazil’s extraordinarily rich flora, including the early treatment of the species-rich genus *Machaerium*, for which 43 species were recognized. More than a century later, the launch of *Flora e Funga do Brasil* (FFB) online marked a new phase in documenting Brazilian biodiversity. Supported by digitized herbarium collections, integrated national biodiversity databases, and broad taxonomic collaboration, the FFB provides up-to-date, openly accessible monographs for all Brazilian plant, algal, and fungal species, now recognizing 53,699 species. Widely distributed across Brazil and exhibiting pronounced morphological and ecological diversity, *Machaerium* is represented by 74 species in FFB, out of an estimated 130 total, reflecting a substantial increase of approximately 72% compared to FB. We expect this number to grow, as our recent taxonomic studies have identified 11 new species for Brazil – five from the Caatinga, one from the Cerrado, and five from the Amazon – which are currently under morphological and molecular study. Advancing and maintaining a complete, up-to-date monograph of *Machaerium* is essential not only to refine the taxonomy of the genus, but also to highlight the importance of detailed monographic studies in achieving a comprehensive Flora of Brazil, while also supports conservation assessments by enabling the identification of threatened species and priority areas for biodiversity protection.

Subgenomic composition underlies population genetic features in sporophytic apomictic system: new insights from the warm-temperate shrubs *Damnacanthus indicus* and *D. major*

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Sporophytic apomixis is a distinctive reproductive mode in which clonally and sexually derived embryos coexist within a single seed. In such reproductive systems, population genetic features are expected to reflect the relative success of clonal versus sexual offspring, yet the determinants of these patterns remain poorly understood. Here, we investigate reproductive mode, population genetic structure, and polyploid origins in the warm-temperate evergreen shrubs *Damnacanthus indicus* and *D. major*. Micro-CT and flow cytometric seed screening show that tetraploid populations of both taxa reproduce via sporophytic apomixis. Microsatellite analyses reveal strikingly contrasting clonal structures: *D. indicus* comprises 26 multilocus clonal lineages (MLLs), whereas *D. major* is dominated by a single MLL across its range. Phylogenetic analysis of the low-copy nuclear gene *ABC115* indicates contrasting polyploid origins, with *D. indicus* derived from allopolyploidization between closely related diploids (AABB) and *D. major* from hybridization between two allotetraploids sharing a B subgenome (BBA'C'). We propose that the extreme predominance of a single MLL in *D. major* reflects strong purifying selection against maladapted recombinant genotypes, likely associated with its asymmetric composite subgenomic architecture, whereas *D. indicus*, with a more stable subgenomic composition, maintains diverse recombinant genotypes. Together, these results indicate that subgenomic composition, rather than ecological factors, underlies population genetic features in sporophytic apomictic systems.

An Integrative Assessment of the Korean Hymenophyllaceae and Aspleniaceae including their cryptic species

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Species delimitation in ferns is challenging due to limited diagnostic morphological characters and frequent hybridization and polyploidization, which generate reticulate evolutionary patterns among closely related taxa. These problems are particularly pronounced in the family Hymenophyllaceae and Aspleniaceae, for which taxonomic treatments in Korea have largely relied on morphological classification alone. To reassess species identities and phylogenetic relationships in these families, this study applied an integrative approach combining cytogenetic data with molecular phylogenetic analyses. For the Hymenophyllaceae, morphological investigations and cytogenetic analyses, together with molecular phylogenetic analyses using one chloroplast region (*rbcL*) and one nuclear region (*gapCp*), revealed an unreported triploid *Hymenophyllum barbatum*, a tetraploid *H. wrightii*, one new hybrid, one unrecorded hybrid, and one cryptic species. Based on these findings, the Korean Hymenophyllaceae are now recognized as six taxa of *Hymenophyllum*, four of *Crepidomanes*, and five of *Vandenboschia*. For the Aspleniaceae, cytogenetic analyses were integrated with molecular phylogenetic analyses using three chloroplast regions (*rbcL*, *trnL-F*, *trnH-psbA*) and one nuclear region (*pgiC*). This approach identified a new triploid *Asplenium* × *castaneoviride*, an octoploid *A. prolongatum*, one new species, one putative new species, and three sterile unrecorded hybrids. As a result, the Korean Aspleniaceae are now recognized as comprising 28 taxa of *Asplenium* and one of *Hymenasplenium*. Overall, this study demonstrates that Korean fern diversity has been underestimated and highlights the importance of integrative cytogenetic and molecular approaches for accurate species delimitation. This framework provides a robust basis for detecting additional new or cryptic fern taxa and for improving our understanding of fern evolution in East Asia.

Ecological and evolutionary study on the Korean *Siderostictae* group of *Carex* (Cyperaceae)

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Carex sect. *Siderostictae*, an early-diverging lineage within *Carex* (Cyperaceae), is of particular interest due to its restricted distribution in East Asia. Of the 13 recognized species, four occur in South Korea: *C. siderosticta*, *C. ciliatomarginata*, *C. okamotoi*, and *C. splendentissima*. While *C. siderosticta* and *C. ciliatomarginata* are widespread across East Asia, *C. okamotoi* and *C. splendentissima* are endemic to Korea and exhibit narrower, partly sympatric distributions. Previous molecular phylogenetic analyses based on nuclear rITS sequences suggested parallel speciation events between widespread and Korean-endemic species pairs (e.g., *C. siderosticta* sister to *C. okamotoi*, and *C. ciliatomarginata* sister to *C. splendentissima*). However, the sister relationship between the *C. siderosticta* and *C. okamotoi* remained ambiguous, as *C. okamotoi* was nested within the *C. siderosticta* clade, likely due to sequence heterogeneities in nrITS. Here, we reconstructed the phylogenetic relationships among the four Korean *Siderostictae* species by cloning the nrITS region to resolve intragenomic variation. We also investigated the ecological drivers of speciation in the two species pairs using species distribution models (SDMs). The cloned nrITS sequences of *C. siderosticta* formed several distinct clusters, while *C. okamotoi* formed a single cluster nested within the *C. siderosticta* clade, supporting a scenario of parapatric speciation from *C. siderosticta*. In contrast, *C. ciliatomarginata* and *C. splendentissima* exhibited a pattern consistent with typical cladogenetic speciation. Ecological niche modeling indicated that niche divergence in these pairs is shaped primarily by ecological filtering and local adaptation rather than by geographic isolation, likely reflecting parapatric and/or sympatric speciation processes. Paleodistribution models revealed substantial range shifts and expansion from the Last Glacial Maximum to the present, while future projections under climate change scenarios predicted species-specific range expansions or contractions. Overall, this study highlights the value of integrating phylogenetic data with SDMs to refine species boundaries and elucidate the evolutionary and ecological dynamics of *Carex* sect. *Siderostictae*.

III. 일반 학술발표

General presentation

2) 포스터 발표

Poster presentation

LOBBY, 1ST FLOOR

Forecasting the suitable habitat and ecological effects of *Rheum nanum* (Polygonaceae) in Mongolia under climate change

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Rheum nanum Siev. (Polygonaceae) is a perennial herbaceous plant distributed throughout cold desert regions of northern China, Kazakhstan, Mongolia, and the Altai Mountains of Russia at altitudes of 700–2000 m a.s.l. This species is mostly distributed on rubble and rocky slopes of knolls, north-facing hill slopes, and nearly dry riverbeds and sandy-pebbly floors of valleys. Notably, the root of *Rh. nanum* is an essential portion of the diet of the critically endangered, restricted distribution Gobi bear (*Ursus arctos gobiensis*, Sokolov and Orlov), comprising roughly 30–35% of the entire autumnal diet. This study utilizes the MaxEnt model, along with field investigation data and online recorded data, selecting 249 effective occurrence points and integrating 23 environmental variables, such as bioclimatic and topographic, to evaluate the distribution patterns and dynamic changes of suitable habitats for *Rh. nanum* under current climatic conditions and four future climate scenarios (SSP126, SSP585). Results show that under current climatic conditions, the potential habitat of *Rh. nanum* spans approximately 504,163.9 km², with high suitability areas concentrated in southern Mongolia. Key environmental factors influencing the species distribution include precipitation of warmest quarter (Bio18), annual mean temperature (Bio1), mean temperature of driest quarter (Bio9), temperature seasonality (standard deviation × 100) (Bio4), mean diurnal range (mean of monthly (max temp - min temp)) (Bio2), and elevation. In future climate scenarios, while the total suitable habitat area remains stable, the area of high suitability is significantly reduced. Specifically, under the SSP5-8.5 scenario, high suitability areas are projected to decrease by 27.84% during 2050. The centroid of high suitability areas is expected to shift northwestward, though a localized southeastward shift is observed under the SSP5-8.5 scenario. The conservation and protection of *Rh. nanum* resources, which is a key component of the forage of the Gobi bear (*Ursus arctos gobiensis*), will be greatly aided by this study, which is based on the current and future distribution predictions of *Rh. nanum*.

자월도, 승봉도, 대·소이작도(인천광역시 옹진군 자월면)의 식물상

나누리^P, 박병준, 조형복, 조승주, 박범균, 조용찬

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자월도, 승봉도, 대·소이작도는 인천광역시 옹진군 자월면에 속하는 유인도서로, 현재까지 이들 지역에 대한 종합적인 식물상 조사가 이루어진 바 없다. 본 조사는 특히 조사 기록이 미비한 대·소이작도를 포함한 이들 도서의 관속식물상을 규명하기 위해 수행되었으며, 현장조사는 2025년 4월부터 11월까지 총 24일간 이루어졌다. 식물 목록은 현지에서 수집한 건조표본, 화상자료를 바탕으로, 국립수목원 산림생물표본관(KH)에 소장된 기존 표본을 함께 검토하여 작성하였다. 조사 결과, 전체 지역에서 119과 394속 611종 16아종 42변종 4품종 2잡종 총 656분류군의 관속식물이 확인되었다. 자월도에서는 99과 285속 392종 9아종 28변종 1품종 2잡종 총 432분류군, 승봉도에서는 99과 286속 384종 7아종 28변종 2품종 1잡종 총 422분류군, 대·소이작도에서는 101과 307속 445종 8아종 32변종 2품종 1잡종 총 488분류군의 관속식물이 각각 생육하였다. 이 중 특산식물은 서울제비꽃, 백운산원추리, 쯤목포사초 등 8분류군, 산림청 지정 희귀식물은 취약(VU) 범주 세뿔석위, 금방망이, 버들금불초 등 4분류군, 약관심(LC) 범주 고란초, 개지치, 두루미천남성 등 9분류군이 확인되었다. 구계학적 특정식물은 VI등급 갯마디풀, 왜미나리아재비 등 4분류군, III등급 병아리꽃나무, 금난초 등 17분류군, II등급 26분류군, I등급 42분류군 총 89분류군이 생육하였다. 외래식물은 총 131분류군이 확인되었으며, 사전귀화식물은 도꼬마리 등 16분류군, 잠재침입식물 일본잎갈나무 등 29분류군, 침입외래식물 소리쟁이 등 86분류군으로 구분되었다. 본 연구는 자월면 일대 유인도서의 식물상을 종합적으로 조사한 최초의 사례로서, 향후 생물다양성 보전과 도서 생태계 관리에 활용될 수 있는 기초 자료를 제공한다는 점에서 의의가 있다.

Categorization of alien plants in the Republic of Korea using a biological invasion framework and their characteristics

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We applied barrier- and stage-based biological invasion frameworks to 428 alien plant taxa listed in the *Checklist of Vascular Plants in Korea* (Korea National Arboretum) and assessed their characteristics, spread levels, and Rabinowitz rarity types. Alien plants in the Republic of Korea were classified into 141 casual alien plants (CAPs) and 287 naturalized plants (NPs), including 56 invasive plants (IPs). The current occurrence of 36 CAP taxa remained uncertain. Among NPs, 96 taxa showed “concerned spread (CS)” or higher, and 17 taxa were designated for management and regulation. Based on introduction time, neophytes accounted for 407 taxa, far exceeding archaeophytes, suggesting that increased international exchange may be associated with alien plant introductions. By spread level, PS was the most frequent category (289 taxa), followed by WS (51), MS (45), NS (22), and SS (21). Rabinowitz rarity analysis indicated that most taxa belonged to the Common type (389), with smaller numbers in Type 1 (24), Type 2 (10), and Type 3 (5). Overall, the proportion of IPs appears low and most taxa fall within low spread levels. However, the dominance of the Common type suggests that many alien plants have broad habitat use and high potential for forming dense populations, implying that invasive plants (IPs) may increase under continued disturbance and climate change. Therefore, continuous documentation and categorization of alien plants, along with systematic monitoring and management strategies, are needed to mitigate future invasion risks.

A Checklist for the Vascular Plants of BANGLADESH

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Botanical exploration in Bangladesh spans more than two centuries, from early colonial-era studies to recent taxonomic revisions. By synthesizing historical literature and contemporary research, the present checklist documents approximately 5,131 vascular plant species across 1,730 genera and 235 families, including native, endemic, and introduced taxa. Continued discoveries indicate that the national flora remains incompletely known. This checklist provides an essential baseline for plant taxonomy, biodiversity research, and conservation planning in Bangladesh, and underscores the country's importance in regional and global floristic studies. The contributions of Dr. SangWoo Lee and KRIBB, particularly in long-term coordination, data verification, integration, and editorial guidance, are gratefully acknowledged as a key component of this work.

국내 자생 국화속(*Chrysanthemum* L.)의 화분 염성 비교

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본 연구는 국내에 자생하는 국화속(*Chrysanthemum* L.)에 속하는 구절초 무리(*Chrysanthemum zawadskii* complex), 산국(*Chrysanthemum boreale* Makino), 감국 무리(*Chrysanthemum indicum* complex)를 대상으로 Aniline blue-Lactophenol 염색법을 이용하여, 종 및 배수성 수준에 따른 화분 염성을 비교함으로써, 자생 집단을 유지하기 위한 생식능력의 특징을 파악하고자 수행되었다. 연구 결과, 대부분의 국화속 식물은 분류군과 배수성에 상관없이 80% 이상의 높은 화분염성을 보이는 것으로 확인되었다. 종별 화분염성의 차이를 비교한 결과 감국과 산국이 구절초에 비해 상대적으로 높은 평균 화분 염성을 보였지만, 통계학적 유의성은 없었다. 구절초 무리 내에서는 석병산 집단(6배체)에서 가장 높은 화분 염성(96.35%)이 관찰된 반면, 설악산 바위구절초 집단(6배체)은 가장 낮은 염성(54.63%)을 보여 동일 종 내에서도 집단 간 화분염성의 차이가 있음을 확인하였다. 2배체로만 구성된 산국의 경우 사곡리 집단이 98.94%의 가장 높은 화분 염성을 보인 반면, 비행기재 집단에서는 가장 낮은 염성(42.27%)이 확인되었다. 감국에서는 유달산 집단(2배체)이 가장 높은 화분 염성(96.20%)을 보였고, 척천리 집단(2배체)이 가장 낮은 염성(65.58%)을 가지는 것으로 확인되었다. 국화속 내에서 배수성이 가장 발달한 구절초 무리에서는 2배체에서 6배체로 배수화될수록 화분 염성이 점진적으로 증가하는 양상이 관찰되었으나, 10배체 집단에서는 감소하는 경향이 확인되었다. 이러한 결과는 국화속에서 배수화에 따른 유전체 중복현상이 생식능력의 저하를 야기하지는 않으며 오히려 6배체에서 안정적인 감수분열이 유지되고 있을 가능성을 시사한다. 또한, 10배체와 같은 고차 배수체에서는 생식적 안정성이 부분적으로 저하될 수 있음을 보여준다. 따라서 국내 자생 국화속은 동일 분류군 내에서 다양한 배수성이 존재하고 이들 집단에서 화분 염성이 전반적으로 높게 유지되어, 모든 분류군이 다음 세대를 생산하고 집단을 유지할 수 있는 상당한 수준의 생식능력을 보유하고 있는 것으로 판단된다.

오대산 일대의 산벚나무(*Prunus sargentii* Rehder) 분포 특성

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산벚나무는 러시아 사할린, 일본 홋카이도 및 우리나라 고산지역에 분포하는 종으로 백두대간 일대에 드물게 자생한다. 그러나 산지에 자생하는 벚나무류를 '산벚나무'로 통칭하거나 조경수로 유통되는 등 명칭 오용 및 실제 인식에 대한 문제가 발생하고 있다. 이에 본 연구는 백두대간 중추에 해당하는 오대산(1,563m)을 대상으로 산벚나무 분포현황을 조사하고, 그 결과를 분석하였다. 조사구역은 백두대간 주 능선인 신배령-두로봉-진고개-노인봉-소황병산-매봉-선자령-대관령과 두로령-비로봉-호령봉-상원사, 운두령-계방산 일대를 포함하며, 총길이 약 70km, 해발고도 750~1,579m이다. 산벚나무 개화기인 2025년 5월 7~8일에 20여 명의 조사원이 NABI LAB 현장조사 솔루션을 이용하여 전자조사표를 작성하였고, 위치 정보와 사진 자료를 실시간으로 데이터베이스화하였다. 조사 결과, 오대산 일대에서 확인한 자생 벚나무류는 336개체이며, 그중 산벚나무는 252개체(75%), 잔털벚나무는 46개체(14%), 기타 벚나무류는 38개체(11%)였다. 산벚나무가 빈번하게 출현한 구간은 해발고도 1,200~1,300m(96개체, 29%), 1,100~1,200m(75개체, 22%)였으며, 1,301m 이상(43개체, 17%), 1,100m 이하(38개체, 15%) 순으로 나타났다. 계방산 일대, 비로봉-호령봉 구간 등 일부 지역에서는 산벚나무가 확인되지 않았다. 향후, 조사지역을 확대하여 산벚나무의 남한 내 분포를 명확히 밝힘으로써 '산벚나무' 명칭에 대한 인식개선에 일조하고자 한다.

