

Welcome to the 14th International Conference of the French Society of Plant Biology



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INTRODUCTION

The Organizing Committee, the Scientific Committee, the Federation of the European Societies of Plant Biology, the French Society of Plant Biology and the Biosciences and Biotechnology Institute of Aix-Marseille welcome you to Plant Biology Europe.

This international meeting covers a wide range of Plant Science topics across multiple disciplines and at different scales.

Among the many different themes that are being addressed during the meeting, a particular emphasis is placed on plants and climate changes, algal biology and bioenergy.

SCIENTIFIC COMMITTEE

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DETAILED PROGRAM

MONDAY 3 JULY

- 09:00 – 09:30 Opening Ceremony – Amphitheater 900
- 09:30 – 10:15 Plenary – Amphitheater 900
Malcom Bennett, University of Nottingham, United Kingdoms
Uncovering the hidden half of plants: discovering novel ways roots sense and adapt to heterogeneous environments.
- 10:15 – 11:00 Plenary – Amphitheater 900
Raffaella Balestrini, National Research Council of Italy (CNR-IPSP), Italy
A central role of root symbionts: the plant response to environmental stresses
- 11:00 – 11:30 Coffee Break
- 11:30 – 13:00 Session 1: Plant and algal development and evolution Plenary Amphitheater 900
Chair: **Yoan Coudert**, CNRS/Ecole Normale Sup. de Lyon, France
- 11:30 – 11:50 **Air channels create a directional light signal to regulate hypocotyl phototropism**
Chrisitan FANKHAUSER
- 11:50 – 12:10 **Understanding how flowering plants build communication devices on their petals**
Lucie RIGLET
- 12:10 – 12:30 **A new framework for root gravitropic response kinetics**
Marta DEL BIANCO
- 12:30 – 12:50 **Developmental patterning of head-like inflorescences in Asteraceae**
Paula Elomaa
- 12:50 – 13:00 **Yoan Coudert**
Q&A



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Session 2: Interfaces with plant and soil microbiota Room 120

Chair: **Raffaella Balestrini**, National Research Council of Italy (CNR-IPSP), Italy

- 11:30 – 11:50 **Impact of double root symbiosis (arbuscular mycorrhiza and nodulation) on nutrient distribution in cereal crop-legume interaction**
Pierre-Emmanuel COURTY
- 11:50 – 12:10 **Evolution of microbial community dynamics during field retting of hemp “*Canabis Sativa L.*”**
Eliane BOU ORM
- 12:10 – 12:30 **Psychrotolerant plant-associated bacteria can enhance cold tolerance in crop plants**
Michelle PERAZZOLLI
- 12:30 – 12:50 **Role of zaxinone a novel growth-promoting apocarotenoid metabolite, in shaping rice rhizomicrobiota**
Teresa MAZZARELLA
- 12:50 – 13:00 **Raffaella Balestrini**
Q&A

Session 3: The genetic architecture of quantitative traits in plants Room 76

Chair: **Martin Lascoux**, Sweden

- 11:30 – 11:50 **Fusing genome simulation and crop models for computer-aided breeding in future environments**
Arnaud DESBIEZ-PIAT
- 11:50 – 12:10 **Regulation of sulfur content in *Arabidopsis thaliana* natural variants**
Daniela RISTOVA
- 12:10 – 12:30 **Pervasive Under-Dominance in Gene Expression Underlying Emergent Growth Trajectories in *Arabidopsis thaliana* Hybrids**
Wei YUAN



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- 12:30 – 12:50 **Reconsidering photoperiod-sensitivity for maize adaption to climate change**
Justine DROUAULT
- 12:50 – 13:00 **Martin Lascoux**
Q&A
- 13:00 – 14:00 Lunch
- 14:00 – 14:45 **Plenary – Amphitheater 900**
Marie Barberon, University of Geneva, Switzerland
Plasticity of root permeability for nutrient acquisition
- 14:45 – 15:30 **Plenary – Amphitheater 900**
Juliette de Meaux, University of Cologne, Germany
Polygenic selection and the evolution of gene expression in Arabidopsis lyrata
- 15:30 – 16:00 Coffee Break
- 16:00 – 17:30 **Session 4: Macro- and micro- nutrients in plants**
Amphitheater 900
Chair: **Jérémy Lothier**, University of Angers, France
- 16:00 – 16:20 **The ability of Sorghum bicolor to cope with ammonium nutrition depends on root PEPC activity**
Marin Pena AGUSTIN JAVIER
- 16:20 – 16:40 **Effect of N And Fe deficiencies in poplar roots and root exudates metabolites**
Maria Teresa CIESCHI VILLALBA
- 16:40 – 17:00 **Regulation of CRFs in plant nitrogen (N) sensing and signalling**
Marina BORGES OSORIO
- 17:00 – 17:20 **To be or not to be: a glimpse of micronutrients role in the prediction of plant tissue fate in soybean embryo axis**
Joao Paulo RODRIGUES MARQUES

