

International Conference on Germplasm of Ornamentals

(7-13 August 2016 /Atlanta, USA)

"Better Ornamental Plants for the Better World!"



ICGO2016

Organization

Hosted by

International Society for Horticultural Science

Organized by

The University of Georgia, USA

Beijing Forestry University, China

Gyeongsang National University, South Korea

American Society for Horticultural Science



Convener



Prof. Dr. Donglin Zhang
University of Georgia, USA
Michael A. Dirr Endowed Chair
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Prof. Dr. Qixiang Zhang
Beijing Forestry University, China
ISHS Ornamental Section Chair
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Prof. Dr. Byoung Ryong Jeong
Gyeongsang National University, South Korea
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This “Programs and Abstracts” is designed by Dr. Xiaoman Zhang, Associate Professor of Hebei Agricultural University, China.

>Welcome Address



On behalf of the International Society for Horticultural Science (ISHS) I am pleased to welcome the participants of the II International Symposium on Germplasm of Ornamentals.

I present my sincere acknowledgment to the hosting institutions ASHS and the University of Georgia (USA) and the co-hosting institutions Beijing Forestry University (China) and Gyeongsang National University (South Korea). It is an honour for the ISHS to collaborate with such distinguished institutions.

My special thanks go to the conveners Prof. Dr. Donglin Zhang, Prof. Dr. Zhang Qixiang and Prof. Dr. Byoung Ryong Jeong for their dedication and enthusiasm in the preparation of what I can anticipate will be a very successful meeting.

The ISHS has over 7,000 members from all over the world, organises about 50 specialised symposia per year and a horticultural congress every four years, and publishes the well-known proceedings series Acta Horticulturae. Our Society's primary aim is to promote and encourage research and education in all branches of horticultural science and to facilitate cooperation and knowledge transfer on a global scale. ISHS membership is open to all interested researchers, educators, students and horticultural industry professionals.

The proceedings of this symposium will be published in Acta Horticulturae, a publication of the ISHS available on-line and subscribed by libraries all over the world. This is our contribution to disseminate scientific knowledge and, in this particular instance, to make ornamental horticulture better known internationally.

I am sure the multiple activities organised with great care by the symposium hosts will meet participant's expectations. The symposium is also the time to relax and to experience the country's hospitality. I wish all participants a fruitful attendance of this symposium where the eventual austerity of some scientific topics will be balanced by the beauty and fragrance of flowers and ornamental plants.

Roderick Drew
President of ISHS

Scientific Committee

Dr. Teresita Amcre (University of Hawaii, USA)
Dr. Neil Anderson (University of Minnesota, USA)
Dr. Guihong Bi (Mississippi State University, USA)
Dr. Silan Dai (Beijing Forestry University, China)
Dr. Rosanna Freyre (University of Florida, USA)
Dr. Mengmeng Gu (Texas A&M University, USA)
Dr. Kim Hummer (US Department of Agriculture-ARS, USA)
Dr. Byoung Ryong Jeong (Gyeongsang National University, South Korea)
Dr. Michelle Jones (Ohio State University / OARDC, USA)
Dr. Jiyuan Li (Research Institute of Subtropical Forestry, China)
Dr. Qinghua Liu (Qingdao Agricultural University, China)
Dr. Huitang Pan (Beijing Forestry University, China)
Dr. Margaret Pooler (US National Arboretum, USA)
Dr. Thomas Ranney (North Carolina State University, USA)
Dr. Carol Robacker (University of Georgia, USA)
Dr. John Ruter (University of Georgia, USA)
Dr. Shouyun Shen (Central South University of Forestry and Technology, China)
Dr. Youping Sun (Texas A&M University, USA)
Dr. Wuyun Ta-na (Paulownia R&D Center, China)
Dr. Nianjun Teng (Nanjing Agricultural University, China)
Dr. Caiyun Wang (Huazhong Agricultural University, China)
Dr. Todd West (North Dakota State University, USA)
Dr. Yin Yi (Guizhou Normal University, China)
Dr. Donglin Zhang (University of Georgia, USA)
Dr. Qixiang Zhang (Beijing Forestry University, China)

Organization Committee

Matthew Chappell (Co-Chair, University of Georgia, USA)
Robert Lee (Co-Chair, PDSI/Transcend Nursery, USA)
Jinying Dong (University of Georgia, USA)
Mengmeng Gu (Texas A&M University, USA)
Xiaoling Jin (Central South University of Forestry and Technology, China)
He Li (University of Georgia, USA)
Scott McMahan (Atlanta Botanical Gardens, USA)
Jia Wang (Beijing Forestry University, China)
Hao Wei (Gyeongsang National University, South Korea)
Chao Yu (Beijing Forestry University, China)
Xiaoman Zhang (Hebei Agricultural University, China)

Speaker



“Agapetes: Jewels of the Himalays”
Dr. Kim Hummer, ISHS Representative
US Department of Agriculture-ARS, USA
Kim.Hummer@ars.usda.gov



“Ornamental Breeding at The University of Georgia”
Dr. John Ruter, Keynote Speaker
University of Georgia, USA
ruter@uga.edu



“Great Woody Plants from Texas”
Dr. Mengmeng Gu, Invited Speaker
Texas A&M University, USA
mgu@exchange.tamu.edu



“Exploitation of Primula maximowiczii, A Wild Perennial Flower In China”
Dr. Huitang Pan, Invited Speaker
Beijing Forestry University, China
13601231063@163.com



“Comparative Analysis of Anthocyanin Biosynthesis Pathway in Different Cultivars of Seecio cruentus Based on Transcriptomics”
Dr. Silan Dai, Invited Speaker
Beijing Forestry University, China
silandai@sina.com



“Investigation on Mechanisms of Embryo Abortion During Chrysanthemum Distant Hybridization”
Dr. Nianjun Teng, Invited Speaker
Nanjing Agricultural University, China
njteng@njau.edu.cn



“Ornamental Plant Exploration around the World”
Mr. Scott McMahan, Banquet Speaker
Atlanta Botanical Garden
smcmahan@atlantabg.org



“Good Genes – Germplasm and Breeding Work Together to Create New Plants at the U.S. National Arboretum”
Dr. Margaret Pooler, Keynote Speaker
US National Arboretum, USA
Margaret.Pooler@ars.usda.gov



“Treasure the Exceptions: Opportunities Arise from Wide Crosses!”
Dr. Neil Anderson, Invited Speaker
University of Minnesota, USA
ander044@umn.edu



“How Microsatellite Null Alleles Affect Genetic Analysis? A Case Study of Maire Yew”
Dr. Yafeng Wen, Invited Speaker, China
Central South Univ. of Forestry & Technology
wenyafeng7107@163.com



“Tissue Culture as A Tool for Mass Propagation and Research of Ornamental Germplasm”
Dr. Byoung Ryong Jeong, Keynote Speaker
Gyeongsang National University
brjeong@gmail.com



“Genetic Diversity, Population Structure, and Conservation Implications of Endangered Endemic Paeonia jishanensis in China”
Dr. Fangyun Cheng, Invited Speaker
Beijing Forestry University
chengfy8@263.net



“Ornamental Plant Breeding and Encore Azalea”
Mr. Robert Lee, Keynote Speaker
Plant Development & Service, Inc.
buddyazaleas@yahoo.com

Woody Plant Research Lab
Department of Horticulture
University of Georgia
Athens, GA 30602, USA
www.woodies.uga.edu



Sponsor

Plant Development Services, Inc.
Department of Horticulture at the University of Georgia
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University of Georgia Research Foundation
Pike Nurseries





International Conference on Germplasm of Ornamentals

(7-13 August 2016 /Atlanta, USA)



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Programs and Tours

Day 1 (Sunday, August 7, 2016): Registration (all day) (www.ashs.org)

Day 2 (Monday, August 8, 2016): Join the ASHS Scientific Program (www.ashs.org)

Day 3 (Tuesday, August 9, 2016): Join the ASHS Scientific Program (www.ashs.org)

Day 4 (Wednesday, August 10, 2016): Valdosta Room (1st Floor)

8:00am: Welcome and Open Remarks, Dr. Donglin Zhang, Convener

8:10am: ISHS Representative, Dr. Kim Hummer

8:20am: ISHS Ornamental Section Chair, Dr. Qixiang Zhang

8:30-10:00am: Oral Presentation --- **New Ornamental Plants**

Chair: Dr. Silan Dai, Beijing Forestry University

8:30am: Keynote Speaker, **Dr. Margaret Pooler, USDA**

“Good Genes – Germplasm and Breeding Work Together to Create New Plants at the U.S. National Arboretum”

9:00am: Todd West, Northern Empress® Japanese Elm and Cinnamon Curles®

Dwarf Korean Birch: New Ornamental Woody Plant Releases

9:15am: Jiyuan Li, Current Germplasm Conservation of Camellias in China

9:30am: Yingmin Lyu, Advance in Transcriptome-based Analyses of Cold

Response and Signaling Pathways of Plant Cold Resistance

9:45am: Qiang Liu, *Symplocos paniculata*, A New Ornamental Plant Species

10:00-10:25am: Break and Poster Session. (outside of Valdosta Room)

Coffee is available in the Georgia PreFunction (Exhibit Hall) from 10-10:30am

10:25-12:00noon: Oral Presentation --- **Selection and Breeding**

Chair: Dr. Youping Sun, Texas A&M University

10:25am: Keynote Speaker: **Dr. John Ruter, University of Georgia**

“Ornamental Breeding at The University of Georgia”