희귀식물의 국가적색목록 평가: 송양나무, 낙동나사말, 진주고추나물, 꼬인용담, 좁은잎사위질빵

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IUCN(세계자연보전연맹) 적색목록 평가기준에 따른 우리나라 자생식물의 절멸위협 평가를 위해 송양나무(*Ehretia acuminata* R. Br.), 낙동나사말(*Vallisneria spinulosa* S. Z. Yan), 진주고추나물(*Hypericum oliganthum* Franch. & Sav.), 꼬인용담(*Gentianopsis contorta* (Royle) Ma), 좁은잎사위질빵(*Clematis hexapetala* Pall.)을 대상으로 2025년 6월부터 10월까지 개체군 정밀분포 및 생육 현황을 조사하고 적색목록 평가자료를 수집하였다. 대상종은 모두 국가적색목록에서 정보부족(DD) 범주로 평가된 바 있다(국립수목원, 2021). 송양나무는 거문도와 제주도에서 81개체, 낙동나사말은 경산, 창녕, 함안 등 낙동강수계 8개소에서 2만 개체 이상, 진주고추나물은 순창, 창원, 함안 등 6개소에서 837개체, 꼬인용담은 태백산 일대에서 102개체, 좁은잎사위질빵은 서산 1개소에서 18개체를 각각 확인하였다. 분류군별 출현 범위(EOO), 점유면적(AOO), 성숙개체수, 위협요인 등을 분석하여 IUCN 평가기준을 적용한 결과, 송양나무는 위기[EN B1+2ab(iii); D], 낙동나사말은 취약[VU B1ab(iii)c(ii)], 진주고추나물은 위기[EN B2ab(ii, iii, iv)], 꼬인용담은 위급[CR B1+2b(iii, v)c(ii)], 좁은잎사위질빵은 위급[CR B1+2ab(ii, iii, v); D] 범주로 판정하였다.

춘천시 도시림인 봉의산, 안마산의 식물상 비교

이영철^P, 김기현, 고아름, 송준우, 임원균, 최영민, 유기억

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봉의산(300m)과 안마산(303m)은 강원도 춘천시에 위치한 도시림으로 접근 경로가 다양해 간섭이 잦은 지역이다. 본 연구는 비슷한 지리적 조건을 가진 두 지역의 식물상을 조사하여 관속식물 현황을 파악하고 비교해 식물의 보존과 관리를 위한 기초자료를 제공하고자 수행되었다. 조사는 2025년 3월부터 10월까지 총 23회에 걸쳐 현장에서 진행하였다. 조사 결과 두 지역에서 채집된 관속식물은 110과 325속 456종 11아종 35변종 5품종 4교잡종으로 총 511분류군이 확인되었다. 장소별로는 봉의산 376분류군, 안마산 358분류군으로 나타났고, 두 지역에서 공통적으로 확인된 분류군은 223종류였으며, 각각의 지역에서만 확인된 종류는 각각 153분류군과 135분류군이었다. 조사된 511종류의 과별 종다양성은 국화과(55분류군), 벼과(34분류군), 장미과(29분류군), 콩과(25분류군)의 순으로 높게 나타났다. 특산식물은 서울제비꽃, 꽃황새냉이 등 9분류군으로 이 중 개나리, 섬초롱꽃, 별개미취, 고려엉겅퀴 등 4분류군은 재배종으로 나타났으며, 희귀식물은 8종류의 재배종을 포함해 쥐방울덩굴, 참배암차즈기 등 총 12분류군이었다. 식물구계학적특정식물은 총 60분류군으로 집계되었으며, 등급별로는 V등급 1, IV등급 11, III등급 13, II등급 12, 그리고 I등급 23분류군으로 나타났다. 이 중 고광나무와 낭아초 등 13분류군은 두 지역에서 공통으로 나타났으며, 29분류군은 봉의산에서, 18분류군은 안마산에서만 조사되었다. 귀화식물은 큰금계국, 왕포아풀 등 총 61분류군으로 29분류군은 두 지역 모두에서 조사되었고, 봉의산 9분류군과 안마산 23분류군은 각각의 지역에서만 볼 수 있었다. 두 지역에서 조사된 귀화식물은 주로 임연부에 분포하였으며, 안마산은 지속적인 경작 활동과 도시개발로 인해 봉의산보다 귀화식물 종류가 많은 것으로 판단된다. 귀화율은 11.9%였으며, 도시화지수는 19.0%로 춘천시 전체 산지 귀화율 7.8%보다 높고, 도시화지수 24.8%보다 낮았다. 생태계교란식물은 돼지풀, 가시박, 단풍잎돼지풀, 애기수영, 미국쑥부쟁이, 환삼덩굴, 서양등골나물 등 총 7분류군이었으며, 특히 서양등골나물은 본 조사를 통해 봉의산에서 처음으로 분포가 확인되어 향후 도심지역 전체로의 확산이 우려된다. 유용도는 식용 184분류군, 목초용 174분류군, 약용 152분류군 순으로 나타났다. 이상의 결과에서 두 지역 식물상을 조사·비교한 결과 전체 분류군 수와 분석된 항목별 분류군 수는 비슷하였으나 식물 종 구성에는 차이가 있는 것으로 나타났다. 그 이유는 봉의산이 도심 가운데 위치하고 인근 지역이 아파트단지, 건물, 도로 등으로 고립되어 있고, 오랫동안 도시화가 진행된 반면, 안마산은 춘천시 동남부에 위치하고 최근까지 인접 지역에 농경지가 분포해 활발한 경작이 이루어졌고, 최근 들어 아파트 건설이나 도로의 확장 등 도시화가 진행되었기 때문이라 생각된다.

아고산대 전나무속 2종(구상나무, 분비나무)의 고사 현황과 지형적 요인

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우리나라 소나무과 전나무속(*Abies*)은 아고산대 식생을 대표하는 주요 수종으로, 최근 기온 상승과 적설량 감소 등 기후변화의 영향으로 고사 현상이 보고되고 있다. 본 연구는 구상나무(*Abies koreana*)와 분비나무(*Abies nephrolepis*)를 대상으로, 고사가 집중적으로 발생하는 지형적 입지 특성을 규명하고자 수행되었다. 연구 대상지는 분비나무의 경우 설악산, 오대산, 태백산, 구상나무의 경우 소백산, 덕유산, 지리산으로 선정하였다. 항공영상을 활용하여 생육목과 고사목을 육안 판독 및 인공지능 기법으로 검출하였으며, 수치지형도를 기반으로 해발고도, 사면향, 경사, 일사량, 지형습윤지수(TWI) 등 지형적 요인을 분석하였다. 또한 생육목과 고사목 간 지형 특성 차이를 검증하기 위해 T-test를 수행하였다. 분석 결과, 지리산과 설악산에서는 전나무속 수종이 연속적으로 분포하는 반면, 그 외 공원에서는 불연속적인 분포 양상을 보였다. 지리산 구상나무의 고사율은 약 9.2%로, 해발고도가 높고 남향이며 경사가 급한 지역에서 고사가 집중되었고, 일사량이 높고 지형습윤지수가 낮은 수분 스트레스 환경과 밀접한 관련이 있었다. 설악산 분비나무의 고사율은 약 7.6%로, 서향의 급경사지에서 고사가 주로 발생하여 유사한 지형적 특성을 나타냈다. 불연속 분포를 보이는 다른 공원에서도 대체로 일사량이 높고 지형습윤지수가 낮은 지역에서 고사가 집중되는 경향이 확인되었다. T-test 결과, 대부분의 공원에서 해발고도와 일사량 항목에서 생육목과 고사목 간 유의한 차이가 나타났다. 본 연구는 전나무속 수종의 고사가 분포 하한선의 단순한 이동이 아니라, 기후변화로 인해 수분 스트레스가 증폭되는 특정 지형 입지를 중심으로 발생하고 있음을 제시하며, 향후 아고산대 식생 보전 및 기후변화 대응 전략 수립을 위한 기초자료로 활용될 수 있을 것이다.

설악산국립공원 기후변화 민감종(고산식물) 분포정보 구축 및 취약성 평가 연구

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본 연구는 2025년 설악산국립공원 내 기후변화 민감종(고산식물)을 대상으로 분포현황을 파악하고 향후 기후변화 취약성 평가를 위하여 수행되었다. 문헌조사를 기반으로 분포 예상지역과 조사 경로를 설정하고 출현지점과 서식지 정보를 수집한 결과 총 22종의 분포를 확인하고, 분포좌표 415개를 확보하였다. 조사결과 멸종위기야생생물 II급 4종(기생꽃, 노랑만병초, 장백제비꽃, 홍월굴)과 한국특산식물 1종(산솜다리)을 확인하였다. 또한 국가적색목록 13종 및 식물구계학적 특정식물 18종의 분포가 확인되어 보전 우선 관리가 필요한 분류군이 다수 포함됨을 확인하였다. 공간 분포 특성은 고도 특성(최저·최고고도 및 고도폭(ΔE))과 분포범위(EOO)로 구분하여 분석하였다. ΔE 는 국소형($\Delta E \leq 200m$), 수평형($200m < \Delta E < 600m$), 수직형($\Delta E \geq 600m$)으로 유형화하여 종별 고도 분포패턴을 비교하였다. EOO는 최소불록다각형(MCP) 기반 면적(km^2)으로 산출하여 공원 내 분포의 광범위·국소성을 평가하였다. 전체 분포 고도는 560-1,705m였으며, 최고고도 1,600m 이상에 도달하는 종이 15종(약68%)으로 나타났다. 최저고도 1,300m 이상 종은 11종이었고, 고도폭이 50m 이하의 매우 좁은 분포를 보이는 종은 6종으로 확인되었다. EOO는 0.0-120.609 km^2 범위로 나타났고, 일부 종에서 EOO가 0에 수렴한 것은 실제 분포범위가 좁은 것뿐 아니라, 조사된 좌표 수의 부족의 영향 가능성을 시사한다. 핵심분포지역(Hotspot)은 출현 빈도와 종 중첩도를 기반으로 도출하여 다수 종이 중복 분포하는 구역을 핵심분포지역으로 분석하였다. 본 연구는 2차년도 오대산·태백산·소백산, 3차년도 지리산·덕유산으로 확대 조사한 뒤 누적자료를 기반으로 취약성평가를 수행할 계획이다. 본 연구는 국립공원 차원의 기후변화 적응전략 및 민감종 보전 및 복원 방안(서식지 관리·복원 등) 등 향후 국립공원 기후변화 적응대책 및 관리계획 수립을 위한 방향성을 제시하고자 한다.

덕유산국립공원 관속식물의 다양성과 보전방안

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⁵전남대학교 생물과학·생명기술학과

본 연구는 제5기 덕유산국립공원 공원자원조사를 통해 관속식물상 현황을 파악하고 분석·평가를 통해 공원정책 수립 등 공원관리 기초자료를 제공하고자 수행되었다. 조사는 2025년 4월부터 10월까지 서식지 유형별 조사지점 17개(산림생태계)를 포함하여 전체 공원구역을 85개의 격자(2km×2km)로 구분하여 조사를 수행한 결과 관속식물은 총 109과 295속 총 528분류군으로 확인되었다. 멸종위기 야생생물(식물)은 총 5분류군(I 급: 광릉요강꽃, II 급: 구름병아리난초, 날개하늘나리, 복주머니란, 세뿔투구꽃)이 확인되었으며 한국적색목록종은 위기(EN) 등급인 가문비나무, 구상나무 등 3분류군, 취약종(VU)은 등대시호, 복주머니란 2분류군, 준위협(NT)은 모데미풀 등 2분류군이 확인되었다. 한국특산식물은 금오족도리풀, 나제승마, 숲개별꽃, 어리병풍 등 18분류군으로 확인되었고 식물구계학적 특정종은 총 142분류군(V ~ III등급 56분류군), 외래식물은 14분류군과 생태계교란 생물(식물) 3분류군의 출현을 확인하였다. 본 조사를 통해 기존에 확인되지 않았던 각시고사리, 구름병아리난초, 부산사초, 바늘사초, 사다리고사리, 족제비쑥, 태백개별꽃 등 41종의 서식을 처음 확인하였다. 1기(1993년) ~ 5기(2025년) 결과를 종합하면 덕유산국립공원에는 총 1,335분류군의 관속식물이 분포하는 것으로 확인되었으며, 향적봉부터 남덕유산으로 이어지는 산림지역은 아고산대 식생이 발달하며 기후변화에 취약한 북방계 식물이 잔존하는 피난처로 매우 중요한 의미를 가진다. 따라서 북방계 식물을 포함한 희귀식물의 지속적인 모니터링을 통해 핵심보호지역 생태계의 보전·관리를 위한 노력을 지속하여야 할 것이다.

국립공원 특별보호구역 식물서식지의 지정·관리 현황과 보전 가치

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국립공원은 국가 보호지역으로 기후변화, 서식지 파괴 등 위협에 처한 생태계와 생물다양성 보전을 위한 피난처이자 멸종위기 야생생물의 67.7%가 분포하는 핵심 생태계이다. 국립공원공단은 국립공원 생태계와 주요 생물자원을 보호하기 위하여 「특별보호구역」을 지정·관리하고 있다. 현재 특별보호구역은 식물서식지, 동물서식지, 자연휴식지 등 3개 유형으로 구분되며, 「자연공원법」 제28조에 따라 21개 국립공원에 총 213개소가 관리되고 있다(2007년~). 본 연구에서는 특별보호구역으로 지정된 식물서식지를 대상으로 지정 및 관리현황 등을 종합적으로 소개하고, 보전적 가치와 중요성을 공유하고자 한다. 식물서식지 유형은 19개 국립공원에 96개소(면적 27.2km²)가 지정되어있으며, 기생꽃, 물석송, 자주땅귀개, 한란 등 보호대상식물 42종 대상 89개소, 아고산식물 군락, 습지 등 취약 생태계 대상 7개소가 이에 해당한다. 보호종을 기준으로는 복주머니란 대상 9개소(소백산, 월악산, 덕유산), 노랑붓꽃 대상 6개소(변산반도, 내장산), 광릉요강꽃 대상 5개소(설악산, 덕유산) 등이 있다. 국립공원공단은 특별보호구역의 관리를 위해 우선적으로 출입 단속 및 보호시설 설치로 인위적 간섭을 최소화하고, 나아가 주기적인 모니터링을 통해 개체군 현황, 서식지 위협요인, 서식 환경 등을 조사하여 보전 방안을 수립하고 이행한다. 또한 특별보호구역 지정·변경·해제를 위한 평가 기준 고도화 연구, 위협요인 진단체계 구축 및 맞춤형 관리 전략 마련 연구 등을 통해 핵심 서식지 관리를 강화하고, 국립공원 생태계의 건강성 향상에 기여하고 있다. 본 연구를 통한 특별보호구역 식물서식지의 현황 공유가 향후 핵심 보호지역 관리 및 보전정책 강화에 기여할 것으로 사료된다.

**New record of *Henckelia mishmiensis* (Gesneriaceae) from Kachin State,
Northern Myanmar**

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The genus *Henckelia* Spreng. (Gesneriaceae) is a species-rich group distributed across South and East Asia, comprising approximately 83 species. Its centers of diversity are recognized in the Eastern Himalayas, Northeastern India, and Southwest China. In Myanmar, the genus was previously reported to include 18 taxa, following recent floristic updates. During a botanical expedition in Kachin State, northern Myanmar (2017-2019), a population of acaulescent, lithophytic *Henckelia* was discovered on shaded rock surfaces. Based on diagnostic morphological characteristics, including its whorled leaves, complete absence of bracts, and solitary flowers, the specimens were identified as *Henckelia mishmiensis* (Debbarman ex Biswas) D.J.Middleton & Mich.Möller. The floral morphology is further characterized by funnel-shaped corollas with a white tube, violet lobes, and yellow markings in the throat. The discovery of *H. mishmiensis* in Kachin State represents the first record of this species in Myanmar, increasing the known diversity of the genus in the country to 19 taxa.