- 17:20 – 17:40 **Unravelling the spatiotemporal component of carrier-mediated nutrient transport in Arabidopsis thalian roots**
Kevin ROBE
- 17:40 – 17:50 **Jérémy Lothier**
Q&A
- Session 5: Domestication in retrospect and the future of breeding**
Room 120
Chair: **Maud Tenailon**, CNRS, Paris-Saclay, France
- 16:00 – 16:20 **Changes in competitive ability over the course of durum wheat domestication are mediated by plant functional traits**
Taina LEMOINE
- 16:20 – 16:40 **Genetic and phenotypic diversity in timothy and a closely related species**
Yousef RAHIMI
- 16:40 – 17:00 **Genome-wide association studies on DNA pools identifies promising maize landraces and genomic regions to develop next generation varieties**
Stéphane NICOLAS
- 17:00 – 17:20 **Soil, climate and host genotype shape the seed transmissible microbiome structure in the fonio cereal**
Heribert HIRT
- 17:20 – 17:30 **Maud Tenailon**
Q&A
- 17:30 – 17:50 **FESPB Award for Best Young Scientist**
Adaptation and mitigation strategies for grapevine response to climate change based on its physiology
Nazareth Torres

Session 6: Chromosomes and chromatin dynamics
Room 76

Chair: **Mathilde Grelon**, IJPB, Versailles, France

16:00 – 16:20 **Chromatin dynamics during fertilization of a liverwort, *Marchantia polymorpha***
Tetsuya HISANAGA

16:20 – 16:40 **Identification of the first synaptonemal complex central element proteins in plants**
Marion PEUCH

16:40 – 17:00 **Horizontal gene transfer in *Hordeum* species**
Marek SZECOWKA

17:00 – 17:10 **Mathilde Grelon**
Q&A

17:10 – 17:30 **FESPB Award for Best Young Scientist**
Exploring the Genetic Variability of Bean Germplasm for Nutritional Benefits
Carla Sofia Santos

TUESDAY 4 JULY

09:00 – 09:45 Plenary – Amphitheater 900
Kirsten Bomblies, ETH Zürich, Switzerland
Getting organised – the (re)evolution of fertility after genome duplication

09:45 – 10:30 Plenary – Amphitheater 900
Karel Riha, CEITEC MU, Brno, Czech Republic
P-bodies and post-transcriptional gene regulation in plant reproduction and stress response

10:30 – 11:00 Coffee Break

11:00 – 12:30

Session 7: Plant responses to abiotic stresses (Session 1)
Amphitheater 900

Chairs: **Laurent Laplaze**, IRD, Montpellier, France
Abdelazziz Smouni, Université Mohamed V, Rabat, Maroc

11:00 – 11:20 **Improving tomato plant growth under salt and heat stress – rhizosphere-based solutions**
Bruno SOUSA

11:20 – 11:40 **Coupling chloroplast activity to environmental constraints: TOR set the brake on photosynthesis**
Stefano D'ALESSANDRO

11:40 – 12:00 **RabA-mediated plasma membrane trafficking increases plant tolerance to drought and heat**
Yehoram LSHEM

12:00 – 12:20 **New insights on magnesium deficiency-induced molecular alterations in *Arabidopsis thaliana***
Armand D. ANOMAN

12:20 – 12:30 **Laurent Laplaze & Abdelazziz Smouni**
Q&A

Session 8: Plant reproduction: mechanisms and evolution
Room 120

Chair: **Susana Coelho**, MPI, Germany

11:00 – 11:20 **The F-box protein UFO controls flower development by redirecting the master transcription factor LEAFY to new cis-elements**
François PARCY