10:55am: Invited Speaker, **Dr. Huitang Pan, Beijing Forestry University**

“Exploitation of *Primula maximowiczii*, A Wild Perennial Flower In China”

11:15am: Yongzhong Chen, Method for Determinating the Age of *Camellia oleifera* Ancient Trees



- 11:30am: Bangping Cai, Biodiversity of Excellent Ornamental Plant
Euscaphis japonica (Thunb.) Kanitz
- 11:45am: Guihong Bi, Effects of Biofungicides on Controlling Rose Black Spot
- 12noon: Prepare for the tour and box lunch will be provided at Pike
- 12:30 pm: Pick up from Sheraton Atlanta (Front Entrance)
165 Courtland Street NE, Atlanta, GA 30303
- 12:45pm: Arrive at Pike Nurseries/Garden Center
2410 Camellia Ln NE, Atlanta, GA 30324
About 6.6 miles, 15 minutes
- 2:30pm: Depart from Pike Nurseries/Garden Center
- 4:00pm: Arrive at Atlanta Botanical Gardens in Gainesville, GA
1911 Sweetbay Dr., Gainesville, GA 30501
About 54.6 miles, 1 hour 21 minutes
- 4:30pm: “Ornamental Plant Breeding and Encore Azalea”
By Mr. Robert Lee, Plant Development & Services, Inc.
- 5:00pm: Tour of Atlanta Botanical Garden in Gainesville
- 6:00pm: Welcome Dinner at Atlanta Botanical Garden in Gainesville
Full cash bar!
- 7:00pm: “Ornamental Plant Exploration around the World”
By Mr. Scott McMahan, Atlanta Botanical Garden
- 8:00pm: Depart from Atlanta Botanical Gardens in Gainesville
- 9:30pm: Return to the Sheraton Atlanta
About 56 miles, 1 hour 22 minutes

Day 5 (Thursday, August 11, 2016): Valdosta Room (1st Floor)

- 8:00-9:45am: Oral Presentation --- **Germplasm Resources**
Chair: Dr. Teresita D. Amore, University of Hawaii
- 8:00am: Invited Speaker: **Dr. Kim Hummer, USDA-ARS**
“*Agapetes*: Jewels of the Himalays”
- 8:20am: Invited Speaker: **Dr. Mengmeng Gu, Texas A&M University**
“Great Woody Plants from Texas”
- 8:40am: Invited Speaker: **Dr. Yafeng Wen, How Microsatellite Null Alleles Affect Genetic Analysis? A Case Study of the Maire Yew**
- 9:00am: Minhuan Zhang, Germplasm Resources and Evaluation of Peony in Hunan, China
- 9:15am: Xiaoling Jin, Germplasm Resources and Distribution of Chinese Magnolias
- 9:30am: Longqing Chen, Registered Cultivars in *Chimonanthus* Lindl.
- 9:45-10:10am: Break and Poster Session. (outside of Valdosta Room)
- 10:10-12:00pm: Oral Presentation --- **Ornamental Exploration and Utilization.**
Chair: Dr. Rosanna Freyre, University of Florida
- 10:10am: Invited Speaker: **Dr. Neil Anderson, University of Minnesota**



“Treasure the Exceptions: Opportunities Arise from Wide Crosses!”

10:30am: Fei Wu, Research on Comprehensive Evaluation and Landscape Application with 62 Varieties of American *Lagerstromia indica*

10:45am: Lin Xiang, A Modified P Code Model Determined the Perianth Formation in *Cymbidium goeringii*

11:00am: Liuqing Yang, Photosynthetic Physiological Response Under Drought Stress and Garden Application of *Sedum emarginatum*

11:15am: Teresita D. Amore, Rebuilding Hawaii’s *Anthurium* Germplasm Collection for Cultivar and Species Preservation, Breeding, and Biotechnological Research

11:30am: Guixia Jia, Exploring Photoperiod Regulation and Breeding of *Lilium* × *Formolongi*

11:45am: Hongzhi Wu, Key Factors Affecting Conservation in Vitro and Rapid Propagation of Wild Ornamental *Gentiana*

12:00-1:00pm: Lunch on your own

1:00-3:05pm: Oral Presentation --- **Applications of Modern Technology**

Chair: Dr. Todd West, North Dakota State University

1:00pm: Keynote Speaker: **Dr. Byoung Ryong Jeong**, Gyeongsang National University

“Tissue Culture as A Tool for Mass Propagation and Research of Ornamental Germplasm”

1:30pm: Invited Speaker: **Dr. Silan Dai**, Beijing Forestry University

“Comparative Analysis of Anthocyanin Biosynthesis Pathway in Different Cultivars of *Senecio cruentus* Based on Transcriptomics”

1:50pm: Kaifeng Ma, Flower Color Chimera May Regulated by circRNA in *Prunus mume*

2:05pm: Wen Xing, Development and Characterization of EST-SSR Markers by Transcriptome Sequencing in *Rhododendron*

2:20pm: Chao Yu, Construction of a Genetic Linkage Map and QTLs Analysis for Phenotypic Traits in Tetraploid Roses

2:35pm: Peng Jiang, De Novo Transcriptome Assembly and Analysis of Clarkia Petal

2:50pm: Ming Sun, Molecular Cloning and Expression Analysis of a Monoterpene Synthase Gene Involved in Floral Scent Production from Lily (*Lilium* ‘Siberia’)

3:05-3:30pm: Break and Poster Session. (outside of Valdosta Room)

3:30-4:15pm: **Graduate Student Oral Competition (Chaired by Dr. Peng Jiang)**

3:30pm: Nathan Maren, Hybrid Analysis of Somatic Fused Lilac (*Syringa* spp.)

3:45pm: Hansen Fu, Comprehensive Evaluation of Landscape Application Potential for Wild Ornamental Plants in Hubei, China

4:00pm: Jaser Aljaser: Exponential Growth of Gladiolus ‘Glamini’ under the Influence of Plant Growth Regulators



- 4:15-6:00pm: Oral Presentation --- **Conservation and Sustainability**
Chair: Dr. Guihong Bi, Mississippi State University
- 4:15pm: Invited Speaker: **Dr. Fangyun Cheng**, Beijing Forestry University
“Genetic Diversity, Population Structure, and Conservation Implications of Endangered Endemic *Paeonia jishanensis* in China”
- 4:35pm: Invited Speaker: **Dr. Nianjun Teng**, Investigation on mechanisms of embryo abortion during *Chrysanthemum* distant hybridization
- 4:55pm: Ming Cai, Breeding Fragrant Crape Myrtles Using *Lagerstroemia caudata*, A Native Germplasm to China
- 5:10pm: Donghuan Liu, The Resources Evaluation and Landscape Application of *Hosta* Cultivars
- 5:25pm: Neil Anderson, Collecting Horticulturally-useful Traits in the Wild: Methodology to Maximize Genetic Gain and Minimize Risk
- 5:40pm: **Dinner Announcement** / Spring Meadow Nursery, Mr. Tim Wood
- 6:00-7:00pm: Committee Meeting (for selecting next Conference (3rd) host and site)
- 7:00pm: Sponsor’s Dinner (TBA)

Day 6 (Friday, August 12, 2016):

- 8:30 am: Pick up from Sheraton Atlanta (Front Entrance)
165 Courtland Street NE, Atlanta, GA 30303
- 10:00am: Arrive at Angel Creek Nursery Inc.
1130 Adams Road, Bishop, GA 30621
About 69 miles, 1 hour 23 minutes
- 11:00am: Depart from Angel Creek Nursery Inc.
- 11:15am: Arrive at Southeastern Growers Inc.
2240 Macon Hwy, Watkinsville, GA 30677
About 6.6 miles, 9 minutes
- 2:00pm: Depart from Southeastern Growers Inc.
- 2:15pm: Arrive at UGA Horticulture Farm
1221 Hog Mountain Road, Watkinsville, GA 30677
About 10 miles, 12 minutes
- 3:15pm: Depart from UGA Horticulture Farm
- 3:30pm: Arrive at UGA Trial Gardens
Athens, GA 30602 (UGA Campus, nearby the Coliseum)
About 5.6 miles, 13 minutes
- 4:00pm: Banquet and Closing Remark, (GA Center, UGA Campus)
Full cash bar from 3:30-5:30pm
- 6:00pm: Depart from UGA campus
- 8:00pm: Return to the Sheraton Atlanta and the symposium adjourn!
About 70 miles, 1 hour 41 minutes.6:45pm

Day 7 (Saturday, August 13, 2016): Departure



New Ornamental Plants

Good Genes – Germplasm and Breeding Work Together to Create New plants at the U.S. National Arboretum

Margaret Pooler
USDA/ARS U.S. National Arboretum
10300 Baltimore Ave., Bldg. 010A
Beltsville, MD 20705, USA
Margaret.Pooler@ars.usda.gov

The U.S. National Arboretum was established in 1927 and occupies 446 acres in Northeast Washington, D.C. Its mission is to enhance the economic, environmental, and aesthetic value of ornamental and landscape plants through long-term, multi-disciplinary research, conservation of genetic resources, and interpretative gardens and exhibits. With an emphasis on collections, germplasm, and breeding, the USNA has released over 650 new cultivars of woody ornamental plants, including Glenn Dale azaleas, cold hardy camellias, disease resistant crapemyrtles and American elms, diverse viburnums, and hybrid pyracantha, magnolia, hibiscus, red maples, lilacs, flowering cherries, and hollies. All of these plants illustrate the importance that germplasm has on addressing disease and pest problems and bringing new plants to the landscape. This talk will provide a case study of how plant exploration and evaluation led to the development of disease-resistant plants (crapemyrtles), and will showcase some of the past and future trees and shrubs from the National Arboretum.