국내 *Triglochin maritima* L. complex에 대한 형태학적·세포학적 분석 및 *Triglochin asiatica* (Kitag.) Á.Löve & D.Löve의 분류학적 재평가

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지채속(*Triglochin* L.)은 지채과(Juncaginaceae)에 속하는 일년생 및 다년생 식물로, 전세계적으로 약 35종이 분포하는 것으로 알려져 있다. 국내에서는 지채(*Triglochin maritima* L.)와 물지채(*Triglochin palustris* L.) 2종이 자생하는 것으로 보고되어 있으며, 물지채는 강원도 내륙에 제한적으로 분포하는 반면, 지채는 한국 연안 전반에 널리 분포한다. 국내에 분포하는 지채 집단은 개화시기에 따라 두 분류군으로 구분된다. 봄(5월)에 개화하는 분류군은 잎보다 긴 화서, 가는 잎, 털이 많은 주두, 그리고 구형에 가까운 열매를 가져 기존에 알려진 *T. maritima*의 형태적 특징과 일치하였다. 반면, 가을(9월)에 개화하는 분류군은 화서보다 길고 넓은 잎, 소수의 털이 있는 주두, 그리고 가늘고 긴 열매를 가지는 것으로 확인되었다. 봄 개화형 분류군은 동해안과 서해안 전반에 분포하였으며, 가을 개화형 분류군은 주로 서해안 일부 지역과 제주도에 분포하였다. 특히 서해안 안면도를 포함한 일부 지역에서는 두 분류군이 동일 지역 내에 서로 분리된 집단을 형성하고 있었다. 세포학적 분석 결과, 봄 개화형 지채의 염색체는 $2n = 120$ 의 20배체였으며, 가을 개화형 지채의 염색체는 $2n = 48$ 인 8배체로 확인되었다. 또한 flow cytometer를 이용한 유전체 크기를 측정한 결과, 봄 개화형 지채는 2.4 pg, 가을 개화형 지채는 0.94 pg으로 측정되어, 배수성과 일치하는 경향을 보였다. 형태학적 및 세포학적 결과를 종합하면, 국내에 분포하는 지채는 서로 다른 두 분류군으로 인식되는 것이 타당하다고 판단된다. 본 결과는 러시아, 한국, 일본 등 동아시아 지역에 분포하며 기존에 *T. maritima*의 이명으로 처리되었던 *Triglochin asiatica* (Kitag.) Á.Löve & D.Löve를 독립된 종으로 인식해야 함을 과학적으로 뒷받침한다. 이에 따라, *T. asiatica*를 한국 자생식물로 인식하고, 해당 분류군에 대해 “아시아지채”라는 새로운 국명을 제안하고자 한다.

**A study of the external morphology and sexual system
of *Mercurialis leiocarpa* (Euphorbiaceae)**

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The genus *Mercurialis* L. (Euphorbiaceae) comprises eight species worldwide and has been widely used as a model system for studying sexual systems and plant evolution. *Mercurialis leiocarpa* Siebold & Zucc. is mainly distributed in East Asia, including Korea, and is native to the southern regions of Korean Peninsula. Although European-Mediterranean species, such as *M. annua* L., have been extensively studied, comprehensive investigations of the East Asian species *M. leiocarpa* remain lacking. In this study, we conducted a detailed examination of the external morphological and micromorphological characteristics of *M. leiocarpa* and documented representative external features through descriptions and photographic plates. Our results indicate that Korean populations of *M. leiocarpa* exhibit trioecy, with monoecious and dioecious individuals occurring simultaneously. Micromorphological traits of leaves and pollen grains were analyzed using scanning electron microscopy to assess intersexual morphological differences, revealing distinct variations in pollen and other micromorphological features among sexual forms. To further elucidate these findings, additional studies on the reproductive biology and phylogeny of *M. leiocarpa*, including sex ratio, sexual function, ploidy levels, and pollination biology, are required.

Comparative leaf micromorphology, palynology, and ITS sequence variation in
Arisaema thunbergii subsp. *geomundoense* and *A. thunbergii* subsp. *thunbergii*
(Araceae)

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The genus *Arisaema* Mart. (Araceae Juss.) comprises approximately 180 species distributed worldwide across tropical and temperate regions. In Korea, six species and one subspecies are recognized. *Arisaema thunbergii* Blume subsp. *geomundoense* S.C.Ko is an endemic Korean subspecies, traditionally distinguished by the color and wrinkled texture of its spadix appendage. However, a recent study of chloroplast genome of the genus *Arisaema* suggested that *A. thunbergii* subsp. *geomundoense* should be treated as a synonym of *A. thunbergii* subsp. *thunbergii*. The present study aimed to provide a detailed description and taxonomic assessment of *A. thunbergii* subsp. *geomundoense* based on micromorphological observations and comparative sequence analyses. Leaf cuticular micromorphology and palynology revealed no significant differences between *A. thunbergii* subsp. *geomundoense* and *A. thunbergii* subsp. *thunbergii*. In addition, we detected that no single-nucleotide polymorphism (SNP) regions were in the internal transcribed spacer (ITS) sequences between the two taxa. These findings support previous plastome-based results and confirm that *A. thunbergii* subsp. *geomundoense* should be regarded as synonym of *A. thunbergii* subsp. *thunbergii*. Nevertheless, some studies have proposed that *A. thunbergii* subsp. *geomundoense* is instead synonymous with *A. thunbergii* subsp. *urashima* (H.Hara) H.Ohashi & J.Murata, an endemic subspecies of Japan. Further comprehensive studies on the *A. thunbergii* complex are therefore necessary to resolve clarify taxonomic boundaries and achieve a robust taxonomic revision of the genus *Arisaema*.

AI-powered automated identification of riparian invasive alien plants on the Korean peninsula using citizen science data

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Invasive alien plants are non-native species that threaten biodiversity by exhibiting rapid growth and reproduction beyond their native ranges. Timely monitoring is essential for effective management, yet expert surveys are costly and time-consuming. Citizen science platforms, such as iNaturalist and NATURING, offer large-scale monitoring opportunities; however, accurate identification is challenging without taxonomic expertise, especially during non-flowering stages. We developed a deep learning model to identify invasive alien plants in riparian habitats of the Korean Peninsula using citizen science images. The model was trained on nine invasive alien species and 21 morphologically similar native or non-target species. A curated dataset from NATURING and iNaturalist covered variation across growth stages and organs. We applied ResNet, a deep learning model, and evaluated its performance using F-score, accuracy, and confusion matrices. This study shows the potential of AI-assisted tools to enhance citizen science-based monitoring and education on invasive alien plants, highlighting the research value of citizen science data and improving identification reliability.

한국산 산사나무(*Crataegus pinnatifida*)의 분류학적 연구

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동아시아에 분포하는 산사나무(*Crataegus pinnatifida*)는 국내에서 털산사, 넓은잎산사, 가새잎산사, 좁은잎산사 등 4개의 변종으로 알려져 왔으나, 변종 간 형태적 경계가 모호하여 분류학적 이견이 지속되어 왔다. 특히 Flora of China와 국가표준식물목록(Korea National Plant List)등 기관별 기재가 상이하여 이들의 실제 규명이 필요한 실정이다. 본 연구는 화분학적 및 분자계통학적 분석을 통해 한국산 산사나무류의 분류학적 위치와 계통적 유연관계를 규명하고자 하였다. 재료는 2025년 4월부터 11월까지 강원도 및 경기도 일대에서 채집된 산사나무 종류를 대상으로 하였다. 화분학적 연구는 Livingstone 방법을 다소 변형한 방법으로 초산분해한 뒤 주사전자현미경(SEM)으로 관찰하였으며, 분자계통학적 연구는 엽록체 DNA(cpDNA) 3개 구간(*matK*, *rbcL*, *trnH-psbA*)의 염기서열을 분석하였다. 화분학적 분석 결과, 모든 분류군에서 3구형(tricolporate)으로 관찰되어 분류군 간 유의미한 차이가 확인되지 않았다. 분자계통학적 연구 결과에서는 넓은잎산사와 좁은잎산사가 하나의 단일 분계군을 형성하며 계통수의 기저부에 위치하였고, 그 외의 분류군들은 하나의 계통군을 이루었으며, 이 중 산사나무와 털산사가 서로 밀접하게 묶이는 sub-clade를 형성하였다. NCBI에 등록된 중국산 개체들의 엽록체 서열은 높은 지지도로 하나의 분계군을 형성하였으며, 중국에 분포하는 산사나무에서는 엽록체 유전자 수준에서 유의미한 분화가 관찰되지 않았다. 이러한 결과는 현재 형태형질의 유사성을 근거로 하나의 종으로 취급되고 있는 산사나무종류가 분자계통학적 관점에서 독립된 분류군으로 재평가될 여지를 보여주며, 이에 대한 후속 연구의 필요성을 지지한다.

Taxonomic revision of Korean *Salix* section *Subalbae* evidenced by morphological and plastome phylogenetic analyses

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The section *Subalbae* belongs to subgenus *Salix* and is considered parallel to the European-West Asian section *Salix*, although some classifications include it within that section. Members of section *Subalbae* are characterized by lanceolate leaves with narrow apices and densely serrate margins. In this study, we examined extensive morphological characters and conducted comparative plastome-based phylogenetic analyses of three Korean species: *Salix babylonica*, *S. pseudolasiogyne*, and *S. pierotii*. Although these species share general morphological characteristics, several taxonomically informative differences were identified, including branch architecture, style development, and anther color. Principal component analysis (PCA) revealed partial overlap among species, but characters related to the sizes of leaves, bracts, ovaries, stamens, and styles contributed significantly to species differentiation, indicating that traditional taxonomic characters remain informative. Plastome phylogenetic analysis of 27 *Salix* species resolved two major clades corresponding to subgenera *Chamaetia/Vetrix* and *Salix*. The three focal species clustered with *S. koreensis* and *S. matsudana* within subgenus *Salix*, but formed two distinct groups. Despite previous treatments of *S. pseudolasiogyne* and *S. matsudana* as synonyms of *S. babylonica*, our results reveal clear distinctions among these taxa. Overall, the combined morphological and plastome-based phylogenetic evidence supports recognizing *S. babylonica*, *S. pseudolasiogyne*, and *S. pierotii* as distinct taxonomic entities within section *Subalbae*.

New insights into *Oxytropis* (Fabaceae) diversity in Mongolia: description of a new species

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Oxytropis L., comprising more than 600 species worldwide, is one of the largest and most diverse genera in the Fabaceae. In Mongolia, *Oxytropis* comprises 100 taxa including 13 endemic and 36 subendemic species which is one of the most species-rich genera of Fabaceae and a key component of steppe, mountain, and desert-steppe floras. Despite long-standing botanical exploration, the taxonomy and distribution of Mongolian *Oxytropis* remain incompletely resolved due to morphological similarity among closely related taxa, under-sampling in across regions. Here, we integrate field surveys conducted in Mongolia (2017-2025), examination of herbarium material, and complete plastome-based phylogenetic to reassess species boundaries within the genus. As a result, we currently described the four new *Oxytropis* species from Mongolia based on morphological and molecular evidence: *O. oyunmaae* Munkht. & Baasanm. (sect. *Verticillares*); *O. jamsranii* Munkht. & Baasanm. (sect. *Xerobia*); *O. dariimaae* Munkht. & Baasanm. (sect. *Verticillares*), and *O. ikhbogdicus* Munkht., Baasanm. & H.J.Choi (sect. *Mesogaea*). In addition, *O. sobolevskajae* Pjak, previously described in the Republic of Tuva, Russia, is newly recorded to the Mongolian flora. Our results highlight that Mongolian dryland and montane landscapes still harbor overlooked legume diversity and emphasize the need for continued integrative taxonomic work to support biodiversity inventories and conservation planning.

Improving the current knowledge of *Astragalus* species (Fabaceae) in Kazakhstan, central Asia based on phylogenetic relationship and morphological notes

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In the case of many previously described *Astragalus* species, more than 3,100 species worldwide, particularly those that are endemic and rare, there is a lack of critical information, such as wild photo illustrations, taxonomic notes, and genetic resources. We investigated the taxonomic status and phylogenetic relationships of 26 *Astragalus* species including 3 endemics to Kazakhstan, using samples collected in 2025 to address this gap. We sequenced the internal transcribed spacer (ITS) of all studied *Astragalus* species. In the phylogenetic tree, all *Astragalus* species were monophyletic and had the same topology as reported in previous studies. Our phylogenetic tree was divided into two primary clades. Clade I included species of the subgenera *Calycophysa* and *Caprinus*, whereas Clade II included species of the subgenera *Cercidothrix* and *Trimeniaeus*. In Clade I, each section was well-separated from the others, except for the sections *Chaetodon*, *Eriocerus*, and *Dissitiflori* in the subg. *Cercidothrix*. The taxonomic positions of some *Astragalus* species, based on morphological and molecular evidence, are also discussed. The detailed illustrations and species documentation presented in this study will serve as significant references for future taxonomic and identification studies of this genus.

우리나라 식물명 검증을 위한 초기 식물문헌 분석: 『조선식물향명집』

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식물명의 정확한 사용은 분류학적 정보 소통과 연구 자료의 신뢰성에 필수적이다. 그러나 문헌에 따라 국명에 대응하는 학명이 상이하거나 그 실체가 명확하지 않은 경우가 있다. 이에 산림청 국립수목원은 식물명 표준화를 위해 국가표준식물목록을 구축하였다. 다만 국가표준식물목록 구축 과정에서 참고된 「한국식물명고」는 국명 출전 기록을 정리한 문헌이지만, 학명-국명 간 대응 관계를 체계적으로 검토·정리한 자료는 아니므로 현행 목록에서도 학명-국명 연계의 일관성 부족이나 오류 가능성이 존재한다. 따라서 초기 문헌에 기록된 식물명의 출처와 변천 과정을 추적하고, 원기재문과 명명학적 근거에 기반하여 학명-국명 관계를 재검토하는 연구가 필요하다. 본 연구는 이러한 접근을 실제로 적용한 첫 사례로서, 1937년에 출판된 초기 식물명 목록인 「조선식물향명집」에 수록된 1,944분류군을 대상으로 학명과 국명의 변화를 체계적으로 재검토하였다. 본 연구에서는 현행 분류 체계 및 국제식물명명규약(ICN)을 기준으로 학명의 적법성·유효성, 명명자 표기, 이명 관계 및 오적용 여부를 검토하고, 국명은 국가표준식물목록의 추천국명과 비교하여 대응 관계의 일치 여부를 분석하였다. 그 결과, 조선식물향명집의 학명 가운데 현행 표준 학명과 일치하는 분류군은 268분류군에 불과하였으며, 1,676분류군에서 불일치가 확인되었다. 학명 오기는 명명자, 속명, 종소명, 변종·품종소명 등 다양한 유형으로 나타났고, 특히 명명자 표기 오류와 종소명 변경이 주요 오류 유형으로 확인되었다. 국명은 국가표준식물목록의 추천국명과 동일한 분류군이 1,184분류군이었으나, 760분류군에서는 단순오기, 개칭 또는 분류학적 재처리에 따른 차이가 확인되었다. 학명-국명 관계를 종합하면 정명 883분류군, 이명 724분류군, 오적용 207분류군이 확인되었고, 비합법명(나명 포함) 64분류군, 서명 54분류군, 동명 11분류군, 출처 불명확 1분류군으로 분류되었다. 또한 조선식물향명집이 원기재에 해당하는 학명은 12분류군(이명 4, 비합법명 8)으로 확인되었다.

자생 꿀풀과 덩굴광대수염(*Glechoma grandis*) 분포 보고

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한국에서는 지금까지 꿀풀과(Lamiaceae) 긴병꽃풀속(*Glechoma*)에 긴병꽃풀[*G. longituba* (Nakai) Kuprian.] 1종만이 분포하는 것으로 알려져 왔다. 그러나 본 연구를 통해 *Glechoma grandis* (A.Gray) Kuprian.가 제주도 일대에서 자생함이 확인되었다. 이 분류군은 국제 식물명 데이터베이스들 상에서 대체로 독립된 종으로 취급되며 일본, 중국 동남부 및 대만에 분포하는 것으로 보고되어 왔다. 반면 일본·대만 등 일부 국가의 분류 처리에서는 이를 *G. hederacea*의 아종 또는 변종으로 처리해 왔다. 국내 문헌에서도 해당 분류군에 대한 인식은 혼재되어 왔다. 『조선식물향명집』(1937)에서는 긴병꽃풀의 학명을 *G. hederacea* var. *longituba*로 기록하였다. 이후 『한국쌍자엽식물지』(1974)는 우리나라에 덩굴광대수염에 해당하는 분류군의 존재를 인식하고 이를 *G. hederacea* var. *grandis*로 처리하는 한편, 꽃부리가 긴 개체를 *G. hederacea* var. *longituba*로 별도로 표기하였다. 그러나 두 분류군의 경계를 명확히 검증하기 보다는 동일종으로 간주하는 통합적 견해를 제시하였고, 이후 국내에서는 이러한 구분이 충분한 재검토 없이 통합되면서 결과적으로 긴병꽃풀 1종만 분포하는 것으로 오인되어 온 측면이 있다. 현지 조사 결과, 제주도 집단은 꽃받침 열편 선단부의 형태와 소포의 상대적인 길이 등에서 긴병꽃풀(*G. longituba*)과 형태적으로 구분되는 특징을 보였다. 또한 한국·일본·중국에서 수집한 40집단 48개체를 대상으로 nrITS 계통분석을 수행한 결과, 제주도 집단은 일본산 *G. grandis* 개체군과 가까운 계통적 관계를 형성하였으며, *G. longituba* 집단과는 별도의 계통군으로 분리되는 양상을 보였다. 이러한 결과는 한국에서 기존에 *G. longituba*만 분포하는 것으로 인식되어 왔으나, 『한국쌍자엽식물지』에서 언급된 덩굴광대수염(*G. grandis*)이 국내에 실존할 가능성을 실증적으로 뒷받침한다. 다만 현재 확인된 국내 표본과 집단이 제한적이므로, 향후 내륙 지역을 포함한 추가 조사와 표본 축적을 통해 국내 분포 범위와 종 경계를 정밀하게 검증할 필요가 있다.