11:20 – 11:40 **Timely endosperm elimination in *Arabidopsis* requires a programmed cell death pathway regulated by NAC transcription factors**
Nicolas M. DOLL

11:40 – 12:00 **MAP Kinase signaling in cell polarity – a lesson from the plant tolerance to drought and heat**
Martin BAYER

Session 11: Organellar biology

Room 120

Chair: **Ben Field**, BIAM, Marseille, France

- 15:30 – 15:50 **CRY1-to-GUN1 anterograde pathway promotes early PSII biogenesis**
Chaajun CUI
- 15:50 – 16:10 **Genetic inactivation of mitochondrial complexes I and IV in Physcomitrium patens: deciphering the role of respiration in plant bioenergetics and primary metabolism**
Antoni Mateu VERA VIVES
- 16:10 – 16:30 **Role of mitochondrial activities in the under-ground early development of Arabidopsis seedlings**
Livia MERENDINO-ISENI
- 16:30 – 16:50 **Cytoneuclear interactions in auto- and allopolyploids of Festuca-Lolium complex**
Jana SZECOWKA
- 16:50 – 17:00 **Ben Field**
Q&A

Session 12: Comparative genomics

Room 76

Chair: **Bruno Contreras-Moreira**, CSIC Zaragoza, Spain

- 15:30 – 15:50 **The first pan-genome of a non-vascular plant broadens the understanding of land plants adaptation to their environment**
Chloé BEAULIEU
- 15:50 – 16:10 **Adapting CRISPR from Physcomitrium patens to sexually dimorphic moss, Ceratodon purpureus**
Emilie-Katherine TAVERNIER
- 16:10 – 16:30 **The evolution of Arabidopsis centromeres**
Fernando RABANAL

- 16:30 – 16:50 **Divide and conquer: Evolutionary adaptations of the plant cytoskeleton during cell division**
Katharina BÜRSTENBINDER

- 16:50 – 17:00 **Bruno Contreras-Moreira**
Q&A

- 17:00 – 18:00 Poster Session A

WEDNESDAY 5 JULY

- 09:00 – 09:45 Plenary – Amphitheater 900
Aline Muyle, CEFE – CNRS Montpellier, FRANCE
Gene DNA methylation in plants: selective pressures and sex chromosome evolution

- 09:45 – 10:30 Plenary – Amphitheater 900
Bruno Contreras-Moreira, CSIC, Zaragoza, Spain
Learning to build and interrogate the pangenome of Brachypodium distachyon

- 10:30 – 11:00 Coffee Break

- 11:00 – 12:30 Session 13: Plant adaptation to climate change
Amphitheater 900
Chairs: **Laura de Gara**, Italy

- 11:00 – 11:20 **Partial root drying of maize grown in a split-root system leads to local and systemic metabolic adjustments and hydraulic redistribution**
Monika WIMMER

- 11:20 – 11:40 **Two examples of genome-wide evolutionary responses of European forest trees to past climate changes**
Martin LASCOUX

- 11:40 – 12:00 **Exploring phenotypic space for mining genotypes and alleles in maize**
Janas RODRIGUEZ

12:00 – 12:20 **Impact of development-induced structural changes on drought responses of winter oilseed rape leaf – NMR relaxometry, water relations and multi-omics investigations**
Pierre-Nicolas BOULCH

12:20 – 12:30 **Laura de Gara**
Q&A

Session 14: Epigenetic mechanisms and responses in plants
Room 120

Chair: **Leandro Quadrana**, France

11:00 – 11:20 **Uncovering the gene expression regulatory mechanisms underlying self-incompatibility dominance networks in Arabidopsis**
Rita A. BATISTA

11:20 – 11:40 **Global increase of the nuclear transcriptional regime during Arabidopsis photomorphogenesis: effects on gene expression**
Clara RICHEL-BOURBOUSSE

11:40 – 12:00 **Deciphering the epigenetic and molecular logic of WOX5 function in the columella stem cell niche of Arabidopsis thaliana**
Ning ZHANG

12:00 – 12:20 **Mechanism of E3 ubiquitin ligase SIXERICO1/3 regulating high temperature resistance in tomato plants**
Kaixin WANG