Northern Empress® Japanese Elm and Cinnamon Curles® Dwarf Korean Birch: New Ornamental Woody Plant Releases

Todd P. West
North Dakota State University
Fargo, ND 58102, USA
todd.p.west@ndsu.edu

The North Dakota State University (NDSU) Woody Plant Improvement Program (WPIP) has been servicing the Northern Great Plains for 60 years, beginning germplasm trial evaluations in 1954. The program has evaluated 200+ genera and 3,000+ species and cultivars of trees and shrubs. Recently, two new releases were made from the NDSU WPIP. ‘Burgundy Glow’ is a new cultivar of *Ulmus davidiana* Planch. var. *japonica* (Sarg. ex Rehd.) Nakai (common name is Japanese elm). ‘Burgundy Glow’ is a very hardy small to medium sized growing elm with a rounded crown, open branching, and attractive summer and fall foliage. Fall foliage of ‘Burgundy Glow’ changes from green to apricot-orange to burgundy-red before leaf senescence.

‘Burgundy Glow’ is approximately 8.5 m tall with a crown width of 7.0 to 7.5 m after 35 years and is a smaller stature tree as compared to the species. It is adapted to USDA cold hardiness zone 3b to 7 and performs well on a wide range of soil types. This smaller statured elm selection is suitable for use as a small to medium sized ornamental tree in urban landscape planting areas. This is especially relevant where available space or overhead power lines are a concern and where hardiness of other elm cultivars may be an issue. ‘Burgundy Glow’ is sold under the trademark Northern Empress® (U.S. Trademark Reg. No. 4,662,503, registered Dec. 30, 2014) ‘CinnDak’ is a new cultivar of *Betula costata* Trautv. (common names include Korean, Manchurian or costata birch). ‘CinnDak’ has a compact dwarf habit with a well-branched crown and ornamental exfoliating colored bark. ‘CinnDak’ is approximately 2.7 m with a crown width of 2.4 to 2.7 m after 30 years where seasonal growth over the last five years averaged 18.0 cm. It is adapted to USDA cold hardiness zones 3a – 7 and performs well on a wide range of soil types. This compact selection is suitable as a small tree specimen in the landscape, with multi-season interest, as a result of high quality summer foliage, reliable golden fall color, and high quality ornamental exfoliating bark. ‘CinnDak’ is sold under the trademark Cinnamon Curls® (U.S. Trademark Reg. No. 4,668,972, registered Jan. 6, 2015).

Current Germplasm Conservation of Camellias in China

Jiyuan Li^{1*}, Ni Sui², He Libo^{1,3*}

1. Research Institute of Subtropical Forestry, Chinese Academy of Forestry, No.73 Daqiao Rd. Fuyang District, Hangzhou, Zhejiang 311400, P.R.China

2. School of Marine Sciences, Ningbo University, No.818 Fenghua Rd., Jiangdong District, Ningbo, Zhejiang 315211, P.R.China

3. College of Horticulture and Landscape Architecture, Hunan Agricultural University, No 1 Nongda Rd., Changsha, Hunan 410128, P.R.China

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This paper deals with the general introduction of current germplasm conservation of ornamental camellias in China. During last decades, great achievements have been made for genetic germplasm conservation for camellias in China. For in situ conservation, four yellow camellia species at National Fangcheng Gold Camellia Natural Reserve in Guangxi Autonomous Region were officially conserved first time in 1986. The wild *Camellia japonica* resources are being well conserved in Changmenyan island at Qingdao City and Zhoushan Islands in Zhejiang Province. The only wild *C. azalea* (*C. changii*) population is being conserved at E’huangzhuang Provincial Natural Reserve in Guangdong Province. Several wild *C. reticulata* and other camellia species forests with large area have been found in southwestern China recent years. Large amounts of ancient camellia trees are grown in temples, natural conserves, parks, gardens, yards, sightseeing zones throughout South China. For ex situ conservation, numerous camellia species botanical gardens and camellia cultivar gardens have been built both in mainland and Taiwan of China, of which eight have been recognized as international camellia garden of excellence by the ICS since

2003. On the other hand, we are facing big challenge in conservation of newly-found camellia resources. In fact, most of wild camellia species resources are being endangered although China is rich in camellia resources. The major factors include building new roads, regeneration by other cash tree species, harvesting as fuel wood in mountainous areas and using as ornamental plants in urban areas. China is taking a number of positive measures to establish new natural reserves or broaden existing natural reserves at national or provincial level. Some new research projects have been supported by the central or local governments in an effort to enlarge wild population of camellias.

***Diospyros kaki* Thunb. ‘Zhongshi 3’ for Both Fruits and Ornamentals**

Jianmin Fu¹; Peng Sun²; Donglin Zhang³; Weijuan Han²; Songfeng Diao² and Fangdong Li¹,
1Paulownia Research & Development Center of China, State Forestry Administration,
zhengzhou, China

2Paulownia Research & Development Center of China, State Forestry Administration,
Zhengzhou, China

3Department of Horticulture, University of Georgia, Athens, GA 30602, USA
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A new cultivar, *Diospyros kaki* Thunb. ‘Zhongshi 3’, was selected from natural populations in Xingan County of Henan (China) for its colorful foliage as ornamentals and taste fruits for fresh fruit production in July 2009. Grafted plants from 2010 to 2015 retained the unique features of colorful foliage. The plant is a deciduous tree with dense and yellow branches. The leaves are papery with various colors during the growing season. Newly sprouted leaves, <6.5 cm in length, are reddish brown (RHS Color Chart, 173A) and full extended leaves, about 14 cm, bright yellow (1B). Both new sprout and full-extended leaves are oblong or obovate with acute apex and cuneate leaf base. The veins of mature leaves are in red (RHS 44B) or reddish (RHS 32A). The unique dense branches and bright yellow foliage made ‘Zhongshi 3’ different from other cultivars of *Diospyros kaki*. Fruits of ‘Zhongshi 3’ are edible, which ripe in middle October with orange red color. The fruits are ellipsoid, to 10cm in diameter. ‘Zhongshi 3’ had tap root systems and it grows well in warm climate and on good drainage soil. It grows well under lower fertility and drought conditions. The recommended cultivation regions of ‘Zhongshi 3’ are the same as majority of other *D. kaki* cultivars.

***Symplocos paniculata*, A New Ornamental Plant Species**

Qiang Liu¹; Youping Sun²; Jinzheng Chen³; Peiwang Li³; Changzhu Li³; Lijuan Jiang¹ and Genhua Niu²,

1Central South University of Forestry and Technology, Changsha, Hunan, China

2Texas A&M AgriLife Research at El Paso, Texas A&M University, El Paso, TX,



3Hunan Academy of Forestry, Changsha, Hunan, China
liu.qiangcs@163.com

Symplocos paniculata is a widespread species in China with unique ornamental characteristics such as dark green leaves, fragrant creamy white flowers, sapphire-blue berries, and rough yellowish-brown and corky bark. It is easy to grow, tolerant to drought condition and high soil salinity and resistant to pests; thus it is considered a potential ornamental plant for urban landscapes. Attentions have been recently paid to the development and utilization of its fruit oil for bio-diesel production; however, little research-based information is available on its potential on ornamental usage. This paper highlights the progress of the selection of novel cultivars and reviews the propagation techniques including seed propagation, cutting, grafting, and tissue culture. Such information plays a vital role in the development of this species for commercial production for green industry.

Poster Session. (Outside of Valdosta Room)

Germplasm Resources and Cold-resistance Breeding of Mei, An Ornamental Woody Plant

Qixiang Zhang

Beijing Key Laboratory of Ornamental Plants Germplasm Innovation & Molecular Breeding,
National Engineering Research Center for Floriculture and College of Landscape Architecture,
Beijing Forestry University, Beijing, China
zqxbjfu@126.com

Mei (*Prunus mume* Sieb. et Zucc.), originated in the Hengduan Mountains region in China, was domesticated as an important ornamental and fruit plant more than 3,000 years ago. Here, we review two important issues about the distribution of germplasm resources of mei and its cold-resistance breeding progress. Mei has an abundant warehouse of wide and semi-wide resources mainly distributed in southwestern region. Through long-term selection and breeding, mei has been domesticated to produce about 350 varieties in 15 distinct regions stretching 20 provinces, some of which exist in more than 200 year trees (known as ancient mei). It is observed that there are 75 ancient mei identified in six southwestern and southeastern provinces. Also, tremendous effort has been made to select mei for cold regions, especially ‘Three-North Areas’ of China. By crossbreeding with apricot, a highly cold-hardy species, many cold-resistance varieties, such as ‘Yan Xing’, ‘Hua Hudie’, and ‘Shan Taobai’, have been cultivated in the past more than 60 years. These varieties can tolerate and resist cold temperature of -15 to -35°C. As an ornamental woody plant, mei has proven itself to be an important fuel for studying the evolution and diversification of genus *Prunus*.