Report of the introduced plant *Angelica pubescens* Maxim. in Korea

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Angelica pubescens Maxim. (Apiaceae), a plant native to Japan and Taiwan, was found in Gyeongsangnam-do (Goseong, Jinju, Haman, and Hapcheon), Korea. Although it resembles the native *A. dahurica*, it is distinguished by longer lower cauline leaf blades; finer leaflet-margin serration; bracts absent and bracteoles absent or rarely one; simple hairs on the mericarp surface; and vittae 3 per vallecule and 6-8 on the commissure. The species appears to be naturalized in Korea and is currently restricted to Gyeongsangnam-do; however, habitat suitability modeling under current and future climate scenarios (SSP1-2.6, SSP3-7.0, SSP5-8.5) predicts a northward expansion of climatically suitable areas with warming. Meanwhile, the young shoots of *A. pubescens* are often confused with those of *Aralia cordata* var. *continentalis* (Araliaceae). In *The Japanese Standards for Non-Pharmacopoeial Crude Drugs*, *A. pubescens* is recorded under the medicinal name “Dokhwai (独活),” which is the same name used for *Ar. cordata* var. *continentalis* in *The Korea Pharmacopoeia*. In addition, given that *A. pubescens* is most commonly distributed around villages in Hapcheon, where medicinal cultivation trials are frequently conducted, it is possible that this species was intentionally introduced for use as “Dokhwai (独活);” however, further investigation is needed to clarify the introduction pathway. These findings suggest that introductions driven by confusion in plant names, together with insufficient post-introduction management, can lead to establishment and spread in natural ecosystems, highlighting the need for systematic monitoring and management of introduced plants.

New generic classification for Korean *Peucedanum* L. (Apiaceae) species based on deep phylogenomic study

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The phylogenetic relationships among Korean *Peucedanum* taxa and other *Peucedanum* s.l. which comprises approximately 140 species, have not yet been thoroughly investigated. In addition, it is necessary to re-evaluate the taxonomic validity of the genus *Kitagawia* which was defined by morphological evidences and partially included Korean *Peucedanum* taxa. From this study, we generated and annotated the chloroplast genome sequences of 11 *Peucedanum* taxa from Korea (excluding *P. coreanum*) and related species, *Sillaphyton podagraria*. Furthermore, we conducted codon usage bias analysis and identification of repetitive sequences to examine the molecular characteristics of each taxon. To assess the phylogenetic relationships between Korean *Peucedanum* and related taxonomic groups in family Apiaceae, we constructed phylogenetic trees using Maximum Likelihood (ML) and Bayesian Inference (BI) methods based on 49 taxa including 37 retrieved sequences and 12 newly obtained from this study. In addition, we estimated the divergence time for each node of the trees. As a consequence, Korean *Peucedanum* taxa were divided into two groups, one (clade A) included ten taxa resolved as a monophyletic and another (*P. japonicum*) was clustered with *Sinopeucedanum* group (clade B). Based on mericarp anatomy of representative species from each clade, clade A shared key characteristics of the genus *Kitagawia* having elongated, lignified cells on the mesocarp. According to the concept of the genus *Kitagawia*, which was well supported by morphological and molecular evidences, ten *Peucedanum* taxa from clade A were supported to be recognized as genus *Kitagawia*. Among them, five were newly transferred to the genus *Kitagawia* from this study. It is estimated *Kitagawia* diverged from *Peucedanum* s.l. at approximately 3.27 Ma, mainly during the Pliocene-Pleistocene interval.

Comparative seed morphology and surface micromorphological characters of ten *Rhododendron* species

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Taxonomic studies of *Rhododendron* have largely focused on palynology, molecular phylogeny, and external morphology, whereas seed morphology and seed-coat micromorphology remain comparatively underexplored. In this study, we examined seeds of ten East Asian *Rhododendron* species to evaluate the taxonomic usefulness of seed morphological characters. Overall seed morphology was documented using electron micrographs, and seed-coat micromorphology was assessed based on diagnostic surface characters, including surface pattern, anticlinal wall, periclinal wall, ridge pattern, ridge density, and ridge morphology. Most species shared a broadly striate surface pattern, yet interspecific variation was evident in the configuration of anticlinal walls and ridge characters. Additionally, both basal wings and apical wings were observed in *R. aureum* and *R. brachycarpum*, while apical wings were observed in *R. micranthum* and *R. mucronulatum*. The seed size, shape, presence of appendages, and surface micromorphological characteristics can be considered for species identification within the genus. Collectively, the combination of gross seed morphology and seed-coat micromorphological characters provides practical features for species discrimination within *Rhododendron* and offers foundational data for further taxonomic research, with potential relevance to restoration and seed-based species authentication studies.

Cirsium vlassovianum Fisch. ex DC. (흰잎영경귀)의 실체

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영경귀속(*Cirsium* Mill.)의 흰잎영경귀(*C. vlassovianum* Fisch. ex DC.)는 Turczaninow가 1831년 러시아 아무르강 유역과 프리모르스키 북부 지역에서 채집한 표본에 기초하여 Fischer ex De Candolle (1837)에 의해 발표된 신종이다. 이후 Maximowicz (1874)는 본 종의 분포 범위를 한국, 만주, 트란스바이칼, 아무르강 하류 지역, 우수리, 한카, 사할린, 일본까지 확장하여 보고하였다. 국내도감 및 선행연구에서 흰잎영경귀는 표본에 근거하여 국내에 분포하는 것으로 언급되어 왔으나, 실제 자생 개체에 대한 현장 확인은 이루어지지 않았다(Chung, 1956; W. Lee, 1996; Y. Lee, 1996; Song and Kim, 2007; Kang, 2020). 본 연구에서 국내에 소장된 흰잎영경귀 표본을 재검토한 결과, 1965년 인천광역시 옹진군 백령면과 대청면 소청리에서 채집된 표본만이 흰잎영경귀로 확인되었으며, 그 외의 표본들은 고려영경귀 [*Cirsium setidens* (Dunn.) Nakai]의 오동정으로 밝혀졌다. 이에 본 연구에서는 표본 정보를 토대로 현장 조사를 수행하여 흰잎영경귀의 자생지를 직접 확인하였고, 이를 통해 국내 분포 및 자생 여부를 명확히 규명하였다. 또한, 본 종의 형태학적 특징을 명확히 하기 위하여 기재문, 도판 및 검색표를 제시하였다.

등골나물속(*Eupatorium*)의 외부 형태학적 및 분자계통학적 연구

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한국에 분포하는 등골나물속(*Eupatorium*) 등골나물(*E. chinense*), 골등골나물(*E. lindleyanum*), 벌등골나물(*E. fortunei*), 향등골나물(*E. tripartitum*), 제주등골나물(*E. japonicum*), 갈래등골나물(*E. makinoi*) 등 6분류군에 대한 기준표본 및 원기재문 재검토, 외부 형태학적 연구, nrDNA ITS에 기반한 분자계통학적 연구를 수행하였다. 본 연구에서 처음으로 국내에 분포하는 벌등골나물(*E. fortunei*)의 분류학적 실체를 확인하였으며, 외부 형태학적 연구 결과, 줄기의 털 유무, 잎의 형태 및 열편 발달, 엽맥, 엽병의 발달 유무, 잎의 선점 유무, 두상화서 및 총포의 형태, 화관의 선모, 갯털의 길이는 각 분류군을 구분하는 데 유용한 형질로 확인되었다. nrDNA ITS5-4구간을 이용한 최대우도법(Maximum Likelihood) 분자계통학적 연구 결과, 대부분의 분류군의 비교적 명확한 계통군을 형성하여 형태적 분화 양상과 전반적으로 일치하는 경향을 보였다.

특성조사요령(TG) 제·개정을 위한 목본류 특성조사: 소나무, 다래, 명석딸기, 밤나무

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특성조사요령(TG; Test Guideline)은 「식물신품종보호법」에 의해 품종의 특성을 설명하는 데 필요한 사항과 재배심사에 필요한 특성을 조사하여 정리한 지침이다. 산림청 국립산림품종관리센터는 2008년부터 현재까지 조경수, 특용, 산채 등 산림식물자원 368건의 TG를 제·개정하였다. 본 연구는 소나무(*Pinus densiflora* Siebold & Zucc.), 다래(*Actinidia arguta* (Siebold & Zucc.) Planch. ex Miq.), 명석딸기(*Rubus parvifolius* L.), 밤나무(*Castanea crenata* Siebold & Zucc.) 등 4종에 대한 수종별 자생지 생육환경 및 개체별 특성을 조사하였으며, 이를 바탕으로 모든 형질을 통합·분석하여 TG 작성에 유용한 특성형질을 선별하였다. 소나무는 전국 6개 지역(양주, 고성, 태안, 장흥, 봉화, 함양)에서 161개체를 대상으로 86개 형질, 다래는 자생지 5개 지역(인제, 원주, 순천, 봉화, 울릉) 및 재배지 3개 지역(화성, 원주 2개소)에서 279개체를 대상으로 132개 형질, 명석딸기는 6개 지역(양평, 강릉, 보령, 제천, 순천, 고령)에서 123개체를 대상으로 80개 형질, 밤나무는 자생지 3개 지역(홍천, 부여, 함양)과 재배지(국립산림과학원 어천시험림)에서 139개체를 대상으로 92개 형질을 조사하였다. 종합적인 조사 및 형질 분석 결과, 소나무는 수형, 수관 형태, 줄기 분지성, 수피 색, 가지 방향, 잎 길이, 수구화수 성전환 유무, 암구화수 색, 구과 길이 및 직경 등 32개 형질, 다래는 나무 성, 가지 단면 형태 및 색, 수꽃 길이, 암꽃 직경, 열매 형태, 당도 등 35개 형질, 명석딸기는 가지 색, 가지 수, 잎 길이, 꽃잎 형태, 열매 길이 등 32개 형질, 밤나무는 잎 길이, 화서 수, 미상화서 길이, 밤송이 수, 견과 낙과 유형, 당도 등 41개 형질을 TG 특성으로 선정하였다.

한국산 자작나무속(*Betula* L.) 열매 형태에 의한 분류학적 연구

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자작나무속(*Betula*)은 주로 북반구에 분포하며 전 세계 약 60종이 보고되고 있다. 국내에서는 북한에 자생하는 자작나무와 좀자작나무를 제외한 개박달나무(*Betula chinensis* Maxim.), 거제수나무(*B. costata* Trautv.), 물박달나무(*B. dahurica* Pall.), 사스래나무(*B. ermanii* Cham.), 박달나무(*B. schmidtii* Regel) 5종이 분포하는 것으로 알려져 있다. 본 속의 열매는 분류학적 주요 형질로 알려져 있으나, 현재 일부 외부형태학적 연구만이 이루어졌으며, 국내의 미세형태학적 연구와 해부학적 연구는 전무한 실정이다. 따라서 북한에 자생하는 좀자작나무와 자작나무를 제외한 한국산 자작나무속 5종을 대상으로 열매의 외부형태 및 미세형태학적 연구와 해부학적 연구를 수행하여 분류학적 유용 형질을 조사하였다. 열매는 모두 소견과로 외부형태학적 및 미세형태학적 연구 결과에 따라 열매의 크기, 날개 너비, 표면 털의 분포가 분류학적 유용 형질로 파악되었다. 해부학적 연구의 경우 퇴화된 내과피를 제외한 외과피와 중과피의 두께와 구조에서 유의미한 차이가 확인되었다. 외과피는 두께, 세포의 층 수, 세포 형태, 탄닌 세포의 유무와 날개 구성, 중과피는 두께, 층 수, 2차 세포벽 두께 등이 분류학적으로 유용한 형질임이 파악되었다.

도서·연안에 분포하는 비름과 17종의 비교해부학적 연구:
적응 형질과 연속형성층을 중심으로

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비름과(Amaranthaceae s.l.)는 극지방을 제외한 전 세계에 널리 분포하며, 건조지역·해안사구·염습지 등 극한 생육환경에 적응한 분류군을 다수 포함한다. 염생식물(halophytes) 또는 내염성식물(salt-tolerant plants)은 다육화나 수분저장조직 발달 등 유사한 해부학적 형질이 공통적으로 관찰되며, 이러한 수렴 형질은 여러 분계군에서 독립적으로 나타나기 때문에 외부 형태만으로 분류군 경계를 설정하기에는 어려움이 있다. 해부학적 형질은 외부 형태를 보완하고 환경에 대한 적응 형질과 분류학적 적응 형질을 구분하는 데 유용한 근거가 된다. 본 연구에서는 비름과 17종(가는갯는쟁이, 창갯는쟁이, 둥근잎명아주, 양명아주, 취명아주, 냄새명아주, 좁은잎명아주, 명아주, 솔장다리, 수송나물, 통통마디, 호모초, 나문재, 좁은해홍나물, 칠면초, 기수초, 해홍나물)의 뿌리·줄기·잎·화경 등 영양기관을 대상으로 파라핀 포매 및 Safranin O-Fast Green FCF 이중염색을 통해 해부학적 형질을 비교하고 생육환경에 대한 적응 형질을 고찰하였다. 관찰 결과, 염생 분류군이 포함된 *Salsola*, *Salicornia*, *Corispermum*, *Suaeda* 속에서 수분저장조직이 확인되었다. 솔장다리와 수송나물을 제외한 대부분의 분류군은 양면엽이었으나 책상·해면조직의 구분이 불명확한 위양면엽(subisobilateral) 특징을 보였다. 크란츠(Kranz) 해부구조는 양명아주, 취명아주, 솔장다리, 수송나물에서 관찰되었고, 솔장다리와 수송나물은 salsoloid형에 해당하였다. 또한 17종 모두의 뿌리 및 줄기에서 연속형성층(successive cambia)에 기반한 2차생장이 확인되었다. 연속형성층은 주로 석죽목에 속한 분류군에서 보고되며 염생 환경과의 기능적 연관성이 제기되어 왔다. 반복적 유관속 증가(vascular increments)와 결합조직(conjunctive tissue)의 교대 배열은 저장·전도 조직의 반복 배치를 통해 염분 스트레스로부터 물·이온의 분산 및 수분 상태 안정화에 기여할 수 있는 것으로 알려져 있다. 다만 해당 형질은 염생식물에만 제한되지 않으므로 생육환경과 형질 발현을 함께 고려해야 한다. 본 연구는 비름과 17종의 해부학적 비교 정보를 제시하였고 수렴 형질의 진단뿐만 아니라 분류학적 적응 가능성과 생태적 시사점을 논의하였다.

국내 분포 개자리속(*Medicago* L.) 및 토끼풀속(*Trifolium* L.) 종자의 형태학적 분류

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본 연구는 사료작물인 알파파의 산림 내 작물재래원종(Crop Wild Relatives: CWR)에 해당하는 개자리속(*Medicago*) 중 국내 도입종 잔개자리(*M. lupulina*), 좁개자리(*M. minima*), 자주개자리(*M. sativa*), 개자리(*M. polymorpha*)와 근연속인 토끼풀속(*Trifolium*) 내 토끼풀(*T. repens*), 노랑토끼풀(*T. campestre*), 애기노랑토끼풀(*T. dubium*), 붉은토끼풀(*T. pratense*)을 대상으로 형태를 기반으로 한 분류 유용성을 확인하기 위하여 진행되었다. 연구재료는 국립백두대간수목원 시드뱅크에 보존되고 있는 국내 수집 종자를 사용하였다. 형태는 외부형태와 미세형태를 바탕으로 분석하였으며, 외부형태는 스펙트럼이미지 분석기와 광디지털현미경을 이용하였다. 미세형태는 가속전압 15kv, WD 10~15mm에서 주사전자현미경을 이용하여 촬영하였다. 외부형태 분석 결과, 각 형질은 종 간 차이가 확인되었으나, 잔개자리의 집단 내에서도 크기 등 일부 형질의 유의한 차이가 확인되었다. 이에 따라, 외부 형태의 경우에는 종간의 분류에는 유용하지 않다고 판단하였다. 다만, 종자의 dorsal view는 각 집단 간의 차이의 유의성이 나타나지 않음에 따라, dorsal view의 경우에는 종자의 1차 분류에 있어서 유용함이 확인되었다. 종자의 미세 형태 분석 결과, 모든 종에서 표면에 큐티클층이 존재하였다. 종자 표면의 세포 병충벽의 경우, 개자리속의 경우에는 spherical 형태로 표면에는 돌기 없이 smooth(평활상) 형태로 존재하는 반면, 토끼풀속의 경우에는 불규칙한 구조로 표면에는 rugose(주름형)와 faveolate(유공상) 형태로 존재한다. 미세형질의 경우에는 개자리속 내에서 종 간 뚜렷한 차이가 확인되지 않으며, 토끼풀속의 경우에는 형태에 차이가 확인된다. 추가로, 노랑토끼풀의 경우에는 종자의 전체 형태에서 foveate(오목형) 형태가 나타나는 것이 확인되어 다른 종들과 뚜렷하게 구분되는 것이 확인되었다. 이를 바탕으로 형태 기반 계통 분석 결과, 작물에 해당하는 자주개자리는 개자리, 좁개자리가 유연관계가 가까운 것으로 확인되었고, 이는 동시 진행된 분자 계통분석 결과와도 일치한다.