12:20 – 12:30 **Leandro Quadrana**
Q&A

Session 15: Mechanics and stress responses
Room 76

Chair: **Benoit Landrein**, France

11:00 – 11:20 **Limited water stress modulates expression of circadian clock genes in Brachypodium distachyon**

roots and induces differential response of proline-metabolism related genes
Janos GYORGYEV

11:20 – 11:40 **Dynamics of the calcium signal elicited by mechanical stimulation of Arabidopsis root**
Sébastien THOMINE

11:40 – 12:00 **Multiscale modelling of cell adhesion and separation in plants**
Rawen BEN MALEK

12:00 – 12:20 **It's just a phase: Structural characterization of LLPS and its role in temperature sensing in plants**
Chloe ZUBIETA

12:20 – 12:30 **Benoit Landrein**
Q&A

12:30 – 13:30 Lunch

13:30 – 14:30 Poster Session B

14:30 – 15:30 Poster Session C

15:30 – 16:00 Coffee Break

16:00 – 17:30 Round table Plant Act

THURSDAY 6 JULY

09:00 – 09:45 Plenary – Amphitheater 900
Rosa Lozano-Duran, University of Tübingen – ZMBP, Tübingen, Germany
How to conquer a plant using just eight genes: learning from geminiviruses

09:45 – 10:30 Plenary – Amphitheater 900
Gwyneth Ingram, CNRS Lyon, FRANCE
Controlling communication during reproductive development: The genesis and roles of apoplastic barriers

10:30 – 11:00 Coffee Break

11:00 – 12:30

Session 16: Plant Immunity
Amphitheater 900

Chair: **Rosa Loranzo-Duran**, Germany

11:00 – 11:20 **Investigating antiviral defenses protecting plant stem cells and germline**
Marco INCARBONE

11:20 – 11:40 **Gradual immune system maturation in the root affects plant microbe interaction**
Elhanan TZIPILEVICH

11:40 – 12:00 **Role of the plasma membrane signalling during plant virus propagation**
Sébastien MONGRAND

12:00 – 12:20 **Engineering danger sensing and signaling in plant immunity: use of oligosaccharins to enhance durum wheat resistance to fusariosis**
Valentina BIGINI

12:20 – 12:30 **Rosa Loranzo-Duran**
Q&A

Session 17: Photosynthesis: understanding and progress in its manipulation
Room 120

Chair: **Xenie Johnson**, CEA CNRS AMU, France

11:00 – 11:20 **From Algae to Sea Slugs: Functioning of Stolen Chloroplasts in Animal Cells**
Luca MORELLI

11:20 – 11:40 **Two vacuolar channels from the ALMT family regulate C4-organic acids metabolism**
Roxane DOIREAU

11:40 – 12:00 **From oxidative stress to antenna quenching: regulation of qH-energy dissipation in plants**
Aurélie CREPIN

12:00 – 12:20 **Chloroplast redox status modulates leaf development via changes in proteasomal activity and endoreduplication index**
Arce ROCIO CECILIA

12:20 – 12:30 **Xenie Johnson**
Q&A

Session 18: The genetics of natural variation of plant-plant interactions
Room 76

Chair: **Fabrice Roux**, Montpellier, France, Christophe Robaglia, BIAM, Marseille, France

11:00 – 11:20 **Evolution of cooperation in post-green revolution durum wheat cultivars**
Michel COLOMBO

11:20 – 11:40 **Chromatin regulation of and by gene islands in plants**
Louis-Valentin METEIGNIER

11:40 – 12:00 **Identification of genes and metabolites controlling plant-plant interaction**
Sophie JASINKSI

12:00 – 12:20 **Molecular bases of plant-plant interactions: identification of the molecular pathways depending on ESC-1, a RLK involved in the competitive response in Arabidopsis thaliana**
Marie INVERNIZZI

12:20 – 12:30 **Fabrice Roux**
Q&A

12:30 – 13:00 Closing Plenary

COMPARATIVE GENOMICS

0005-A CENTROMERES IN COMMON BEAN (*PHASEOLUS VULGARIS*): LESSONS LEARNED FROM CHROMOSOME SCALE GENOME ASSEMBLIES

Gianluca TEANO^{1*}; Juan C. ALVAREZ-DIAZ²; Christophe KLOPP²; Marion VERDNAUD¹; Stéphanie PFLIEGER¹; Ariane FRATIAS¹; Andrea PEDROSA-HARAND²; Valérie GEFFROY¹