***Utilization of *Kalmia latifolia* L. Germplasm as Ornamentals**

He Li; Donglin Zhang and Matthew Chappell

Department of Horticulture, University of Georgia, Athens, GA 30602, USA

susuzx98@uga.edu

Kalmia latifolia L. (mountain laurel) is an evergreen shrub with attractive flowers in heath family and a promising ornamental plant for southeastern United States. It distributes naturally from southern Maine west to central Ohio and south to east Louisiana and northwest Florida and forms dense bush in rocky and sandy soil. The natural diversity and effect of selection and breeding since early 1960 had yielded about 170 cultivars with various habits, many sizes of foliage, separate to united petals, and wide ranges of floral patterns and flower colors. Field exploration, cultivation survey in gardens and various landscapes, and nursery visits in the last three years concluded that mountain laurel is much more popular in the northeast US than that of the southeastern states. The breeding effect of Dr. Richard Jaynes in Connecticut has significantly increased availability of cultivars, adaption, and market shares of mountain laurel in the northeastern states. Less than 10 cultivars are sold in Georgia and southeastern states due to limited heat tolerance. Field exploration from north Georgia, to Alabama, to Florida (Pensacola) indicated that wild mountain laurel plants did widely distribute in warm regions and had vigorous growth. We have collected and propagated these germplasm resources for breeding many more heat-adapted cultivars for the southeastern US gardens and landscapes.

*Student Poster Competition

Cold Hardiness of Nine Introduced Evergreen *Ilex* Cultivars

Shouyun Shen, Zeng Wen, Chai Yixia, Jin Xiaoling

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One of key features to introduce new ornamental plants is their cold hardiness. Nice hybrid evergreen *Ilex* cultivars were introduced from US and evaluated in Changsha (China) for their cold hardiness. The 2nd and 3rd leaves from the terminal of each cultivar were collected in January 2015 and treated with 0, -5, -10, -15, -20, and -25 C. The results concluded that LT50 for all nine cultivars was between -14.1 and -34.9C. much lower than mean lowest temperature (-1C) in January. With the temperature decreased, the concentrations of MDA were increased, SOD and soluble protein increased firstly, then decreased. Free proline concentrations were cultivar dependable, increased as temperature went down or increased firstly, then decreased. All nine cultivars were hardy in Changsha and other regions in China should refer to their cold hardiness rank as the following: *Ilex* cultivars was: *I. glabra* 'Shamrock' (LT50: -34.9C) > *I. x attenuata* 'Forsteri' (-25.4C) > *I. crenata* 'Schwoebel Compacta' (-22.7C) > *I. vomitoria* 'Anna's Choice'

(-19.6C) > *I. cassine* ‘Tensaw’ (-18.8C) > *I. x meserveae* ‘Blue Maid’ (-18.2C) > *I. x attenuata* ‘Bronze Beauty’ (-17.9C) > *I. vomitoria* ‘Oscar’s Dwarf’ (-17.1C) > *I. x attenuata* ‘Savannah’ (-14.1C). The results also were similar to the recommended USDA hardiness zones for each cultivar.

Keywords: *Ilex* cultivars, cold hardiness, semi-lethal temperature, the membership function

Research on China New Floral Crops of Gesneriaceae

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There are about 150 genus, 3700 species in Gesneriaceae in the world, of which approximately 58 genus and 470 species distribute in China, and most of them are famous ornamental perennials with beautiful flowers and leaves, and can be cultivated as pot flowers and garden plants in warm regions. The mountainous areas from southwest to south in China are the very important areas of modern distributions and differentiation of Gesneriaceae plants. Guangxi is lying in the centre of these areas. The genus of which it owns of Gesneriaceae is the most in China. The diversities and richness of species in Gesneriaceae are very high degree in Guangxi. It is very great significance of systematic researches for ornamental resources of Gesneriaceae in Guangxi. Several investigations on wild Gesneriaceae were made in Guangxi successively. Based on the full investigation, a set of technical system was found. The researches were extended from the characteristic of botany in Gesneriaceae to the cultivation of introductions and domestication, reproduction technologies, relationship analysis of some species in Primulina, test of cross-breeding, etc. It has basically been established a relatively system for further industrialized operation.

Key words: Gesneriaceae, Germplasm resources, Breed, Propagation

Mixed bud and Flower Development of *Geranium koreanum* (Geraniaceae)

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Geranium koreanum is a wild flowers that is distributed in Qingdao area of China. Little is

known about the mixed bud and flower development in *G. koreanum*. In this text, development of flower and mixed bud of *G. koreanum* was described. The morphogenesis, surface structure, and growth period of the organs were examined in detail using scanning electron microscope and dissecting microscope. The mixed bud initiated from a flat apical meristem. In addition, the stipule and leaf primordia arose first as a circle ridge around the margin of the main apex. Subsequently, the hemispherical apex was spited into two hemispheres, forming terminal- and floral- bud primordia, respectively. The development of mixed bud completed at the formation of terminal, floral and lateral buds, young leaves and stipules. Floral development began when cymule primordium was separated from terminal bud primordium. The abaxial and adaxial bracteole primordia arose first and grew like leaves, followed by the initiation of sepal primordia and lateral bracteole primordia at floral-bud meristem. Sepals continued to develop and embraced the floral buds eventually. Then the petal and stamen primordia appeared. The growth of petal primordia was slower compared with stamen primordia. The stamens became stalked and formed anther locules. The petals also became stalked but remained thin and small. Then the carpels commenced as five-angled ring and gradually formed five ovary locules. Finally, all organs including corolla and gynoecium enlarged rapidly and quickly. The corolla became longer than the short stamens and later long stamens. The gynoecium does the same nearly at the same time. When the gynoecium and corolla surpass the long stamens, the floral bud is almost ready to open. These results above uncover the process of mixed bud initiation and flower development of *G. koreanum*.

Keywords: Morphology, Organogenesis, Scanning electron microscopy, Inflorescence

Screening Drought-tolerant Pepper Cultivars using Multivariate Statistical Analysis

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Drought is one of the major factors that limit chili pepper production in Guizhou, China. Drought tolerant chili peppers are necessary maintain the chili pepper yield and decrease the input cost for agricultural production. Seed germination and seedling growth of 20 pepper cultivars that were treated with PEG-induced drought stress were investigated. Principal component analysis, membership function, and clustering analysis were used to examine the drought tolerance of 20 pepper cultivars based on the morphological and physiological indicators. The results indicated that the drought resistance coefficients (the coefficient of drought resistance is that the difference between the stress value and the control value is ratio to control value) of germination rate, germination potential, plant height and chlorophyll content showed significant differences among the cultivars. The eight indicators fell into five principal components and 90.8% of the original information was reserved. cluster analysis using the principal component scores classified 20 pepper cultivars into three groups. 'Biggie Chile', 'Hungarian Yellow Wax', 'Red Cherry Hot', 'Serrano', 'Sweet banana', and 'Variegata' were drought-sensitive cultivars;

‘Anaheim’, ‘Caribbean Red Hot’, ‘Cayenne Long Thin’, ‘Fooled You’, ‘Mohawk’, ‘Pompeii’, ‘Portugal Hot’, ‘Tabasco’, ‘Thai’, ‘Treasures Red’, and ‘Yolo Wonder’, had intermediate drought tolerance. ‘Ethem’, ‘Jalapeno Early Hot’, and ‘Purple Beauty’ were drought-tolerant cultivars. These results provide useful information for selecting drought tolerant cultivars for further breeding research in Guizhou.

Fertility Evaluation of Interspecific Hybrids between *Lagerstroemia indica* and *L. speciosa*

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To breed elite crape myrtle cultivars with combination of complementary traits from *Lagerstroemia indica* and *L. speciosa* which have different ornamental appeal, interspecific crosses were performed. However, it is hard to carry out backcross or sib mating due to the poor fertility of most interspecific hybrids, which hampered gene introgression and ideal progeny generation. In F1 populations, no open-pollinated seed pods were observed, except one progeny (Lis-ZD6) of *L. indica* ‘Zixia’ × *L. speciosa*. It was similar to *L. indica* in morphology and was proved to be true interspecific hybrid by SSR analysis. To elucidate the reasons for fertility difference among different F1 progenies, a random representative sterile hybrid (Lis-FD1) of *L. indica* ‘Fenjing’ × *L. speciosa* and Lis-ZD6 were investigated. The results showed that pollen grains of Lis-FD1 had no germination ability. Pollen tubes of *L. speciosa* and *L. indica* ‘Creole’ were detected in ovules of Lis-FD1 48 h after pollination, while enlarged ovaries began to abscise at 72 h after pollination and failed to produce seeds, which suggested that the barriers occurred during post-fertilization phases. By contrast, Lis-ZD6 showed 25.90% pollen germination rate, and the pollen tubes of *L. speciosa* and *L. indica* ‘Creole’ were found to penetrate into ovules of Lis-ZD6 48 h after pollination. The results indicated that Lis-ZD6 can be used as either male or female parent for further *Lagerstroemia* breeding programs, while Lis-FD1 may be used as female parent through embryo rescue culture. Morphological measurements revealed that progenies with similar phenotype to *L. speciosa* were sterile, while those similar to *L. indica* showed relatively high fertility.