Comparative seed micromorphology of Euphorbiaceae in Korea and its taxonomic significance

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In the world, Euphorbiaceae comprises about 330 genera and 6,500 species. It mainly distributed in the tropical and subtropical regions, with some species extending into temperate areas. In Korea, about 20 species are distributed in eight genera. This study examined 17 species distributed in Korea, including the endemic species *Euphorbia fauriei* and *Glochidion chodoense*, and the two alien species *E. maculata* and *E. nutans*. The classification followed Engler's system. Seed micromorphological characteristics are usually considered to be unaffected by environmental factors and are known to be particularly important for identifying the genus *Euphorbia*. Seed micromorphological characteristics were examined using scanning electron microscopy (SEM). Taxonomically important characteristics were identified as seed size, seed shape, caruncle presence and shape, seed ornamentation, seed surface microsculpture, shape of the periclinal wall and anticlinal wall, these characteristics were useful for interspecific identification. In particular, *G. chodoense*, *Flueggea suffruticosa*, *Phyllanthus urinaria*, and *P. ussuriensis*—taxa formerly treated within Euphorbiaceae—were all observed to have a sectoroid, three-sided seed shape. Accordingly, these four species are better treated within Phyllanthaceae under the APG IV system rather than Euphorbiaceae of Engler's system.

Spore Morphological Study of Korean Island and Coastal Lycophytes and Pteridophytes (II)

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This study analyzes spore-based reproductive traits of native ferns distributed in island, coastal, and inland regions of Korea, aiming to establish a morphological dataset for taxonomic research and biodiversity conservation. Because fern spores are extremely small and difficult to identify visually, advanced microscopic analysis is required for accurate taxonomic interpretation. Spore morphology of 100 taxa occurring mainly in island and coastal regions was investigated over a two-year period. These taxa represent 23 families 49 genera were examined using living materials and verified voucher specimens collected since 2024. Taxonomic treatment followed the Pteridophyte Phylogeny Group I (PPG I) classification system. Spore characters were documented using standardized English terminology, with quantitative data provided for major diagnostic features, including polar axis length (P), equatorial diameter (E), laesura length, and spore wall ornamentation. Each taxon was illustrated using light microscopy (LM) and field-emission scanning electron microscopy (FE-SEM) images to facilitate detailed comparison. The results were compiled into 「Spore Atlas of Korean Island Ferns I」, providing an essential reference for fern taxonomy, reproductive trait studies, and biodiversity conservation.

Sequence characteristics of Korean chestnut trees (*Castanea*, Fagaceae)

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Chestnut (*Castanea*, Fagaceae) comprises ecologically and economically important nut tree species with a cultivation history in Korea exceeding 1,500 years as a vital food source. Despite widespread cultivation, detailed nucleotide sequence variation patterns across natural and cultivated populations of Korean chestnuts remain poorly understood, impeding effective germplasm conservation and breeding efforts. In Korea and Japan, *Castanea crenata* Siebold & Zucc. (Korean/Japanese chestnut, locally “bamnamu”) is distributed, whereas *C. mollissima* Blume (Chinese chestnut, locally “yakdanbam”) is native to China. In northern Korea, natural hybrids between these species, known as “Yakbamnamu” occur due to the predominantly insect-pollinated, outcrossing nature of chestnuts and overlapping distributions. In 1958, severe damage from the chestnut gall wasp (*Dryocosmus kuriphilus*) caused widespread mortality of native and cultivated trees in Korea. To recover production, blight- and gall wasp-resistant cultivars were imported from Japan and integrated with Korean local germplasm in extensive breeding programs. This study characterized the genetic features of Korean native *C. crenata* using chloroplast and nuclear markers from over 100-year-old individuals. We sequenced three chloroplast regions (*rbcL*, *matK*, and *trnL* intron/*trnL-trnF* intergenic spacer) and the nuclear ribosomal ITS (nrITS) region, with cloning to resolve intragenomic polymorphisms in nrITS. Results identified two distinct chloroplast haplotypes in Korean *C. crenata*, clearly differentiated from those of *C. mollissima*. nrITS analysis detected at least three sequence types per species, with some Korean *C. crenata* individuals containing additional *C. mollissima*-type sequences, indicating introgression from *C. mollissima*, likely through historical natural hybridization events (e.g., Yakbamnamu ancestry). These findings facilitate reliable identification of hybrid-origin individuals (Yakbamnamu) and inference of maternal (cpDNA-uniparental) and paternal/biparental (nrITS) lineages. This integrated molecular approach offers valuable insights into the origins of Korean chestnut populations, supports conservation of native genetic resources, and informs future breeding for resilient, high-quality cultivars.

미기록종 꼭두선이과 신안백정화(*Serissa serissoides* (DC.) Druce) 분포 보고

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꼭두선이과(Rubiaceae) 백정화속(*Serissa*)의 *Serissa serissoides* (DC.) Druce가 한반도 서남해안에 자생하는 것이 본 연구에서 처음으로 확인되었다. *Serissa serissoides*는 중국 장시성(Jiangxi, 강서성)에서 처음 보고되었으며, 현재까지 중국 안후이성, 푸젠성, 광둥성, 광시성, 후베이성, 장쑤성, 장시성, 저장성 및 대만에 분포하는 것으로 알려져 있다. 한반도에서는 이 종이 2021년 전남 신안군 암태도 박달산 기슭 동사면에서 처음 발견되었으며, 해발 10-50 m 높이에서 200여 개체가 생육하는 것으로 조사되었다. *Serissa serissoides*는 잎, 화서, 꽃, 열매, 종자의 형태적 특징에 있어 같은 속의 백정화(*S. japonica* (Thunb.) Thunb.)와 뚜렷이 구별된다. 본 종은 신안군에서 처음 발견되었기에 '신안백정화'로 국명을 부여하였다. 신안백정화(*S. serissoides*)와 백정화(*S. japonica*) 형태적 특징 비교, 신안백정화의 정기준표본 및 본 연구기간 발견지에서 확보한 표본의 사진, 그리고 속 내 유일(唯二)한 상기 2종 간의 대조되는 특징을 보여주는 검색표 등을 제시한다.

Plastid genome characterization of the African endemic legume *Humularia*

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The papilionoid legume genus *Humularia* currently has 34 species distributed across Central and Eastern Sub-Saharan Africa. It was described in 1954 in an attempt to resolve the taxonomic complexity between *Bryaspis* and *Geissaspis* and is morphologically distinct from these related genera by the combination of emarginate inflorescence bracts and panduriform standard petals. To expand genomic knowledge of *Humularia* and provide a foundation for phylogenetic, taxonomic, and evolutionary studies, as well as to support future research on genetic diversity and conservation, the presented study was conducted on comprehensive plastid genome characterization of seven species: *H. elisabethvillena* (Brunudi), *H. reekmansii* (Tanzania), *H. apiculata*, *H. kapiriensis*, *H. minima*, *H. pseudoaeschynomene*, and *H. rosea* (Zambia). We used genome skimming sequencing methods to assemble the plastomes. The *Humularia* plastomes range from 155,462 to 156,160 bp in length and with a GC content of 35.6%, comprising 127 genes, including 82 protein-coding genes, 37 tRNAs, and 8 rRNAs. A plastome-based phylogeny including available sequences from GenBank strongly supported a monophyletic *Humularia* as sister to the African genus *Kotschya*. However, rigorously confirming the monophyly of *Humularia* will require a broader taxon sampling within the largely polyphyletic genus *Aeschynomene* in the Dalbergia clade.

Genome skimming provides phylogenetic insights into the taxonomic treatment of a Korean population of *Leuzea chinensis* (Cardueae; Asteraceae)

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The genus *Leuzea* DC. (= *Rhaponticum* Ludwig; Cardueae; Asteraceae) is notorious for its intricate taxonomic boundary and controversial infrageneric classification. Of approximately 30 species recognized in the genus, only two species have been recorded in East Asia: *L. uniflora* (L.) DC. and *L. chinensis* (S. Moore) Susanna. A recent investigation reported a new occurrence of *L. chinensis* in the Korean Peninsula, while this species has been previously considered endemic to China. This novel finding led us to propose three alternative hypotheses to explain the disjunct distribution of *L. chinensis* between Korea and China: 1) homoplasy between two distinct lineages; 2) vicariance of a lineage through paleoclimatic and paleogeographic changes in East Asia; and 3) dispersal from widely distributed Chinese populations to a narrowly confined Korean population. To resolve the phylogenetic relationships among *L. chinensis* populations and elucidate the origin of the Korean population, we assembled nuclear ribosomal and chloroplast genomic sequences using a genome-skimming approach. Phylogenetic analyses based on both nuclear and chloroplast data inferred a close relationship between the two East Asian *Leuzea* species and strong monophyly of *L. chinensis*, making the homoplasy hypothesis less plausible. The robust monophyly of geographically disjunct *L. chinensis* populations rather suggested scenarios involving either ancestral/recent dispersal or vicariance. Ongoing studies will further dissect the genomic signature of two mutually exclusive hypotheses, ultimately clarifying the taxonomic delimitation and evolutionary trajectory of the Korean *L. chinensis* population.

Chloroplast genome sequencing of three *Viola* species and comparative plastome analysis within *Viola* subsect. *Rostratae* (Violaceae)

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In this study, we report complete chloroplast genomes of three species within *Viola* subsect. *Rostratae* (*V. faurieana*, *V. jordanii*, and *V. rostrata*) and perform comparative plastome analyses of 11 taxa to reassess phylogenetic relationships and series-level classification. The three species possessed chloroplast genomes of 158,179 to 158,489 bp (GC content: 36.1-36.2%) in length, each comprising 84 protein-coding genes, 8 rRNA genes, and 37 tRNA genes. IRscope analysis revealed the formation of $\Psi ndhF$ in *V. jordanii* at the IR-SSC boundary. mVISTA analysis showed that nucleotide variation was concentrated in non-coding regions of the LSC and SSC, with East Asian taxa of ser. *Rosulantes* exhibiting similar patterns of variation. Phylogenetic analysis strongly supported the monophyly of subsect. *Rostratae* (BP=100, PP=1.00). At the series-level, European ser. *Arosulatae* diverged in the most basal position and was distinct from East Asian taxa, whereas ser. *Rosulantes* and ser. *Mirabiles* formed a supported clade. Within ser. *Rosulantes*, East Asian taxa formed a distinct clade. These findings indicate that biogeographic patterns, which have not been adequately incorporated into previous studies, serve as an important character for series-level delineation and warrant a reassessment of the current classification system. Although the present study is based exclusively on chloroplast genome data, future work should integrate nuclear DNA data and additional morphological characters and employ time-calibrated phylogenetic analyses to clarify divergence times and historical distribution within subsect. *Rostratae*.

백서향나무 종복합체의 분자계통학적 연구

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국내 자생하는 백서향나무와 그 근연종은 중국, 대만, 일본, 한국 등 동아시아 지역에 분포하는 양상을 보인다. 본 연구에서는 백서향나무(*Daphne kiusiana* Miq), 서향(*Daphne odora* Thunb.), 제주백서향(*Daphne jejuensis* M. Kim)을 포함하여 국내외에 자생하는 백서향나무류와 중국 및 대만에 자생하는 근연종들로 구성된 집단을 이하 '백서향나무 종복합체(*Daphne kiusiana* complex)'로 명명하고, 이들을 대상으로 계통학적 유연관계를 밝히고자 하였다. 백서향나무 종복합체는 잎의 형태나 화서 등 몇 가지 형태적 형질을 중심으로 분류되어 왔으나, 최근 연구에 따르면 화서당 꽃의 수, 화탁통의 길이, 그리고 화탁통 외부 표면의 털 밀도 여부를 제외하면 종 단위에서 형태적 형질만으로 이들을 명확하게 구분하기 어려운 것으로 보고되고 있다. 본 연구에서는 백서향나무 종복합체의 핵 리보솜 ITS 구간과 엽록체 전장유전체를 이용하여 계통학적 유연관계를 분석하였다. 그 결과, 서향은 잡종 기원으로 나타났으며, 개체마다 서로 다른 부모종 조합을 갖는 것으로 확인되었다. 또한 핵 ITS 및 엽록체 전장유전체 기반 계통분석 결과, 자생하는 백서향나무 종복합체는 한반도를 기준으로 (한반도 동남부-일본) 지역의 East clade와 (한반도 서남부-중국) 지역의 West clade로 구분되는 두 개의 독립적인 계통으로 구성되어 있음을 보여주었다. 더 나아가, 한국·중국·일본의 세 지역별로 엽록체 전장유전체가 지리적으로 구조화되어 있음을 확인하였다.

**Analysis of genetic diversity among populations of
Menyanthes trifoliata using SSR markers**

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Genetic diversity and population structure of *Menyanthes trifoliata* were investigated using microsatellite (SSR) markers to evaluate patterns of genetic variation among geographically isolated populations. A total of 30 individuals from four regions—Korea, Japan, Russia, and the United Kingdom—were analyzed. Genetic diversity indices, analysis of molecular variance (AMOVA), and principal coordinate analysis (PCoA) were used to assess within- and among-population variation. At the species level, *M. trifoliata* maintained relatively high genetic diversity despite its clonal growth habit and fragmented wetland habitats. In contrast, genetic diversity varied markedly among populations. AMOVA revealed that a substantial proportion of genetic variation was partitioned among populations, indicating restricted gene flow. PCoA further demonstrated clear genetic structuring corresponding to geographic origin, separating East Asian and European populations. Korean populations showed pronounced genetic distinctiveness, likely reflecting long-term geographic isolation, habitat reduction, and their location at the eastern margin of the geographic range. These patterns are consistent with post-glacial range expansion followed by regional isolation and limited dispersal in wetland environments, highlighting the importance of conserving geographically distinct populations.

Phylogenetic relationships of the Korean *Angelica* (Apiaceae) inferred from the complete chloroplast genome

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The genus *Angelica* L. (Apiaceae) comprises approximately 110 economically valuable species. Despite numerous morphological and phylogenetic studies, the taxonomic classification of *Angelica* species remains complex and controversial. As a result, chloroplast genome sequences have been extensively employed to elucidate these relationships. In this study, the complete chloroplast genomes of four *Angelica* species were newly sequenced. The chloroplast genome sizes ranged from 146,989 to 147,416 bp, with a consistent GC content of 37.8%. All genomes exhibited the typical quadripartite structure, comprising a pair of inverted repeats (IRs; 17,811–18,166 bp) separated by a large single-copy region (LSC; 93,189–93,600 bp) and a small single-copy region (SSC; 17,743–17,924 bp). Each chloroplast genome contained 113 unique genes, including 79 protein-coding genes, 30 transfer RNA genes, and four ribosomal RNA genes. Extensive IR expansion and contraction events were observed among the *Angelica* species. Based on these structural variations, the *Angelica* chloroplast genomes were categorized into six distinct types. Genetic divergence analysis revealed that the psbM–psbD region exhibited the highest nucleotide diversity ($\pi = 0.05233$). Phylogenetic reconstruction based on complete chloroplast genomes resolved *Angelica* as paraphyletic, forming three distinct clades. These results provide valuable genomic resources and offer new insights into the evolutionary history and phylogenetic relationships of *Angelica* and the broader Apiaceae family.