¹ (1) Université Paris-Saclay, CNRS, INRAE, Univ Evry, Institute of Plant Sciences Paris-Saclay (IPS2), 91405, Orsay, France (2) Université de Paris, CNRS, INRAE, Institute of Plant Sciences Paris-Saclay (IPS2), 91405 Orsay, France; ² Plateforme Bioinformatique, Genotoul, BioInfoMics, UR875 Biométrie et Intelligence Artificielle, INRAE, Castanet-Tolosan, France
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Common bean (*Phaseolus vulgaris*) is the most important grain legume for human consumption. We generated two highly contiguous chromosome-scale genome assemblies of genotypes BAT93 and JaloEEP558 using PacBio HiFi sequencing and chromosome conformation capture data (Hi-C). In common bean, centromeres are defined by two unrelated satellite repeats, CentPv1 and CentPv2, which associate with the centromere-specific histone H3 (CENH3). CentPv1 is present in 8 chromosomes, while CentPv2 is present on the other 3. Published results proposed these two repeats as mutually exclusive. Surprisingly, in 5 chromosomes of BAT93 and JaloEEP558 HiFi assemblies, both CentPv1 and CentPv2 repeats co-localized. To confirm this specific feature of chromosomes harboring both CentPv1 and CentPv2, we performed Chromatin Immune precipitation of CENH3. Mapping these data on the HiFi genomes, in combination with methylation data will shed light on the evolutionary history of centromeric repeats in common bean.

0006-A INTERPRETING THE CHEMODIVERSITY IN A PHYLOGENETIC CONTEXT: A CASE STUDY OF THE GENUS *NEPETA*

Tijana BANJANAC^{1*}; Branislav SILER¹; Tamara LUKIC¹; Uros GASIC¹; Luka PETROVIC¹; Dragana MATEKALO¹; Skoric MARIJANA¹; Jasmina NESTOROVIC ŽIVKOVIĆ¹; Slavica DMITROVIC¹; Milica MILUTINOVIC¹; Neda ANICIC¹; Jelena BOZUNOVIC¹; Biljana FILIPOVIC¹; Milos TODOROVIC¹; Danijela MISIC¹

¹ Department of Plant Physiology, Institute for Biological Research "Siniša Stanković" – National Institute of the Republic of Serbia, University of Belgrade, Bulevar despota Stefana 142, 11060 Belgrade, Serbia
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Nepeta L. is the largest genus of the Lamiaceae family. The species of this genus are famous for their biopesticidal potential and medicinal properties. Within the genus, we found considerable variability in the qualitative and quantitative content of iridoid and phenolic compounds. Using state-of-the-art metabolomics techniques (UHPLC/LTQ-Orbitrap MS, GC/MS, UHPLC/DAD/(+/-)HESI-MS2), we comprehensively assessed the overall diversity of

iridoids and phenolics in the selected chemodiverse *Nepeta* taxa at the intra-species level. To reconstruct phylogenetic relations among the selected chemodiverse taxa from across the *Nepeta* genus, genomic ITS molecular marker and two maternally inherited plastid DNA regions (trnL-trnF and rbcL) were analyzed. A consensus phylogenetic tree was constructed to interpret the distribution of the most abundant iridoid and phenolic compounds. It was not possible to uncover clear regularities between phylogenetic relationship and chemotype affiliation.