Investigation on Resources of *Hemerocallis* in North China

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The various colors and adaptable of daylilies(*Hemerocallis*) make them be widely used in landscaping as flower borders, gardens and road green belts. The natural distribution of daylilies covers East Asia to Russia's Siberia and mainly in China. 11 of 14 species in *Hemerocallis* native to China. There are problems of classification and evolutionary relationships among populations, such as naming and classification confusion, unclear distinction between species and varieties, variation exists with different geographical groups, natural hybrid populations, the difference between day and night flowering in *Hemerocallis*. Therefore comprehensive and systematic investigation of the population should be studied in origin China. Based on the literature and investigating all 383 collections of wild daylilies of herbarium specimens in the Herbarium, Institute of Botany, CAS (PE), 5 species and 1 variant of wild daylilies are collected in Shandong, Shaanxi, Heber Province and Beijing. In addition, a field investigation has been conducted in Saihanba National Forest Park in HeBei Province and Plots have been set to be recorded the elevation, slope, habitat, associated plants and biological characteristics of daylilies. Currently, by analyzing the data, this study shows that daylilies are mainly distributed in the moist areas of forests and the valley plains, the maximum average coefficient of variation within populations is the length of the bracts(86.28%) in *Hemerocallis lilio-asphodelus* and number of buds(21.39%) in *Hemerocallis citrina*. The mainly factors among polulations is the height of plants in *Hemerocallis minor*. This research will provide guidance for further study in daylilies. About analysis within populations and among populations and molecular markers remains to be studied. In addition, more resources will be collected.

Investigation and evaluation of wild drought resistant germplasm of chrysanthemum and related genera

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In view of the severe drought problems all over the world, we investigated chrysanthemum genus and near source of germ-plasm in north and central China(Inner Mongolia, Hebei, Henan, Anhui, Hubei, Hunan, Shandong and Fujian provinces) , collected sixteen species of germplasm of *Chrysanthemum* and related source, then evaluate their drought resistance. According to their wild habitats, primarily identifying drought resistance, selected 6 drought resistance, measured photosynthetic characteristics and physiological indexes.*Opisthopappus taihangensis* Ling, *Filifolium sibiricum*, *Ajania fruticulosa* Ledeb., *Chrysanthemum indicum* L., *Chrysanthemum mongolicum* Ling *Chrysanthemum lavandulifolium*. of drought experiments were carried out to set up the drought group and the normal watering group. Determination of photosynthetic

characteristics, photosynthetic rate (PN), transpiration rate (TR), stomatal conductance (CD); physiological and biochemical indexes: content of chlorophyll (CHL), Leaf Proline Content (pro), leaf relative conductivity (RC). The reduced amplitude of Light photosynthetic rate, transpiration rate and stomatal conductance of *Opisthopappus taihangensis* Ling, *Filifolium sibiricum*, *Ajania fruticulosa* Ledeb. is the smallest. Three indexes change rate with an average of 33%, 34% and 36.7%. Three indexes of *Chrysanthemum lavandulifolium* decreased greatly, the rate of change of mean value was 67%, the drought is the worst. *Opisthopappus taihangensis* Ling, *Filifolium sibiricum*, *Ajania fruticulosa* Ledeb, *Chrysanthemum indicum* L. between these four species of relative conductivity change has no significant difference, the cell membrane penetration increased amplitude significantly less than the others, drought resistance is better. Six kinds of free proline content increased, *Chrysanthemum lavandulifolium*, *Chrysanthemum mongolicum* Ling and *Chrysanthemum indicum* the three kinds of the largest increase, an increase of 45%-83%. No significant difference in the change of chlorophyll content, but chlorophyll content of *Chrysanthemum lavandulifolium* and *Chrysanthemum mongolicum* Ling *chrysanthemum* reduced 11%-25%, poor drought resistance. Comprehensive evaluation of the above species, to water stress of drought resistance from strong to weak as follows: *Opisthopappus taihangensis* Ling, *Filifolium sibiricum*, *Ajania fruticulosa* Ledeb., *Chrysanthemum indicum* L., *Chrysanthemum mongolicum* Ling *Chrysanthemum lavandulifolium*.

***Pardancanda norrisii*: Real Iris**

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Pardancanda norrisii is the offspring of *Iris dichotoma* and *I.domestica*, which is a good group with ornamental traits, such as rich colors and a large number of flowers. The parents are native to China and both bloom in summer. The 6 populations (2 parents populations, F1, F2 and 2 backcross populations) were observed and measured in their blooming period. The results showed that: the flower color of F1 was purple and Y×F1 (backcrossing with *I.dichotoma*) was different degrees of purple, which were both different from that of either parents, who were respectively orange and white. While F2 and F1×S (backcrossing with *I.domestica*) developed flowers possessing richer variations, colors ranging from yellow, orange, pink, purple, red, and bicolor, and the variation of F2 hybrids was higher than F1×S. In addition, there were some flowers with no spots in *P. norrisii*, while their parents had orange spots and purple veins respectively. Therefore, *P. norrisii* can provide abundant variations through continuous self-crossing and backcrossing with *I.domestica*. We can conjecture that the variation of



continuous self-crossing populations was higher than backcross populations accord to the Mendelian Law. But now, it can not sure that the variation of which population was the highest. And the abundant variation is conducive to the selection of new varieties with novel flower colors in *P. norrisii*.

Selection and Breeding

Ornamental Breeding at The University of Georgia

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The University of Georgia Department of Horticulture is well-known for its ornamental plant breeding efforts. Beginning in the 1990's with faculty such as Will Corley, Michael Dirr and Allan Armitage these efforts are being continued today by John Ruter, Donglin Zhang, Matthew Chappell and Carol Robacker. Dr. Ruter works on herbaceous and ornamental plants, including the following genera: *Abutilon*, *Agapanthus*, *Berberis*, *Camellia*, *Cupressus*, *Helianthus*, *Heliopsis*, *Hibiscus*, *Ilex*, *Lagerstroemia*, *Pavonia*, *Platycladus*, *Prunus*, *Rhaphiolepis*, *Stokesia*, *Thermopsis*, and *Thuja*. Dr. Zhang's Woody Plant Research Lab focuses on alternative *Camellia* species, *Distylium*, Edible Landscape Plants, *Gardenia*, *Hydrangea*, *Ilex*, *Lagerstoremia*, *Loropetalum*, *Magnolia*, *Nandina*, Ornamental Trees, *Syzygium*, and *Viburnum*. Dr. Chappell cooperates with Dr. Ruter and Dr. Zhang on the following breeding projects: *Acer buergerianum* and *Acer saccharum* var. *barbatum*, *Baccharis*, heat tolerant *Hosta*, and *Kalmia*. Dr. Robacker's work focuses on genera such as *Abelia*, *Schizachyrium*, *Spigelia*, and *Vitex*. Ornamental breeders currently have over 50 herbaceous and ornamental selections under commercial evaluation for potential release to industry. An overview of UGA breeding programs will be given along with an introduction to the Trial Gardens at UGA.

Exploitation of *Primula maximowiczii*, A Wild Perennial Flower in China

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Primula maximowiczii, a wild perennial sub-alpine species that grows naturally in northern China, is a potential garden plant and pot-grown floral crop. In this research, 8 natural populations of *P. maximowiczii* were surveyed with phenotypic variation, pollen morphological traits and genetic diversity. Of these, 40 natural variants with different flower colors were conserved. To establish commercial propagation and cultivation technique system, the effects of photoperiod, light quality, temperature, fertilizing and GA3 treatments on growth and development of *P. maximowiczii* were studied. The results showed that seedlings which were sprayed with 10mmol/L GA3 solution and fertilized once every 5 days with nutrient solution of EC=1.5 mS/cm grew best. Plants grown under supplementary lighting with red fluorescent light tubes bloomed earlier and had higher net photosynthetic rate. The dormancy of *P. maximowiczii* in autumn and winter was induced by the decrease of day length, and the dormant plants sprouted rapidly and grew quickly under extended day length or night interruption treatment. The plants grown under 16-hour day length at 1C kept vigorous and strong growth. Additionally, GA3 treatment promoted the dormant plant germination and growth, especially under short-day conditions. Cold storage (-2C) significantly promoted adult dormant plants of *P. maximowiczii* germinating and flowering, and with the cold storage time extended, the scape height and flowering rate were increased. In addition, seeds and dormant swollen bud under -2C cold storage for 2-4 months could be used as materials to establish successfully a stable and efficient in vitro propagation system, which provided an ideal way for germplasm conservation.

Method for Determinating the Age of *Camellia oleifera* Ancient Trees

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The determination of ancient tree's age has important practical significance for the protection and the development and utilization of the ancient tree resources. Ring numbers and diameters of seventy-one trunk and branches were investigated. These data were analyzed using nine types of multivariate regression models. The errors and precisions of all models were compared. The model $y = -0.07x^2 + 7.92x + 5.38$ ($P < 0.05$, $R^2 = 0.92$) was selected for determining the age of the tree. This equation also serves a valuable reference other ancient trees with a diameter ranging from 13.6 cm to 56 cm. The oil-tea trees age was also measured using image processing method. The error between image processing method and ring number method ranged from 10 to 22 years. The method can accurately measure trees age without any limitation of the diameter.

Biodiversity of Excellent Ornamental Plant *Euscaphis japonica* (Thunb.) Kanitz.

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Euscaphis japonica (Thunb.) Kanitz is a species in Staphyleaceae, small deciduous trees or shrubs, growing in mountain valleys or open forests, distributed in most provinces of China, especially in areas south of the Yangtze River to Hainan, and ranges in Japan, Korea and Vietnam. In recent years, this species is grown as a very popular ornamental tree because its pericarp is red color in ripened fruits, which can be hanging on the tree long time from September to the second year in March. The investigated results show that there are much morphological variances in the species, such as the bark color is from grey to grayish brown, the leaflet blade shape is elliptic to oblong-ovate or sometimes oblong-lanceolate, rarely ovate, the adaxial leaflet color is yellowish green to bottle green, the pericarp color is initially pale green and finally light red to red brown during fruit ripening, the seed number in a follicle is 1 to 3, and so on. A new variety was found in southwest of Fujian, China. It had been described as *E. japonica* (Thunb.) Kanitz var. *wupingensis* B. P. Cai et Z. R.Chen. The new variety is easy discriminated from the protospecies by its pericarp with yellow color. Furthermore, a new cultivar with white leaflet blades was selective bred from the cultivated plants, named as *E. japonica* (Thunb.) Kanitz ‘Silver’ B. P. Cai.