Phylogenetic incongruence and hibrid origin of *Spiraea trichocarpa* Nakai (Rosaceae) revealed by transcriptome and plastome data

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The genus *Spiraea* L. (Rosaceae) comprises approximately 80-120 species distributed across temperate and subtropical regions of the Northern Hemisphere. Based on morphological characters, the genus has traditionally been divided into four sections. However, recent phylogenetic studies have shown that these sections are not monophyletic, particularly sect. *Chamaedryon*, and phylogenetic incongruence has been reported among different gene trees. To investigate the evolutionary history underlying these issues, we conducted a comprehensive phylogenetic reconstruction using transcriptome and plastid genome (plastome) data from 16 *Spiraea* taxa distributed in the Korean Peninsula, with *Aruncus dioicus* included as an outgroup, representing a total of 17 taxa. A total of 705 single- or low-copy nuclear genes were identified through orthologous gene selection and paralog removal. Phylogenetic analyses based on these nuclear genes revealed that *Spiraea trichocarpa* occupied two alternative phylogenetic positions, forming a sister relationship with five species of sect. *Chamaedryon* in 388 single-gene trees, while appearing as sister to sect. *Glomerati* in 317 single-gene trees. Species network inference using all 705 single-gene trees consistently supported a hybrid origin of *S. trichocarpa* across five proposed hypotheses, suggesting that it likely arose through hybridization between the common ancestor of the five species in sect. *Chamaedryon* and the common ancestor of sect. *Glomerati*. Phylogenetic analysis based on maternally inherited plastome data placed *S. trichocarpa* as sister to sect. *Glomerati*, indicating that the common ancestor of sect. *Glomerati* served as the maternal lineage. A haplotype-resolved genome study is currently underway to address this hypothesis in greater detail.

Chloroplast genome comparison, phylogeny, and molecular evolution of five endemic *Potentilla* (Rosaceae) species in Mongolia

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Potentilla sensu lato, a taxonomically complex genus within the Rosaceae, comprises approximately 300 taxa worldwide. Thirteen *Potentilla* taxa, each restricted to limited localities, are currently recognized as endemic to the Mongolian flora. Therefore, the effective conservation of *Potentilla* faces significant challenges due to habitat loss caused by climate change and overharvesting. In this study, we utilized high-throughput sequencing to compare the complete chloroplast genomes of five endemic *Potentilla* species to Mongolia and to evaluate their phylogenetic relationships and local evolutionary patterns. The complete plastomes of the five endemic *Potentilla* species was 156,273-156,395 bp long and exhibited typical quadripartite structure. Genome annotation revealed 113 unique genes, including 79 protein-coding genes, 30 tRNA genes, and four rRNA genes. Two intergenic regions (*ndhF-rp32* and *rp32-trnL*) in the SSC region showed markedly high diversity among chloroplast genomes. Analysis of selection signatures identified two genes (*rpoC1* and *ycf1*) under positive selection. These genes may play important roles in the adaptation of these species to specific geographical environments. The present study provides valuable information on the chloroplast genomes of five endemic *Potentilla* species to Mongolia and lays a foundation for future phylogenetic research and molecular marker development.

한국산 진고사리속(개고사리과) 외잎진고사리의 기원 분석

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개고사리과(Athyriaceae) 진고사리속(*Deparia*)은 동아시아 온대 및 아열대 지역을 중심으로 약 70여 종이 분포하며, 국내에는 약 14종이 자생하는 것으로 알려져 있다. 특히 sect. *Deparia*의 분류군들은 빈번한 잡종화와 배수화 현상으로 인해 종간 경계가 모호하고 연속적인 형태변이를 보인다. 이 속의 진화과정에서 잡종화의 중요성은 꾸준히 제기되어 왔으나 일본이나 중국 등 주변국에 비해 한국 내 자생 잡종 분류군에 대한 연구는 미비한 실정이다. 국내에 자생하는 외잎진고사리는 제주도의 일부 지역에 국한되어 분포한다. 본 분류군은 형태적으로 일본에서 보고된 버들참빛(*Deparia lancea*)과 탐라진고사리(*Deparia petersenii* var. *petersenii*)의 잡종에서 기원한 *Deparia* × *tomitaroana*, 또는 버들참빛과 진고사리(*Deparia japonica*)의 잡종으로 추정되는 *Deparia* × *lobatocrenata*와 유사하지만 정확한 기원은 불분명하다. 따라서 본 연구에서는 분자계통학적 분석과 세포학적 분석을 통해 자생 외잎진고사리의 정확한 기원을 밝히고자 하였다. 핵 DNA (*CRY2*) 및 엽록체 DNA (*matK*, *trnL-F*) 분석결과 외잎진고사리는 버들참빛을 모계로, 진고사리를 부계로 하여 형성된 잡종으로 밝혀졌다. 또한 유세포 분석 결과 외잎진고사리의 유전체 크기는 부모 종들의 중간값을 나타내어 이러한 잡종 기원을 뒷받침하였다. 위 결과를 종합하여 국내 자생 외잎진고사리는 버들참빛과 진고사리의 잡종인 *D.* × *lobatocrenata*임을 최종적으로 확인하였다.

Plastid genome based phylogenetic analysis and identification of molecular markers for cultivated taro (*Colocasia esculenta*) in Korea

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Taro (*Colocasia esculenta*) is a culturally and nutritionally important crop with a long history of cultivation in Korea. However, the genetic diversity of cultivated taro in Korea and its phylogenetic relationships with global taro remain insufficiently understood, and molecular tools for lineage discrimination of cultivated taro are still limited. In this study, we analyzed the complete plastid genomes (plastomes) of four cultivated taro samples from South Korea (CESKR01-CESKR04), conducted phylogenetic analyses, and identified plastome-based molecular markers for lineage discrimination and cultivar management. The analyzed plastomes exhibited a typical quadripartite structure, with sizes ranging from 162,376 to 162,546 bp. Phylogenetic analyses clearly resolved the two major cultivated taro plastid lineages (CI and CII). CESKR01, CESKR02, and CESKR03 belonged to the temperate-associated CII haplogroup, whereas CESKR04 was placed within the tropical-associated CI haplogroup, indicating the presence of distinct plastid lineages among cultivated taro in Korea. Based on comparative plastome analyses, plastid simple sequence repeat (cpSSR) and single nucleotide polymorphism (cpSNP) markers were developed, and a total of eight informative markers were selected. These markers provide an effective tool for plastid lineage discrimination in cultivated taro and have applications in germplasm management.

Genetic structure and the potential for cryptic divergence in the Ulleung Island population of *Viburnum furcatum* (Adoxaceae)

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Island biodiversity often displays complex and unpredictable evolutionary patterns. Ulleung Island, a volcanic oceanic island located in the East Sea, is well known for its high level of endemic plant diversity. However, to fully understand the origins of biodiversity on Ulleung Island, it is also essential to investigate non-endemic taxa that are distributed both on the island and the mainland. *Viburnum furcatum* Blume ex Maxim. (Adoxaceae) is a representative non-endemic deciduous shrub found in temperate mountainous regions across Ulleung Island, Jeju Island, and Japan. In this study, we conducted Genotyping-by-Sequencing (GBS) on 95 individuals from 15 populations across Ulleung Island, Jeju Island, and Japan, generating a total of 102,656 SNP loci. Genetic diversity analysis revealed that the Ulleung population had the highest observed heterozygosity (0.215) and the lowest inbreeding coefficient (-0.087), indicating a genetically stable and independently structured population. STRUCTURE, PCA, and maximum likelihood (ML) phylogenetic analyses also showed that the Ulleung population formed a distinct genetic cluster, clearly separated from populations in Jeju and Japan. Pairwise F_{ST} values revealed strong genetic differentiation, with a maximum value of 0.781 between Ulleung and other regions. These results suggest that, despite being a non-endemic species, the Ulleung population of *V. furcatum* has diverged genetically due to geographic isolation. Although morphologically similar to conspecific populations, the Ulleung population exhibits clear genetic distinctiveness, indicating that cryptic divergence may be occurring within this island population.

A population genetic study of *Lysimachia acroadenia* (Primulaceae) from Korea and Japan

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Lysimachia acroadenia Maxim., a perennial herbaceous plant has been found only in Korea and Japan. The distribution in Korea is very restricted in the forested wetlands on Jeju Island and the southern coastal regions of Korea. This species is easily distinguished from other species by the branching pattern, peppery leaves, loosely arranged racemes and glowing spheroidal seed sacs although there appeared some taxonomic confusions with *L. leucantha*. In order to investigate the genetic variations and populational divergence in this species we obtained genome-level of sequence data using the ddRAD-seq method from 67 individuals in Korea and Japan. A total of 17,896 high-quality SNPs were identified and used to assess genetic diversity, population differentiation, and genetic structure. PCoA and STRUCTURE analysis were further conducted to evaluate genetic clustering patterns and admixture among populations. Our results showed the low genetic differentiation among populations within Jeju Island, whereas strong differentiation between inland and Jeju Island populations. In addition, we found that the Korean and Japanese populations were clearly diverged suggesting a limited contemporary gene flow. Taken together, these results suggest that *L. acroadenia* diverged into Korean and Japanese lineages, and that inland Korean populations were likely originated more recently from Jeju populations.

Is there *Suaeda heteroptera* in Korea? A molecular phylogenetic analysis suggests the hybrid origin of Korean *S. heteroptera* between *S. maritima* and *S. heteroptera*.

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The genus *Suaeda* (Amaranthaceae) comprises halophytes widely distributed in coastal marshes and tidal flats, with several species such as *S. glauca*, *S. japonica*, *S. malacosperma*, and *S. maritima* (or *S. australis*) naturally occurring in Korea. Despite their ecological importance, taxonomic identification remains challenging due to high morphological plasticity and a lack of clear diagnostic characteristics, alongside long-standing questions regarding the potential invasion of *S. heteroptera* from Eastern China and reticulate evolution among closely related taxa. To clarify these taxonomic confusions and elucidate the existence of *S. heteroptera*, we collected *Suaeda* specimens with both polymorphic and distinct morphological traits along Korean coastal regions and conducted phylogenetic analyses using chloroplast DNA markers (*rpl32-trnL*, *psbA-trnH*) and nuclear ITS. Our results revealed inconsistent group clustering and significant genetic admixture, particularly involving *S. maritima* and *S. heteroptera*, suggesting complex evolutionary relationships not explainable by simple bifurcating phylogenies. Notably, the data support a hypothesis of a hybrid origin for Korean *S. heteroptera*, potentially arising from hybridization between Korean *S. maritima* and Chinese *S. heteroptera*. These findings enhance our understanding of genetic diversity, hybridization, and ecological differentiation within Korean *Suaeda*, providing critical insights for the taxonomy, conservation, and biogeography of halophytes.

**Complete chloroplast genome of *Solanum carolinense* (Solanaceae),
an invasive plant in Korea**

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Solanum carolinense L., belonging to the family Solanaceae, is a perennial herb or subshrub. *S. carolinense* has become naturalized in Korea as an invasive species, forming a stable population that has grown naturally with native plants for more than 10 years. However, its chloroplast genome structure and complete sequence have not yet been reported. Therefore, we determined the complete chloroplast genome sequence of *S. carolinense* using genome sequencing, assembly, and annotation. The analysis revealed that the plastome exhibited the typical quadripartite structure of most angiosperms, comprising a large single-copy (LSC) region, a small single-copy (SSC) region, and a pair of inverted repeats (IRs). The total length of the chloroplast genome was 155,315 bp with a GC content of 37.6%. The quadripartite structure of the chloroplast genome consisted of an LSC region of 86,160 bp, an SSC region of 18,459 bp, and IRs of 25,348 bp each. It contained 129 genes, including 84 coding sequences (CDSs), 37 tRNA genes, 8 rRNA genes, and one pseudogene. Maximum likelihood (ML) analysis was conducted using 78 CDSs extracted from the chloroplast genomes of 40 species. The analysis revealed that *S. carolinense* is closely related to *S. aridum* Morong and *S. hieronymi* Kuntze. These results provide a molecular basis for phylogenetic and evolutionary studies of the genus *Solanum* and present a fundamental chloroplast genomic resource for future invasion biology research.

Chloroplast genome assembly and phylogenetic analysis of two Korean endemic plants: *Inula minipetala* and *Semiaquilegia quelpaertensis*

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In this study, we sequenced and analyzed the complete chloroplast genomes of two Korean endemic plants, *Inula minipetala* (Asteraceae) and *Semiaquilegia quelpaertensis* (Ranunculaceae), and report their genomic features and phylogenetic placements. Both plastomes exhibited the typical quadripartite structure of most angiosperms, comprising a large single-copy (LSC) region, a small single-copy (SSC) region, and a pair of inverted repeats (IRs). The chloroplast genome of *I. minipetala*, recently confirmed in Geumsan, was 150,781 bp in length (LSC 82,452 bp; SSC 18,435 bp; IR 24,947 bp) and contained 129 genes in total, including 84 coding sequences (CDSs), 37 tRNA genes, and 8 rRNA genes. The chloroplast genome of *S. quelpaertensis*, distributed on Jeju, was 162,312 bp (LSC 91,355 bp; SSC 17,331 bp; IR 26,813 bp) and comprised 128 genes, including 82 CDSs, 38 tRNA genes, and 8 rRNA genes. Additionally, to elucidate the phylogenetic relationships of the two species with their close relatives, we conducted phylogenetic analyses separately for *I. minipetala* and *S. quelpaertensis* using CDSs extracted from the chloroplast genomes assembled in this study together with chloroplast genomes of congeneric relatives retrieved from NCBI (<https://www.ncbi.nlm.nih.gov>). The results showed that *I. minipetala* is most closely related to *I. linariifolia*, and *S. quelpaertensis* is sister to *S. adoxoides*. This study provides chloroplast genome information for the two species, which can be used not only to support accurate identification and conservation of rare and endemic Korean plants, but also as a foundational resource for future phylogenetic and evolutionary studies of these genera.

The complete chloroplast genome of *Lamium purpureum* var. *purpureum*
(Lamiaceae) and phylogenetic analysis

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The genus *Lamium* L. (Lamiaceae) is the type genus of subfamily Lamioideae Harley and comprises approximately 16–40 species. Members of the genus are primarily distributed in the temperate and subtropical regions of Asia, North Africa, and Europe and some species have become introduced in various areas. In this study, the complete chloroplast genome of *Lamium purpureum* L. var. *purpureum* was newly sequenced. The chloroplast genome is 150,474 bp in length, with a GC content of 38.6%. The genome had a typical quadripartite structure and was composed of two inverted repeats (IRs; 25,506 bp), a large single-copy region (LSC; 82,459 bp), and a small single-copy region (SSC; 17,004 bp). It contained 117 unique genes, including 80 protein-coding genes, 33 transfer RNA genes, and four ribosomal RNA genes. Genetic divergence analysis revealed that the *atpE-ndhC* region exhibited the highest nucleotide diversity ($\pi = 0.11226$). The phylogenetic analysis based on complete chloroplast genomes indicated that *Lamium* forms a monophyletic group. These results represent the first complete chloroplast genome report for *L. purpureum* var. *purpureum* and offer valuable information for further studies of the genus.

Chloroplast genome assembly and analysis of *Richardia brasiliensis* (Rubiaceae, tribe Spermacoceae)

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Richardia brasiliensis, an alien plant discovered in Jeju, belongs to the tribe Spermacoceae, where commonly used chloroplast regions for phylogenetic analyses (e.g., *rbcL* and *atpB*) are relatively conserved, limiting phylogenetic resolution and motivating efforts to identify more variable chloroplast regions. Here, we sequenced and annotated the complete chloroplast genome of *R. brasiliensis* and conducted a basic phylogenetic analysis and a preliminary comparative analysis using the genome of related taxa. The chloroplast genome is 154,573 bp (LSC 84,388 bp; SSC 17,411 bp; IRs 26,387 bp each) with a GC content of 43% and contains 127 genes (82 CDSs, 37 tRNAs, and 8 rRNAs); *atpF* is intronless and *infA* is a pseudogene. Phylogenetic inference based on 77 CDSs indicated that *R. brasiliensis* was most closely related to *Oldenlandia corymbosa*. In a comparative analysis of chloroplast genome variation showed little variation among congeneric taxa, whereas variation was observed among genera in both coding and noncoding regions. In addition, comparisons of IR junctions (JLB, JSB, JSA, and JLA) revealed interspecific differences in the positions of genes such as *rps19*, *ndhF*, and *ycf1*, suggesting the possibility of boundary shifts at the IR junction regions. Because this study included only seven taxa of Spermacoceae, denser taxon sampling with additional chloroplast genome data will be necessary to better resolve relationships and to evaluate structural variation across the tribe. Nevertheless, the complete chloroplast genome of *R. brasiliensis* and the comparative results presented here provide a useful reference and a foundation for future phylogenetic and evolutionary studies of Spermacoceae.