0007-B CHROMOSOME REARRANGEMENT AND GENOME COMPLEXITY IN HEXAPLOID *HIBISCUS SYRIACUS* (*GANGNEUNG* AND *BAEKDANSIM*): INSIGHTS FROM PSEUDOCHROMOSOME ASSEMBLY AND COMPARATIVE ANALYSIS

Hyunjin KOO^{1*}; Sangjin GO¹; Minah JUNG¹; Seongmin HONG¹; Ah-Young SHIN¹; Yong-Min KIM¹

¹ Plant Systems Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, Republic of Korea
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Rose of Sharon (*Hibiscus syriacus*) is one of the most widespread garden shrubs globally and has a complex genome structure resulting from multiple rounds of polyploidization events. We constructed two reference genome assemblies for hexaploid *H. syriacus* accessions with long read sequencing and Hi-C scaffolding. Both varieties had 12 typical groups of chromosomes shown in hexaploid genomes containing three syntenic chromosomes, and two extraordinary groups with four and two syntenic chromosomes. Comparison of genome structures suggested that extensive chromosomal rearrangements occurred in both genomes during consecutive diploidization processes. Further analysis revealed a substantial expansion in Chr9 of Baekdansim, primarily influenced by a repeat burst after the variety divergence event. Population analysis using 94 re-sequencing datasets of worldwide collection of *H. syriacus* indicated the high genomic complexity. Further evolution of *H. syriacus* will be presented in the poster.

0008-B MOLECULAR MARKERS IN THE DETECTION OF INTERSPECIES HYBRIDIZATION – A MODEL STUDY ON THE GENUS *CENTAURIUM* HILL

Tamara LUKIC^{1*}; Branislav SILER¹; Danijela MISIC¹; Jasmina NESTOROVIC ŽIVKOVIĆ¹; Mihailo JELIC²; Milos BRKUSMANIN²; Biljana FILIPOVIC¹; Milos TODOROVIC¹; Tijana BANJANAC¹

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The species of the genus *Centaurium* Hill are characterized by a pronounced phenotypic plasticity, while interspecific hybridization readily occurs. Previous studies reported

hybridization events between *C. erythraea* and *C. tenuiflorum* in the Mediterranean region, but the status of a potentially hybrid taxon (termed "*Centaureum x tenuiflorum*") remains unclear. Therefore, molecular markers (EST-SSR, ITS, and chloroplast DNA markers) were combined and their usefulness in estimating overall genetic variability and in identifying phylogenetic relations between *Centaureum* taxa was scrutinized. Both EST-SSR and ITS markers proved to be well suited to distinguish the parental taxa *C. erythraea* and *C. tenuiflorum*, and a putative hybridogenic taxon "*C. x tenuiflorum*", the last one being more related to *C. erythraea*. Conversely, maternally inherited chloroplast markers (trnL-F, rbcL and psbA-trnH) nominated *C. tenuiflorum* as a donor of plastid.

0009-C
PLANT-TFCLASS: A STRUCTURAL CLASSIFICATION FOR PLANT TRANSCRIPTION FACTORS

Romain BLANC-MATHIEU^{1*}; Renaud DUMAS¹; Laura TURCHI¹; Jeremy LUCAS¹; François PARCY¹

¹ Laboratoire de Physiologie Cellulaire et Végétale
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Transcription factors (TFs) bind DNA at specific sequences to regulate gene expression. This universal process is achieved thanks to their DNA-binding domain (DBD). In mammals, the vast diversity of DBD structural conformations and the way they contact DNA has been used to organize TFs in the TFClass hierarchical classification. Such classification was missing from plants that possess many DBD types absent from mammals. We reviewed DBD 3D-structures and models available for plant TFs to classify most of the 56 recognized plant TF types within the TFClass framework. This extended classification adds six new classes and 35 new families corresponding to DBD structures absent in mammals. Plant-TFClass provides a unique resource for TF comparison across families and organisms.

0010-C
COMPARATIVE ANALYSIS OF CHLOROPLAST GENOMES OF TWO ADENOPHORA SPECIES

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Adenophora verticillata and *Adenophora stricta*, which belong to the family campanulaceae, were well-known as medicinal plants. However, it is very similar shape, especially roots, and has been used as herbal medicine and/or biomaterials regardless of classification. Therefore, in this study, we performed chloroplast genome sequencing to identify a genetic marker that can distinguish these two species. The total reads of *A. verticillata* and *A. stricta* were 247,553,132 and 229,873,920 reads, respectively. As a result of mapping the analytical sequence with *Adenophora triphylla* chloroplast genome as reference, the total number of SNPs in *A. verticillata* and *A. stricta* was 48 and 1,153, of which homozygous SNPs were 44 and 1,107, respectively. These results suggest that the homozygous SNPs between the two

species can be utilized in the development of genetic markers that distinguish the two species.