Effects of Biofungicides on Controlling Rose Black Spot

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Black spot is the most common and serious disease problem on roses (*Rosa* spp.). It is caused by the fungus *Diplocarpon rosae* Wolf. Black spot is especially severe in the South due to the warm, humid climate and long growing season. There are currently no effective ways to control rose black spot. Growers and home gardeners have to rely on frequent sprays of fungicide at 7- to 14-day intervals. In this study, we evaluated the efficacy of several biofungicides, including a novel biofungicide occidiofungin and 3 commercially available biofungicides (Cease, Actinovate, and Regalia), in comparison with 2 conventional fungicides (Honor Guard and Compass) on controlling rose black spot. Rose ‘Orogold’, a black spot susceptible hybrid tea cultivar, was



selected based on growers' recommendation. In general, all fungicide treatments decreased the black spot occurrence, and Honor Guard was the most effective in controlling leaf black spot, especially early in the season. As the season progressed, biofungicides, especially the higher rates of occidiofungin (2, 10, and 50 mg) showed similar or better effects as Honor Guard on controlling black spots, possibly due to the repeated use which increased the effectiveness of the biofungicide treatments. Preliminary data showed that biofungicides have potential to be used for controlling rose black spot, and occidiofungin has the promise to be used as a biofungicide.



Germplasm Resources

Agapetes: Jewels of the Himalays

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The U.S. Department of Agriculture, National Clonal Germplasm Repository (NCGR) at Corvallis that maintains genetic resources for temperate specialty crops. This genebank houses crop wild relatives of *Vaccinium* L., including *Agapetes* D. Don ex G. Don, a cousin in the family Ericaceae. *Agapetes* is a semi-climbing woody shrub native to Southeastern Asia. This genus is found in the Himalayan highlands from India through China to Cambodia, Laos, and Vietnam. During 25 October to 14 November 2015, *Agapetes*, and other species relatives were collected during a Vietnamese-US cooperative expedition in Northern Vietnam. The exploration involved representatives of the Plant Resources Center, Vietnam Academy of Agricultural Sciences in Hanoi, and the NCGR. The exploration was supported through the U.S. National Plant Germplasm System (NPGS) Plant Exploration/Exchange Program. Permissions for collecting were obtained from the Vietnamese Ministry of Agriculture and Rural Development, and the administration of four Vietnamese National Parks. During the expedition, 5 species of *Agapetes*, were collected, doubling the number of species represented in the NCGR. Root samples for propagation and seeds were collected from 1200 to 3100 m elevation. Chilling hours in these habitats were estimated to be 50 to 160 hours per year. *Agapetes* species were lithophytic (epipetric) or epiphytic. The plants simultaneously displayed multiple stages of phenology from bud break to fruit development. Fruit colors of these *Agapetes* wild relatives included pink, bright red, fuchsia, as well as purple to black. Descriptive flower and fruit characters of the *Agapetes* in the NCGR collection will be summarized.

Great Woody Plants from Texas

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Texas is the second largest state in the U.S., in terms of land area. Annual precipitation in Texas ranges from less than 200 mm in the El Paso in West Texas to over 1400 mm in Southeast Texas, and there are ten vegetational areas in Texas. Among hundreds of native and adapted woody



plants in Texas, many have high landscape value. Desert Willow (*Chilopsis linearis*), yaupon holly (*Ilex vomitoria*) and Texas sage (*Leucophyllum* spp.) are examples of commonly used native plants, while *Styphnolobium affine*, *Prunus mexicana* and *Cornus florida* var. *pringlei* are among many other under-utilized plants. Of the same species, provenance from Texas may perform different in landscapes compared ones from other states. Incorporating genetics from Texas in breeding programs may help increase the palette of landscape plants and their adaptability.

How Microsatellite Null Alleles Affect Genetic Analysis? A Case Study of the Maire Yew

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Microsatellite markers are widely used in genetic analysis due to its many advantages. However, the common occurrence of null alleles has not been paid enough attention. In this study, we checked for the occurrence of null alleles and their impact on genetic analysis in four Maire yew (*Taxus chinensis* var. *mairei*) populations. We redesigned the new primers to confirm the existence of null alleles in suspicious loci, some of these loci isolated from *Taxus* congeneric species using cross-species amplification method. The proportion of matching genotypes between new and old primers suggested there could be null alleles in two loci (TC3 and TC4). After amplification with new and old primer pairs, the genetic parameters of two primer sets (old and new) showed that null alleles have significant impact on the genetic analysis. Once corrected null alleles, most populations appeared at HWE, quite different with the data of old primers nearly all the populations were significantly deviated from HWE, as a result of heterozygote deficiencies. On species level, genetic parameters of H_o and H_e values changed from 0.197 and 0.513 to 0.495 and 0.493, respectively. High positive values of fixation indices ($F_{old} = 0.566$) changed to negative values ($F_{new} = -0.015$). Furthermore, analysis from corrected genotypes showed more strong genetic differentiation between populations than before null alleles eliminated, the F_{ST} data were 0.212 and 0.150, respectively.

Germplasm Resources and Evaluation of Peony in Hunan, China

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In order to understand the genetic relationship and genetic diversity of peony in Hunan province, the DNA fingerprints of 47 peony germplasm materials of Hunan province were studied by using ISSR markers. Seven primers selected from 100 ISSR primers could obtain high polymorphism and reproducibility bands. The results showed that total of 77 DNA bands were amplified, and 67 polymorphic bands, counting for 87.01%. Genetic similarity analysis showed that Hunan peony germplasm resources with high genetic diversity. Through the computer software analysis, peony variety tested the average effective number of alleles is 1.395 4, the average Nei's genetic diversity index is 0.248 0, the average Shannon's information index was 0.385 9; Between each type of the similarity coefficient between 0.532 5 ~ 0.961 0, with an average of 0.751 5, is a sign of close genetic relationship between the material. These 47 germplasm resources could divided into 2 groups and 3 subgroups by UPGMA analysis, were distinguish varieties from different sources. It reveals from the molecular level of Hunan local peony varieties, genetic relationship and genetic diversity of Resistance to hot and humid peony varieties breeding work provides theoretical basis.

Germplasm Resources and Distribution of Chinese Magnolias

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Magnoliaceae Family has distributed between Asia and America. There are 16 genera with about 300 species, which mainly distribute in Southeast and East Asia, Southeast of North America, Central America and the variable of South America. China enjoys fantastic resources with 11 genera, nearly 160 species. This paper summarized the resource and geographical distribution of Magnoliaceae Family in China. Hunan province is one of the distribution center of Magnoliaceae plants in China. There are 6 genera with 39 species, including 1 subspecies and 3 varieties.) *Manglietia insignis*, *Michelia crassipes*, *Michelia maudiae* 'Honghua', and *Michelia platypetala* 'Fenyun' are red flower resource of Magnoliaceae in China.

Registered Cultivars in *Chimonanthus* Lindl

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Plants of *Chimonanthus* Lindl. are extensively cultivated in gardens and many cultivars were bred in China. Until now, 19 cultivars have been registered based on ICRA's criterion. The cultivars are: *Chimonanthus praecox* 'Hua Hudie', 'Yangzhou Huang', 'Wai Gang', 'Lü Yun', 'Yingbei Hanzhu', 'Caotang Yunxiang', 'Xiang Yi', 'Huantian Xidi', 'Zao



Hong' , 'Bao Chun' , 'Xingfu Huaxiang' , 'Si Nian' , 'Xingguang Canlan' , 'Huang Xin' , 'Jinse Yangguang' , 'Qianyun Jindie' , 'Xiaran Qianyu' , 'Jinling Hongzhuang' and 'Zhongshan Bai' .

Poster Session. (Outside of Valdosta Room)

Callus Induction and Tissue Culture System of *Lilium tsingtauense*

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Lilium tsingtauense is a rare wild flower, known as a special round leaf group lily with high ornamental values. They have a straight and slender stem and can be used as cut flowers and potted plants. However, little information about the propagation of *L. tsingtauense*. In this paper, scales of bulb and ovaries of *L. tsingtauense* before anthesis (20 to 24mm) were used as materials. An optimal tissue culture system were established. Using 75% ethanol 30s, and 0.1% aqueous mercuric chloride for 12 min to sterilize explants had the better effects, and the contamination rate was 26.67%. When the auxiliary buds multiplication medium added 60 g/L of sucrose, the auxiliary buds exhibited more healthy and stronger. The rate of average differentiation was 7.25, the average height and circumference was 3.45cm and 1.76cm, respectively. In addition, using the ovaries of *L. tsingtauense* as explant for callus induction. We found that the contamination rate was 0 when the explants sterilized in 75% ethanol 30s and 0.1% sodium hypochlorite for 11 min. The medium for callus inducement should better be MS + 2.0 mg/L of 2,4-D+ 30g/L of sucrose. The optimum medium for callus multiplication was MS + 1.0mg/L of 6-BA + 0.2mg/L of NAA + 30g/L of sucrose. The best medium for auxiliary buds multiplication was MS + 1.5mg/L of 6-BA + 0.1mg/L of NAA + 30g/L of sucrose. In rooting culture, treatments on darkness or activated charcoal of 3g/L could build dark microenvironment for root growth. It is beneficial to promote the differentiation of root primordial and the roots emergence occurs two to three days earlier than other treatments. Moreover, CCC of 2g/L increased the concentration of dry weight, which improved the resistance of vitro shoots. These results above gave clear information of callus induction and tissue culture system of *L. tsingtauense*.