Genetic Diversity Patterns of *Rhaphiolepis indica* var. *umbellata* in Korea and China: Implications for Restoration Management

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Rhaphiolepis indica var. *umbellata* (Rosaceae) is an evergreen coastal shrub distributed in southern Korea and China. Owing to its high tolerance to harsh coastal environments, it is widely used in restoration and landscaping. Recently, however, the increasing introduction of foreign plant materials has raised concerns about potential genetic contamination of native populations. To provide a scientific basis for regional genetic resource management, we investigated genetic diversity and population structure of this species. A total of 105 individuals from 12 populations in Korea and China were analyzed using a high-quality reference genome (752,519,896 bp) generated by PacBio long-read sequencing. Multi-sample genotyping identified 15,751 high-quality single nucleotide polymorphisms (SNPs). Genetic diversity analyses showed that Korean populations exhibit higher genetic diversity than Chinese populations. Population structure analyses based on ADMIXTURE and principal component analysis revealed clear genetic differentiation between Korean and Chinese populations, whereas no distinct genetic structure was detected among Korean populations, indicating geographic homogeneity. From the genome-wide SNP dataset, 31 candidate loci were initially selected, and these markers are suggested to be effective in discriminating Korean genetic resources from Chinese populations. Overall, our results demonstrate that Korean populations maintain high genetic diversity without regional structure, yet remain genetically distinct from Chinese populations. This study provides valuable genomic resources and molecular tools to support sustainable restoration and conservation management in Korea.

Draft genome assembly and population genetic structure of *Euonymus japonicus* Thunb.: implications for coastal forest restoration

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Euonymus japonicus Thunb. (Celastraceae) is a widely distributed evergreen shrub with high tolerance to sea winds and salinity, making it suitable for coastal forest restoration. Despite its ecological significance, genetic studies of *E. japonicus* remain limited. Here, we present a draft genome assembly of *E. japonicus* generated using PacBio long-read sequencing. The assembled genome consists of 132 contigs with a total length of 285.3 Mb, an N50 of 8.6 Mb, and 98.1% completeness based on BUSCO analysis, providing a high-quality reference for population genetic analyses. Using this reference genome, we analyzed genetic diversity and population structure of 107 individuals from 13 populations in Korea and China based on 3RAD sequencing and identified 12,357 high-quality single nucleotide polymorphisms. Population structure analyses using ADMIXTURE and principal component analysis revealed partially shared genetic ancestry between Chinese and some Korean populations, suggesting historical connectivity or gene flow across regions. However, analysis of molecular variance (AMOVA) indicated significant genetic differentiation among populations ($F_{ST} = 0.145$, $P = 0.001$), with 14.5% of the total genetic variation attributable to differences among populations, while most variation was distributed within individuals. These results suggest that although *E. japonicus* populations share common genetic backgrounds across East Asia, population-level genetic structure has been maintained. Our study demonstrates that the draft genome assembly enables robust assessment of genetic diversity and population structure in *E. japonicus* and provides valuable genetic insights for the selection and management of plant materials in coastal forest restoration and conservation programs on the Korean Peninsula.

Comparative Genetic Structure of Two Korean *Sorbus* Species:
S. commixta Hedl. and *S. ulleungensis* Chin S. Chang

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The genus *Sorbus* L. s.s. (Rosaceae) comprises approximately 90 species, with five species occurring in Korea. *S. commixta* is widely distributed across East Asia, including Korea, Japan, the Kuril Islands, and Sakhalin (Russia), while *S. ulleungensis* is endemic to Ulleung Island. *S. ulleungensis* has recently been recognized as a distinct species from *S. commixta* based on morphological characteristics. A chloroplast-based molecular study further provided preliminary evidence for genetic divergence between these two species. In this study, we used a genome-wide 3RAD-seq approach to (1) compare the genetic structure of *S. commixta* and *S. ulleungensis*, and (2) examine regional genetic differentiation within *S. commixta* across Korea. We analyzed 10 populations (94 individuals) of *S. commixta* from Korean native habitats and one population (8 individuals) of *S. ulleungensis* from Ulleung Island. Based on a total of 45,933 single nucleotide polymorphisms (SNPs), population structure analyses (admixture, ML tree and PCA) revealed clear genetic differentiation between the two species, consistent with the previous chloroplast-based study. Within *S. commixta*, regional genetic clusters were detected among Korean populations, despite the bird-mediated seed dispersal of berry-like pomes. This geographic genetic structure may be attributed to the habitat characteristics of this species, which primarily occurs in high-altitude regions (approximately 500m to over 1,000m elevation). This study provides genome-wide insights into the genetic structure of Korean *Sorbus* species. Future studies incorporating comprehensive sampling of *S. ulleungensis* across Ulleung Island and *S. commixta* populations from other regions (Japan and Russia) will facilitate understanding of the evolutionary history and divergence patterns of these species.

P3-21. 포스터 발표

The complete plastid genome of Korean endemic *Aster danyangensis* J.Y.Kim & G.Y.Chung (Asteraceae): comparative genomic and phylogenetic analyses

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Aster danyangensis J.Y.Kim & G.Y.Chung, a biennial plant belonging to the Asteraceae family, is Korean endemic species and distributed in Gyeonggi-do, Chungcheongbuk-do, etc and has high scholarly value. This plant is designated as a national rare and endemic plant. Because it grows in specific environments, such as gravel or sandy soil, it is an important indicator of the ecosystem and the potential to be developed as a horticultural species. Furthermore, it is considered evidence of independent speciation in isolated geographic locations, and therefore has important implications for studying biological evolutionary processes. The taxonomic status of *A. danyangensis* J.Y.Kim & G.Y.Chung needs to be clarified. Despite its rarity, the importance of evolutionary research, the importance of biodiversity conservation research, and its potential for horticultural industrial applications, its genome information is lacking, and genetic studies are insufficient. In this study, we assembled the chloroplast genome of *A. danyangensis* J.Y.Kim & G.Y.Chung, a Korean endemic, and performed phylogenetic analysis within the *Aster* and related taxa. The chloroplast genome of *A. danyangensis* J.Y.Kim & G.Y.Chung was 152,451 bp long, and contained a total of 174 genes, including 128 protein-coding genes, 38 tRNAs, and 8 rRNAs. By comparing and analyzing the genetic relationships among various species within the *Aster*, the taxonomic position of *A. danyangensis* J.Y.Kim & G.Y.Chung was clarified. The chloroplast complete genome of *A. danyangensis* J.Y.Kim & G.Y.Chung identified in this study provides a foundation for developing molecular markers that can distinguish *A. danyangensis* J.Y.Kim & G.Y.Chung within the *Aster*.

Chloroplast phylogenomics revealed preliminary phylogenetic relationships among Korean species of *Anemone* (Ranunculaceae)

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Species of *Anemone* (Ranunculaceae) are perennial herbs of enormous horticultural and medicinal importance, yet species relationships within the genus are poorly known. To clarify species relationships among Korean members of tribe Anemoneae, we conducted phylogenomic analyses based on complete plastome sequences. We assembled complete chloroplast genomes from 17 accessions representing eight Korean species, including three species of *Anemonastrum* and five species of *Anemone*, and reconstructed a maximum likelihood plastome phylogeny to infer species relationships. The plastome based phylogeny recovered well-defined clades corresponding to *Anemonastrum* (x=7) and *Anemone* (x=8), revealing robust and well-resolved species relationships within each lineage. In the x=7 lineage, monophyletic *A. flaccidum* was sister to the clade containing the *A. rossii* - *A. baicalense* group and *A. koraiensis*. In the x=8 lineage, *A. raddeana* was found to be monophyletic and sister to the clade that includes the non-monophyletic species *A. amurensis*, *A. reflexa*, and *A. pendulisapala*. Two independent origins were suggested by the plastome data if *A. pendulisapala* is indeed of hybrid origin. Overall, our results demonstrated important utility and value of chloroplast genomes among Korean *Anemone* species. The currently ongoing phylogenomic analysis based on nuclear genomes will shed additional light into elucidating the evolution of major lineages, including the purported hybrid origin of *A. pendulisapala*, in Korean Peninsula.

Characterization of the complete mitochondrial genome of *Koelreuteria paniculata* (Sapindaceae) and comparative analysis within the family

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Koelreuteria paniculata (Sapindaceae) is an economically and culturally important species valued for its ornamental traits, durable wood, and medicinal use. Plant mitochondrial (MT) genomes exhibit complex structures and size variations, providing valuable insights into species identification and evolution. Herein, we report the first complete MT genome sequence of *K. paniculata*. The complete circular genome (610,364 bp; GC 41.4%) contains 58 unique genes: 32 protein-coding, 4 ribosomal RNA, and 22 transfer RNA genes. A 2,047-bp chloroplast-derived fragment containing *rrn16* and *trnV-GAC* was verified to be transferred into the MT genome. Additionally, we identified 197 simple sequence repeats and 352 dispersed repeats, with the longest repeats spanning 2,084 bp. Codon usage favored A/U-ending codons, a conserved feature in terrestrial plants. Moreover, 468 C-to-U RNA-editing sites were predicted across the 32 protein-coding genes (PCGs), with *nad4* being the most affected. For 25 shared PCGs among Sapindaceae species, the mean *Ka/Ks* ratio (0.64) indicated purifying selection; meanwhile, *atp8*, *matR*, and *nad2* showed positive selection, implying adaptive evolution. Phylogenetic analysis of 28 conserved PCGs placed *K. paniculata* within Sapindaceae. Comparative analysis revealed dynamic MT rearrangements within the family. Conclusively, this study contributes to our understanding of the genome architecture and evolutionary dynamics of *K. paniculata*.

Genetic relationships and conservation strategies of *Arisaema takesimense* and *A. serratum* based on 3RAD-Seq analysis

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Arisaema takesimense Nakai is a perennial herb in the Araceae, and is an endemic species to the Korean Peninsula, distributed in moist mountainous habitats on Ulleung Island. This species is currently classified as Least Concern (LC) by the Ministry of Environment of Korea and Near Threatened (NT) by the Korea Forest Service, indicating the need for a re-evaluation of its conservation status based on improved understanding of ecological conditions and genetic characteristics. In addition, *A. takesimense* has been treated as a synonym of its closely related taxon, *A. serratum* (Thunb.) Schott, resulting in ongoing taxonomic ambiguity. This study was conducted with two objectives: (1) to establish conservation strategies for *A. takesimense* through an assessment of its current distribution and population genomic structure, and (2) to investigate the genetic relationships between populations of *A. takesimense* on Ulleung Island and populations of *A. serratum* from the Korean mainland and Jeju Island. First, a total of 54 individuals from five populations on Ulleung Island were analyzed using the 3RAD-Seq approach, yielding 3,753 SNPs. Genetic diversity analysis showed that the mean expected heterozygosity (H_e) was 0.232 and the mean observed heterozygosity (H_o) was 0.208. The mean inbreeding coefficient (F) was 0.072, showing weakly positive values across all populations. AMOVA results indicated that genetic differentiation among populations accounted for only 1% of the total genetic variation, whereas variation among individuals (43%) and within individuals (56%) constituted the majority. PCoA and STRUCTURE analyses revealed no clear population clustering, indicating that populations of *A. takesimense* on Ulleung Island exhibit a genetically homogeneous structure. To further examine genetic relationships between *A. takesimense* and *A. serratum*, an additional dataset including 44 individuals from four populations of *A. serratum* was analyzed, resulting in a total of 2,972 SNPs. Pairwise F_{ST} analysis revealed that the Jeju *A. serratum* populations are more genetically similar to *A. takesimense* than to their inland counterparts, with moderate differentiation observed between the two groups. These results provide fundamental data for re-evaluating the conservation status of *A. takesimense*, establishing effective conservation and genetic diversity management strategies, and for reassessing its taxonomic position.

Population genomics of *Silene jenseensis* at the southernmost limit in Korea
for establishing conservation strategies

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Silene jenseensis is a perennial herb belonging to the Caryophyllaceae, growing on rocky slopes at elevations above 1,300 m in the mountainous northern regions of South Korea. It is known to be distributed in China, Mongolia, and Russia, with Korea marking the southernmost limit of its native range. Its IUCN Red List status is Near Threatened (NT) according to the Korea Ministry of Environment, and Vulnerable (VU) based on the Korea National Arboretum. Despite this, no population-level genetic study has yet been conducted on this species. Here, we present our population genetic analysis findings in 96 samples across six populations based on genome-wide SNPs as markers, to provide useful information for establishing conservation strategies for the species. Analysis of genetic diversity revealed that all populations exhibited low levels of genetic diversity ($He = 0.161$), and elevated inbreeding ($F = 0.781$). PCoA results showed three genetic clusters, while our STRUCTURE analysis identified as the two optimal groups ($K = 2$). The AMOVA results indicated that most of the genetic variation in *S. jenseensis* occurred among individuals (82%), followed by among populations (12%; $F_{ST} = 0.114$) and within individuals (6%). The results of this study are expected to provide important data for the conservation of *S. jenseensis*.

Comparative chloroplast genome analysis of four *Juniperus* species in Korea (Cupressaceae)

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The genus *Juniperus* (Cupressaceae) shows complex species boundaries in Northeast Asia due to overlapping morphological traits and high ecological plasticity. To investigate plastome variation and phylogenetic relationships among Korean *Juniperus* taxa, we conducted a comparative analysis of complete chloroplast genomes. Seven complete plastomes were assembled from whole-genome sequencing, representing four described taxa (*J. chinensis*, *J. chinensis* var. *sargentii*, *J. chinensis* var. *procumbens*, and *J. rigida*), as well as additional *Juniperus* samples collected from Baekdu Mountain and Pohang. Plastome sizes ranged from 127,489 to 128,283 bp with conserved gene content (82 protein-coding, 33 tRNA, and 4 rRNA genes). A reduced inverted repeat (IR) region near duplicated *trnQ*-UUG genes (167-228 bp) was consistently detected, representing a major source of structural variation. Maximum-likelihood phylogenetic analyses generally recovered the separation of sect. *Sabina* and sect. *Juniperus*. *J. chinensis* and *J. chinensis* var. *procumbens* formed a clade, *J. chinensis* var. *sargentii* was recovered as a distinct lineage in plastome-based analyses, and the Baekdu Mountain sample clustered with *J. sabina*. These results highlight the usefulness of comparative chloroplast genome analyses for investigating phylogenetic relationships and evolutionary history within the genus *Juniperus*.

A PacBio HiFi-based draft genome assembly of the Korean endemic species
Rubus takesimensis

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Rubus takesimensis a Korean endemic species restricted to Ulleung Island and provides a useful system for studying genome evolution within the genus *Rubus*. Here, we present a high-quality draft genome assembly of *R. takesimensis* generated using PacBio HiFi long-read sequencing. The final assembly spans 522.5 Mb with a contig N50 of 98.9 kb and a maximum contig length of 36.8 Mb, demonstrating high continuity. The assembly shows high structural consistency with other *Rubus* genomes and exceptional base-level accuracy with a Merqury Quality Value (QV) of 50.69. Analysis of k-mer frequency distributions using Jellyfish and GenomeScope indicated substantial sequence duplication associated with abundant repetitive elements. Transposable elements, particularly LTR retrotransposons of the Gypsy and Copia superfamilies, account for a large proportion of the genome. Genome annotation predicted 62,719 protein-coding genes, and BUSCO analysis recovered 98.4% of conserved orthologs (rosales_odb12), supporting the high completeness of the assembly. Comparative synteny analyses with related *Rubus* species revealed strong chromosomal collinearity, and Ks distribution analysis identified signatures of both recent duplication events and an ancient whole-genome duplication shared within Rosaceae. These results provide a genomic foundation for future studies of diversification and genome evolution in *Rubus*.

Fruiting traits and genetic variation in *Viburnum sargentii* (Adoxaceae)

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Seed dispersal is a key process of the gene flow resulting in patterns of intraspecific genetic variation. The genus *Viburnum* exhibits pronounced interspecific variation in fruit color and maturation patterns, which makes an excellent case to test the relationship between dispersal patterns and genetic structure within a species. Some species produce red fruits in maturity, while others develop into red, as an intermediate stage, and become in black when fully matured. In this study, we examined genetic structure of *V. sargentii*, which produces red fruits matured at the same time. Individuals of *V. sargentii* were collected from selected natural populations in Korea and China, and single nucleotide polymorphism (SNP) data were generated using a genotyping by sequencing (GBS) approach. These data were used to assess population-level genetic diversity and population structure. In addition, haplotype analyses of chloroplast DNA were conducted to examine haplotype diversity and phylogeographic patterns. A total of 30,312 SNPs were generated following GBS filtering. Genetic diversity was generally high across populations, and most populations exhibited admixed genetic compositions, except for several southern populations in the Korean Peninsula. Levels of inbreeding and genetic differentiation among populations were low, suggesting that there are no significant barriers for gene flow among populations. Analysis of three concatenated chloroplast DNA regions identified seven haplotypes, most of which were shared among geographically distant populations. These patterns suggest that long distance dispersal of the seeds should have occurred across the continental East Asia in *V. sargentii*.

Long-read sequencing resolves complex mitochondrial genome structure of *Deutzia paniculata* L. (Hydrangeaceae)

KSPT Workshop

(Jeongwoo Seo¹, Yun-Gyeong Choi², Junhyun Hur³, Hoesu Jeong⁴, Sein Jeong⁴, Minkyung Jung¹, Se-Eun Jung¹, Hyun-Jun Kang², Iseon Kim⁵, Woo-Ho Kim⁶, Yoon-Su Kim², Dohyeon Kwag³, Ji-Eun Lim⁶, Hyeonji Moon¹, Hwa-Jung Suh², Jiye Suh¹, Tae-Soo Jang⁴, Sang-Tae Kim³, Sang-Hun Oh², Seung-Chul Kim⁵, Young-Dong Kim⁶, Sangtae Kim^{1*})

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Plant mitochondrial genomes are characterized by extensive structural variation, frequent rearrangements, and high levels of polymorphism, which often hinder accurate assembly using short-read sequencing alone. Consequently, long-read sequencing approaches are essential for resolving their complex genomic architectures. Here, we report the complete mitochondrial genome of *Deutzia paniculata* Nakai (Hydrangeaceae), an endangered Korean endemic shrub, assembled using a hybrid sequencing strategy that integrates Oxford Nanopore Technologies (ONT) long reads with Illumina short reads. High-molecular-weight DNA was extracted to ensure the recovery of long mitochondrial fragments, enabling reliable structural reconstruction. Long-read data were assembled using POLAP, an assembler specifically optimized for ONT reads and organellar genome assembly, resulting in a highly reliable mitochondrial genome sequence. The assembled circular mitochondrial genome is 582,750 bp in length with a GC content of 45.4% and contains 64 genes, including 36 protein-coding genes (PCGs), 26 transfer RNA (tRNA) genes, and two ribosomal RNA (rRNA) genes. Eleven genes were identified as cis-spliced, whereas *nad2* was confirmed as a trans-spliced gene, reflecting the complex gene organization typical of plant mitochondrial genomes. Phylogenetic analysis based on 17 conserved mitochondrial PCGs revealed that *D. paniculata* forms a sister relationship with species of *Hydrangea*, supporting its distinct evolutionary lineage within Hydrangeaceae. Overall, this study highlights the necessity of long-read sequencing for resolving structurally complex plant mitochondrial genomes and provides a valuable genomic resource for future phylogenetic, evolutionary, and conservation studies of East Asian Hydrangeaceae.

Understanding mitogenome evolution in mycoheterotrophic orchid
Chamaegastrodia shikokiana Makino & F.Maek. (Orchidoideae)

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While plastome reduction in mycoheterotrophic plants is well documented, mitochondrial genome (mitogenome) evolution remains poorly understood—particularly within the Orchidaceae, where no complete mitogenomes from the subfamily Orchidoideae have been reported. Here, we present the complete mitogenome of *Chamaegastrodia shikokiana*, comprising 19 contigs with a total length of 412,787 bp. In contrast to its significantly reduced plastome, the *C. shikokiana* mitogenome retains a nearly full set of protein-coding genes, lacking only four (*nad1* exon1, *rpl2*, *rpl16*, and *rps19*). We identified 21 plastome-derived homologous regions, including photosynthesis-related and housekeeping genes. However, comparative analyses revealed no significant correlation between these transferred regions and elevated substitution rates or altered selection pressure. Although RELAX analysis indicated a mix of relaxed and intensified selection among plastome genes, these patterns were not associated with intracellular gene transfer (IGT). Our findings suggest that plastome-to-mitogenome gene transfer in *C. shikokiana* occurs independently of functional constraints or adaptive significance. This study provides a crucial reference for filling the phylogenetic gap in Orchidaceae and offers new insights into organellar co-evolution in mycoheterotrophs.

Population genetic structure of *Persicaria thunbergii* in Korea revealed by genotyping-by-sequencing

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Freshwater biological resources are important for advancing the bioindustry, and genetic information is essential for their effective utilization. We applied genotyping-by-sequencing (GBS) to *Persicaria thunbergii* to investigate population genetic diversity and structure and to develop population-discriminatory genetic markers. Five populations (AD, GR, YS, JJ, and UL) were analyzed using genome-wide variants, and population structure was assessed using AMOVA, pairwise F_{ST} , PCA, and STRUCTURE. Observed heterozygosity was highest in YS (0.0616) and lowest in JJ (0.0468), while expected heterozygosity ranged from 0.0597 in UL to 0.2034 in YS. All populations showed positive F_{IS} values, indicating heterozygote deficiency. AMOVA revealed nearly equal genetic variation among populations (49.98%) and within populations (50.02%). Pairwise F_{ST} indicated strong differentiation of UL, whereas the remaining populations showed moderate differentiation (0.3-0.4). PCA and STRUCTURE analyses separated UL and JJ from other populations and revealed admixture among AD, GR, and YS. From the GBS data, indel regions were extracted and 30 homozygous markers were selected, enabling population identification and genetic authentication of freshwater plant bioresources

Genotyping-by-Sequencing 기법을 활용한 해국(*Aster spathulifolius* Maxim.)의 종자 이동 구역(Seed Zone) 설정 연구

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종자 이동 구역(Seed Zone, 이하 시드존)은 기후·지형·토양 등 환경 요인의 차이를 고려하여 종자의 수집과 이동 및 활용 범위를 설정하는 개념으로, 복원 사업에서 종자의 현지 적합성과 안정성을 검토하기 위한 기준으로 제시되고 있다. 국화과(Asteraceae)에 속하는 해국(*Aster spathulifolius* Maxim.)은 제주도 및 전국 해안가에 자생하는 다년생 초본으로, 내염성이 우수하여 해안 생태계 복원 과정에서 주요 식생으로 활용되고 있다. 또한 산림청 「산림 복원용 자생식물 공급 및 활용에 관한 고시」에 따라 복원용 자생식물로 지정되어 있어, 종자 관리 및 이동 범위 설정의 필요성이 제기되고 있다. 따라서, 본 연구는 해국의 유전적 다양성과 집단 구조를 분석하여 시드존 설정을 위한 기초 정보를 제공하고자 수행되었다. 전국 5개 시드존 권역 15개 집단에서 수집한 96개체를 대상으로 Genotyping-by-Sequencing 분석을 실시하였으며, 총 27,171개의 SNPs를 확보하였다. 분석 결과, 해국은 비교적 낮은 수준의 유전다양성 ($He=0.164\sim0.318$)을 보였다. PCoA 및 UPGMA 결과에서는 집단 간 유전적 분화 양상이 확인되었으나, 일부 지리적으로 인접한 집단 간에는 명확한 구분이 나타나지 않았다. 또한, STRUTCUTRE 분석에서도 국내 해국 집단의 유전적 구조는 지리적 거리의 영향을 받는 경향을 보였다. 이러한 유전구조 분석 결과는 해안도서권역 1~3 간에는 유전적 유사성이 비교적 유지되고 있는 반면, 해안도서권역 4와 5에서는 유전적 분화가 상대적으로 뚜렷하게 나타나 해국의 시드존 설정에 있어 권역별 유전적 특성을 반영한 차등적 수집 및 관리 전략을 고려할 필요성을 확인하였다.

Structural variation and phylogenomics of *Adenophora* (Campanulaceae) based on complete chloroplast genomes

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The chloroplast genome of the genus *Adenophora* exhibits remarkable structural variation, providing important information for evolutionary and taxonomic studies. In this study, we newly sequenced chloroplast genomes of nine taxa and performed comprehensive analyses of genome structure, repeat sequences, codon usage patterns, and phylogenetic relationships across a total of 19 *Adenophora* taxa, including 10 previously reported genomes. Comparative genomic analyses revealed nine distinct chloroplast genome structural types characterized by extensive large single copy (LSC) region rearrangements and inverted repeat (IR) boundary shifts. Repeat sequences were predominantly concentrated in the LSC region, with clear differences in the number and distribution patterns of repeat sequences among taxa. Codon usage analysis showed consistent genetic characteristics in most species, whereas *A. himalayana* and *A. pinifolia* exhibited unique patterns. Phylogenetic analyses using 76 protein-coding genes (CDS) through both concatenated and multi-locus species tree approaches revealed complex evolutionary relationships, and topological incongruence between the analytical methods suggests that resolving the evolutionary history of *Adenophora* remains a challenging task. Genome structural variations showed no clear correlation with infrageneric classification. This study provides new insights into the molecular evolutionary diversity of the genus *Adenophora* and is expected to serve as fundamental data for future comprehensive systematic research integrating nuclear DNA markers.

The complete chloroplast genome of *Orostachys thyrsiflora* (Crassulaceae) and its phylogenetic implications

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The genus *Orostachys* is primarily distributed in East Asia and is utilized as an ornamental and medicinal plant. Some species have been identified as important plant resources due to their therapeutic effects, including immunomodulation and antioxidant activities. The genus *Orostachys* is divided into two subsections, *Appendiculatae* and *Orostachys*, based on the presence or absence of leaf tip appendages. *O. thyrsiflora*, belonging to subsection *Appendiculatae*, is restricted to certain regions of Russia, including Orenburg and Kurgan, making it of high conservation value. However, no molecular biological studies at the chloroplast genome level have been conducted on this species. Therefore, this study aimed to decode the chloroplast genome of *O. thyrsiflora* for the first time and compare it with closely related taxa. The results revealed that the chloroplast genome of *O. thyrsiflora* was 151,137 bp in length with a G+C content of 37.8%. The cp genome consists of a large single-copy (LSC) region of 82,861 bp, a small single-copy (SSC) region of 16,798 bp, and two inverted repeat (IR) regions of 25,739 bp each. A total of 113 unique genes, including 79 protein-coding genes, 30 transfer RNA (tRNA) genes, and 4 ribosomal RNA (rRNA) genes, were identified, consistent with other *Orostachys* taxa. Phylogenetic analyses revealed that *O. thyrsiflora* exhibited the closest phylogenetic relationship *M. sikokianus* and clustered and formed a sister group to other taxa in subsection *Appendiculatae* (*O. fimbriata*, *O. latielliptica*, *O. japonica*, *O. japonica* f. *polycephala*, *O. margaritifolia*, *O. minuta*). This study reports the complete chloroplast genome of *O. thyrsiflora* for the first time and evaluates its phylogenetic relationships with closely related taxa, providing foundational data for various research fields.

Multiple alternative mitochondrial genome conformations in *Cyperus microiria* Steud.

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Cyperus (Cyperaceae) comprises approximately 600 species worldwide, including about 18 species native to Korean peninsula, and is characterized by considerable ecological and economic importance in wetland ecosystems. *Cyperus microiria* Steud., which is widely distributed in Korea, China, and Japan, remains poorly characterized at the genomic level despite its ecological significance. Plant mitochondrial genomes exhibit highly dynamic architectures driven by extensive structural variation and repeat-mediated recombination, resulting in multiple alternative and polymorphic conformations that are difficult to resolve using short-read sequencing alone. To provide a robust genomic foundation for future evolutionary and comparative studies, we generated a high-quality assembly of the mitochondrial genome of *C. microiria* using a hybrid strategy that combines long-read Oxford Nanopore sequencing with highly accurate short-read Illumina sequencing. The assembled mitochondrial genome exhibited four alternative conformations, reflecting the multipartite and dynamic nature of plant mitochondrial genomes. The complete mitochondrial genome spanned 870,128 bp with a GC content of 41.0% and contained 34 protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, and three ribosomal RNA (rRNA) genes. Comparative analysis across the Cyperaceae and related Poales lineages demonstrated that while core metabolic genes (e.g., *atp*, *cox*, *cob*, *nad*, and *ccm*) are highly conserved, several ribosomal protein genes (specifically *rps* and *rpl* families) have undergone lineage-specific losses or copy-number reductions. These findings align with the rapid evolutionary patterns observed in Poales mitogenomes and provide a robust genomic foundation for future studies on the molecular evolution and phylogenetic diversity of the Cyperaceae.

Characterization of the chloroplast genome of *Tripterospermum japonicum* (Gentianaceae)

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Tripterospermum japonicum is a perennial climbing plant belonging to the genus *Tripterospermum* (Gentianaceae), distributed in Korea and Japan. In Korea, it is restricted to montane edges of Ulleungdo and Jeju Islands. *T. japonicum* is considered a species of high conservation value due to its restricted geographic distribution. Additionally, pharmacological studies have reported the presence of bioactive compounds in its aerial parts, demonstrating its significant value as a medicinal plant resource. This study aimed to decode the chloroplast genome of Japanese *T. japonicum* and perform comparative analysis with previously reported Korean individuals. The complete chloroplast genome sequence of *T. japonicum* was 151,266 bp in length, with LSC, SSC, and IR regions measuring 82,511 bp, 17,589 bp, and 25,583 bp, respectively. A total of 112 genes were identified, including 78 protein-coding genes, 30 tRNAs, and 4 rRNAs. Comparative analysis of chloroplast genomes between Korean and Japanese individuals revealed sequence differences of 1 bp in the *trnR-ACG* gene and 17 bp in the *ycf1* gene, while all other regions were identical. Maximum likelihood phylogenetic analysis showed that the genus *Tripterospermum* formed a strongly supported monophyletic group, with *T. japonicum* positioned as a sister group to *T. nienkui*, *T. filicaule*, and *T. membranaceum*. This study elucidates the chloroplast genome structure and intraspecific genetic variation of *T. japonicum*, providing fundamental data for phylogenetic studies of the genus *Tripterospermum* and biogeographic research of East Asian populations.

Plastid genome sequence of *Viola arcuata* (Violaceae) from Laos

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Viola arcuata Blume is a widely distributed violate species ranging from Indonesia to Russia (Far East). Plastid genomes have previously been reported for samples as *V. arcuata* from Korea and as *V. verecunda* A. Gray from Japan, with the latter often been treated as conspecific. Here, we report the complete plastid genome sequence of *V. arcuata* from a population collected from Northern Laos to investigate geographic patterns of variation in this broadly distributed taxon. The Laotian plastid genome is 157,768 bp in length (GC content 36.3%) and exhibits the typical quadripartite structure of angiosperm plastomes, consisting of a large single-copy (LSC) region of 86,356 bp, a small single-copy (SSC) region of 17,294 bp, and a pair of inverted repeats (IR) each 27,059 bp long. It encodes 112 unique genes: 78 protein-coding genes, 4 ribosomal RNA genes, and 30 transfer RNA genes. Pairwise sequence comparisons revealed 0.765% divergence (1,208 bp differences) between the Laotian and Korean samples, and 0.761% (1,201 bp) between the Laotian and Japanese samples. In contrast, the Korean and Japanese samples differed by only 0.036% (57 bp). This pattern - low divergence between the closely situated Korean and Japanese populations, but substantially higher divergence to the distant Laotian population - is consistent with an isolation-by-distance (IBD) scenario, where genetic differentiation increases with geographic separation. These results provide the first plastid genome data for *V. arcuata* from mainland Southeast Asia and highlight the potential role of geographic distance in shaping plastome variation within this species complex. Further sampling across the range, combined with nuclear markers, will help clarify whether this reflects neutral IBD or contributions from cryptic divergence or historical barriers.

스트레스 처리에 따른 개느삼 기내배양체 성분의 함량 변화와 전사체 분석

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개느삼(*Sophora koreensis* Nakai)은 한국 특산 다년생 관목으로, 자생지가 강원도 일부 지역으로 제한되어 있다. 이 식물은 항암·항염증·항균·항산화·면역조절 등과 관련된 보고된 유용 화합물을 포함하고 있다. 따라서 개느삼의 이차대사산물을 안정적으로 확보하고 생산 조건을 최적화하기 위해, 스트레스 요인이 생장과 성분 생산에 미치는 영향을 통합적으로 규명하는 연구가 요구된다. 따라서, 유용물질로 scopoletin과 squalene을 설정하고, 개느삼 기내배양체에 sucrose(1, 3, 5%) 및 LED 광원(white, red, blue, red:blue = 2:1, 4:1) 스트레스 처리를 적용하여 두 성분의 함량 변화를 평가하였다. Sucrose 농도가 높아질수록 생장이 촉진되었으며, 특히 5% 처리구에서 생중량이 0.98 g으로 증가하였다. Scopoletin 함량은 sucrose 3% 처리구에서 1125 mg/g까지 증가한 후 5%에서 감소하였다. Squalene은 1% sucrose 처리구에서 148 mg/kg으로 증가한 뒤, 이후 농도 증가에 따라 감소하는 경향을 보였다. 이러한 결과는 sucrose 농도가 생장과 유용물질 축적을 조절하는 중요한 요인이 될 수 있음을 시사한다. LED 처리에서는 짧은 파장(blue) 조건에서 squalene 축적이 0.87 mg/g으로 증가하였다. 추가로 전사체 분석에서는 sucrose와 LED 처리구를 대상으로 De novo transcriptome 구축, 기능 주석 및 DEGs 분석하였다. GO 분석에서 64개, EggNOG 분석에서 24개의 기능적 주석이 있었다. 처리구 간 상관관계 비교에서 sucrose 농도 차이가 유전자 발현 차이를 가장 크게 유도하는 핵심 요인으로 해석되었다. LED 조건에서는 red+blue 혼합광보다 blue 단독 처리에서 DEGs 변화가 더 뚜렷하게 관찰되어, 광 조건 또한 특정 대사 관련 유전자 발현과 연동될 가능성을 제시하였다. 향후 최적 조건 탐색을 통해 기능성 성분의 고효율 생산 및 표준화된 생산 시스템 구축이 기대된다.