Keywords: *Lilium tsingtauense*, Callus induction, Tissue culture system

Proteome Analysis of *Lilium lancifolium* in Response to cold stress and ABA induction

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The ecological balance and metabolism activity were caused by changes in expression of differential genes and proteins when plants were subjected to various stresses. *Lilium lancifolium* is a very important cold-resistant wild flower for lily cold resistance breeding. In order to study the response mechanism to stresses (cold and ABA) in-depth, a proteome study was conducted on the basis of 2-D gel electrophoresis. 149 significantly differential protein spots were found by DIGE technology, 21 spots with at least 2-fold altered expressions were analyzed by MALDI-TOF and ESI-MS/MS and 19 proteins were successfully identified. Moreover, the proteins were classified into ‘metabolism process’ (35.1%), ‘response to stress’ (20.7%), ‘energy’ (12.5%), ‘signal transduction mechanism’ (10.1%), ‘others’ (10.0%), ‘protein binding’ (6.2%) and ‘biogenesis of cellular component’ (5.4%). The functional classification of proteins was almost in accordance with that of genes by RNA-seq. Especially, the change and damage to the protein structure caused by low temperature could be relieved after treated with ABA. Our study of differentially expressed proteins associated with metabolic pathways promoted the research of cold-resistance proteins and confirmed the consistency in functional classification between differential genes and differential proteins in *L. lancifolium*, which will be most favorable for further study and deep research of cold-resistance breeding in lily.

The Methods for Breaking Hard Seeds of *Sophora viciifolia* and the Effects of Phytohormones on Seed germination

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Sophora viciifolia, belongs to Papilionoideae of Leguminosae, and is a kind of perennial deciduous thorny undershrubs. The seed coats of *Sophora viciifolia* have slight water and air permeability for containing colloidal matter and waxiness, the development of embryo is mechanically inhibited, resulting in the low germination rate generally. This research used different methods to treat the seeds of *Sophora viciifolia*, and found the highest germination rate was by grinding sandpaper. Our results also showed that ABA inhibited the germination of *Sophora viciifolia* seeds and GA was the opposite which the germination rate reached the highest at 200mg/L GA treatment for 6 days.



Structure and Similarity of Wild *Cymbidium tortisepalum* Communities in Yunnan

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Cymbidium tortisepalum is an endemic and endangered orchid species in southwestern China. Twenty-eight native populations of *Cymbidium tortisepalum* in northwest Yunnan Province were studied from August to October in 2013 and 2014. Morphology, habitat ecological factors, rhizosphere soil nutrient of Wild Cymbidium, and Community structure, characteristics of native populations of *Cymbidium tortisepalum* were investigated. The results are as follow: There is a wide range of ecological adaptability, and leaf length, leaf width, plant height, root length and scape length shows great changes among populations of wild *Cymbidium tortisepalum*. The coefficient of variation is over 15%. Moreover, there is individual short and small number of the *Cymbidium* in few population, degraded significantly. There are 12 tree species, 37 shrub species, 40 herbaceous species in *Cymbidium tortisepalum* populations in three parallel rivers regions (Nujing river, Jinsha river and Lancang river) of northwestern Yunnan Province. Community structure of wild populations is relatively stable, presenting "dual". The tree stratum is composed of *Pinus yunnanensis*, *Cyclobalanopsis glauca*, *Quercus variabilis*, and a small number of fir species; shrub stratum is composed of *Pistacia weinmannifolia*, *Rhododendron delavayi*, *L. umbellata* Thumb, *Quercus spinosa*; *Ophiopogon japonicus*, *Cassia obtusifolia*, *Ficus tikoua* Bur, *Imperata cylindrica* etc. *Cymbidium tortisepalum*'s stable accompanying plant is *Radix* in herb layer. The proportion of Pinaceae and Fagaceae's plants in tree stratum, species of herb stratum, number of tree and herb stratum, were decreased with increasing altitude. The average similarity coefficient in populations of *Cymbidium tortisepalum*'s tree layer is 0.64, a medium similar. Shrub layer and herb layer's average similarity coefficient are 0.12 and 0.15, quite dissimilar.

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Effect of Wide and Narrow Row Cultivating on Virus-free Ginger Development and Yield

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To explore Virus-free ginger planting model. Both wide and narrow row and underwent



cultivating models were explored. The models were average spacing 37.5cm and 20cm spacing plants and wide row spacing 45cm and narrow rows 30cm, 20cm spacing plants. And study the effect of both cultivating models on virus-free ginger development and yield. The result shows compared with the average spacing cultivation, cultivation under way wide and narrow row plants height, leaf, root, yield and nutrient absorption are better.

Pollination Biology of *Michelia crassipes* Y.W. Law

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Michelia crassipes Y.W. Law, a small tree to low shrub in Magnoliaceae, is a great ornamental plant with fragrant and dark purple flowers. It is a great ornamental germplasm resource for breeding Magnolia plants for container production. Field observation in Changsha (China) indicated that its flowers started bloom in late March and continued to early May, for about 50 days. Each flower opened for 4-5 days and pistils are ready before stamens. The highest vitality for accepting pollen is from 9:00am to 12:00 noon in the 2nd or 3rd day after bloom. The outcrossing index (OCI) is 4 and pollen/ovule ratio (P/O) is $2,671 \pm 123$, which indicated that *M. crassipes* should be majorly classified as an allogamous plant. Bagged flowers also produced limited seeds, but seed quality (size and weight) were significantly less than that of artificial cross-pollination flowers. Both fruit-set (73.6%) and seed-set (80%) of cross-pollination flowers were significantly higher than that (23.2%, 75.2%) of the self-pollination ones. *M. crassipes* should be partially recognized as an autogamous plant too. The fruit-set and seed-set percentages of *M. crassipes* × *M. figo* were 80% and 89%, respectively. Unfortunately, the reciprocal cross yielded no success. Further studies should address success and failure of these reciprocal crosses of *M. crassipes* with other Magnolia species.

Key words: *Michelia crassipes*, breeding system, cross-compatibility

Exploring on Wild Flower color polymorphism of *Geranium nepalense* (Geraniaceae): adaptation to pollinators or non-pollinator agents

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Flower color polymorphism is very useful on horticultural traits. It is very common in the cultivated species, but relatively rare in natural conditions. We compared various aspects between white flower plants and pink plants and concluded that (1) Pollinator preference:

Halictidae and syrphidae were the main visitors on both pink and white flower plants in all populations. Halictidae prefer pink to white morph but Syrphidae prefer white to pink one. (2) Reproductive success comparison: No significant difference between two morphs except one population in one year. (3) Flower surface temperature comparison: Temperature of two morphs was not significantly different both in morning and noon, but significantly in evening ($F_{1, 26} = 35.28$; $P < 0.001$). (4) Calcium ion concentration and coming flower: Within a certain range, calcium soil can increase coming flower number than potting soil. Our results indicated that different pollinator groups may discriminate against flower color morph of *Geranium nepalense*; non-pollinator agents such as temperature and calcium ion concentration may maintain flower color polymorphism in natural condition. Therefore, to protect wild color polymorphism resources, we need to protect the corresponding pollinators diversity, and the stability of the abiotic environment.

Comparative Analysis of Volatile Organic Compounds from Fragrant Flowers of *Lagerstroemia caudata* and Fragrance-free *L. indica* Cultivars

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Major volatile compounds were identified in *L. caudata*, a rare fragrant Chinese crape myrtle species, which were not present in eleven *L. indica* cultivars that lack fragrance used as controls. The volatile organic components of fresh flowers were collected via headspace adsorption and analyzed by gas chromatography and mass spectrometry (GC-MS). In total, we detected 77 volatile organic components, of which, 9 were common volatile compounds. Isoprenoid together with alkanes (78.07%-97.7%) dominated the main volatile compounds in all tested materials. The main volatile components of *L. indica* cultivars were 1,1-Dimethyl-3-methylene-2-vinylcyclohexane (5.7%-66.2%), cyclohexane (2.4%-61.3%) and methyl geranate (35.3%-49.2%). Comparatively 12 monoterpenoids and its derivatives were peculiar to *L. caudata*. Among them, isogeraniol (25.79%), citral (13.88%) and β -citral (11.25%) were the major volatile compounds, which may contribute to the characteristic aroma of *L. caudata*. This study provides a foundation for aroma breeding in *Lagerstroemia*.

Saline stress induces physiological and morpho-anatomical changes in three *Chrysanthemum* species

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Chrysanthemum are notable traditional flowers and ornamental crops of China, and are also widely cultivated in Asia, Europe, the United States and many other countries. As soil salinization is increasingly serious and has become a restricting factor of flower production and application in open field, salt tolerance breeding is becoming a new significant direction for chrysanthemum breeding. In order to reveal the salt-tolerant ability of chrysanthemum germplasm, comprehensive study was carried out under NaCl stress on morpho-anatomical and physiological features of three typical chrysanthemum species, which as wild species are crucial germplasm in the origin of Chinese cultivated chrysanthemum. Seedlings of *Chrysanthemum indicum*, *Chrysanthemum lavandulifolium* and *Chrysanthemum nankingense* were stressed under the NaCl concentrations of 360 mmol L⁻¹ for 0 day, 3 day, 6 day and 9 day. Morphological change was recorded every morning at 9-10 am and leaves at 4-8 leaf positions were acquired for physiological and anatomical parameters. The results showed that three species were quite different since 6 day, and only *C. indicum* still kept green growth at 9 day. The membrane permeability, proline and malondialdehyde (MDA) increased over time, while the chlorophyll contents was the opposite. During a period of time, except for little increase in thickness of palisade mesophyll of *C. Indicum*, the epidermis, palisade mesophyll, spongy mesophyll and leaves of 3 species decreased in thickness in addition to the diameter reduce of mid-vein. Moreover, mesophyll cell decompartmentation of *C. lavandulifolium* and *C. nankingense* can be observed under the stress. Conclusions are: 1) Though *C. indicum* showed good adaptation to short-term salt stress, none of the three species were endurable under high salinity; 2) Physiological and anatomical features are relation indexes, while membrane propertie of leave and photosynthetic characteristics, as well as the epidermis and mesophyll tissues, have best relativity with salt stress.

Ornamental Exploration and Utilization

Treasure the Exceptions: Opportunities Arise from Wide Crosses

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Since for many ornamental crops their respective germplasm bases are extremely narrow with genetic limitations, e.g. *Lilium longiflorum*, *Pelargonium peltatum*, etc., there is an imperative need for germplasm collection and employment of wide crossing to evoke genetic change. The downy mildew (*Plasmopara obducens*) outbreak in *Impatiens walleriana* is a modern example of narrow germplasm risks with economic consequences. The perils of not collecting novel germplasm in species relatives include specific crop production requirements, which could have been eliminated if wild species had been collected at the commencement of flower breeding programs. The objective of this research is to present several classic crossing schemes proven to incorporate wild species genes into cultivated crops and minimize hybrid breakdown (incongruity), based on >30 years of breeding research. Congruity Backcrossing and F1 Hybrid Bridging vs. classic Recurrent Backcrossing, based on Edgar Anderson's Iris evolution, the use of introgressive hybridization techniques will be used to demonstrate genetic changes possible in *Phaseolus*, *Lilium* and *Gladiolus*. Direction of crosses to maximize exceptional genetic exchange, ancestral vs. derived species as male or female parents, self-incompatibility status of parents, use of cut styles and removal of transmitting tracts are possible techniques to employ. Use of fast-tracking technique options to hasten generational life cycles in herbaceous perennials can be employed to hasten the rate of progress, e.g. 3 cycles (equivalent to 3 years) truncated into one calendar year for gladioli.

Research on Comprehensive Evaluation and Landscape Application with 62 Varieties of American *Lagerstromia indica*

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Based on the field survey statistics of introduced American *Lagerstromia indica* resource in Beijing Botanical Garden, comprehensively considering its ornamental value, reproduction ability and resistance factors, 17 evaluation indexes are determined, and Analytic Hierarchy Process model about varieties of *Lagerstromia indica* is established. The comprehensive garden application value on 62 varieties of *Lagerstromia indica* were evaluated by this model. The results showed that: 'Cherry Dazzle', 'Peppermint Lace', 'Cheyenne', 'Tonto', 'Queen's Lace' and other 18 kinds of varieties have highest application value, 'Miami', 'Centennial', 'Chisam Fire', 'Bashams Party Pink', 'Catawba' and other 31 varieties have higher garden application value which have moderate or smaller applications; 'Osage', 'Words Fair', 'Caddo', 'Bourbon Street' of 13 kinds of varieties have low garden application value which are not proper for exploiting and utilizing. In-depth analysis of *Lagerstromia indica* varieties of ornamental characteristics and landscape application forms, key recommendation are paid to high value of the varieties. The results of AHP model to evaluate *Lagerstromia indica* variety resources will provide theoretical basis for the future exploitation and utilization of *Lagerstromia indica*

resources.

A Modified P Code Model Determined the Perianth Formation in *Cymbidium goeringii*.

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Cymbidium goeringii is traditional floricultural plant in China, and it is desirable to breed elite double-flowered cultivars. Recent studies revealed that expression changes in an AGAMOUS (AG) orthologous gene could result in double flowers with increased numbers of petals. We isolated a CgAG gene from *Cymbidium goeringii* by RT-PCR and RACE-PCR techniques. Sequence analysis showed that CgAG gene sequences are same in the wild type and double-flowered mutant of *C. goeringii*. The gene contained an open reading frame of 702 bp encoding a putative protein of 233 amino acids. Phylogenetic tree analysis indicated that CgAG belong to C lineage of AG subfamily. Real-time quantitative PCR demonstrated that CgAG had similar expression levels in young flower buds of wild type and double-flowered mutant of *C. goeringii*. In addition, CgAG was strongly expressed in columns, while almost absent in sepals, lateral petals and lips. The results suggested that CgAG may play key roles in column formation of *C. goeringii*. The complex floral architecture of the Orchidaceae presents an exciting opportunity to examine perianth development. In this study, we used a cDNA library of wild-type *C. goeringii* flower buds for transcriptome sequencing. In total, 48,840 unigenes were isolated and eighteen candidate AP1/FUL-, AP2-, DEF-, GLO-, SEP-, and AGL6-like genes were identified. Phylogenetic analysis was highly correlated with protein domain identification. qRT-PCR results showed that CgDEF1, CgSEP2, and CgAGL6-1 were only strongly detected in the sepals and petals (SP), and were significantly down-regulated in the lips. CgDEF3, CgDEF4, and CgAGL6-3 were expressed highly in the lips and lip-like petals, but were detected minimally in the sepals. Yeast two-hybrid analysis indicated that CgDEF1 and CgGLO formed a heterodimer. CgAGL6-1, CgSEP2, and CgDEF1 formed higher order protein complexes with the assistance of the CgGLO protein, and both CgAGL6-1 and CgSEP2 formed a heterodimer. CgDEF3 and CgDEF4 could interact independently with CgGLO and CgAGL6-3, respectively; whilst, the CgAGL6-3 formed a homodimer. We propose that a modified Perianth code model can explain *C. goeringii* perianth formation. Furthermore, the L-quartet (CgDEF3/CgAGL6-3/CgAGL6-3/CgGLO) and (CgDEF4/CgAGL6-3/CgAGL6-3/CgGLO) promoted lip formation, whereas the SP-quartet (CgDEF1/CgAGL6-1/CgSEP2/CgGLO) promoted SP formation.



Photosynthetic Physiological Response Under Drought Stress and Garden Application of *Sedum emarginatum*.

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The *Sedum emarginatum* plants are collected from Nanyue Mountain in Hengyang, Hunan Province. By using artificial climate chamber, the sedums are divided into five groups to have different treatments over 60 days in order to test their drought resistance. The five treatments are CK (relative water content 75~80%), mild drought stress (RWC55~60%), moderate drought stress (RWC35~40%), and severe drought stress (RWC15~20%), extreme drought stress (RWC0~10%). The results indicate, from the natural saturation deficit indicators, even though *Sedum* leaves that under severe drought stress cause water deficiency after 20 days of treatment, the surface of leaf blade still remains glossy green after 40 days of treatment. After 10 days under extreme drought condition, heavy moisture loss occurs and affected normal plant growth; From the plasma membrane permeability indicator, mild to severe drought stress had little impact on *Sedum* leaves, however, after 20 days of extreme drought, *Sedum*'s plant growth is severely damaged. When approaching day 40 of treatment, this impact reaches its maximum; From the chlorophyll relative content indicators, it is clear that mild and moderate drought stress had minor impact on leaf chlorophyll content. The leaf chlorophyll content is significantly affected under severe drought stress since day 10, starting with increase of chlorophyll content then the chlorophyll content continue to decline. Chlorophyll content decreases rapidly with increasing drought stress time; From the chlorophyll fluorescence parameters indicators, mild to severe drought stress for the first 30 days had little effect on F_v/F_m value, after 20 days of extreme drought stress, F_v / F_m value decreased. 40 days of mild to severe drought stress has little impact on F_v/ F_m values and the ETR value, extreme drought stress at day 10 began to significantly reduce the F_v / F_m and ETR value; Mild to severe drought stress had minor impact on qP value while extreme drought stress at day 20 significantly decrease qP value. After placing the *Sedum emarginatum* on rooftop for 1 year, it showed that in the absence of artificial watering, while part of the *Sedum emarginatum* population died in the summer, this *Sedum* species survived and returned the next Spring. After planting in container box on outside wall of building, it showed that *Sedum emarginatum* grew well with lush flowering and with a hundred percent coverage, which provided great landscape appearance.

Rebuilding Hawaii's *Anthurium* Germplasm Collection for Cultivar and Species Preservation, Breeding, and Biotechnological Research

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Anthurium is the third most important floriculture crop in Hawaii, grown mainly as a cut flower. The University of Hawaii (UH) has a well-established anthurium breeding program since 1950, with a germplasm collection assembled from backyard growers, hobbyists, researchers and collection trips from countries of origin prior to the 1993 adoption of the Convention on Biological Diversity. Substantial losses to the UH greenhouse collection from the mid-1980s to the 1990s occurred due to bacterial blight. In 2014, a key collaboration between the UH and the USDA Pacific Basin Agriculture Research Center arose to collect species, heritage and commercial varieties with important horticultural attributes. The germplasm collections are housed in greenhouses in three separate locations on Oahu (UH) and Hawaii Island (USDA and UH), as an insurance against adverse weather events such as hurricanes or strong winds that may damage the greenhouses, or unforeseen pest or disease outbreaks. Complementing the greenhouse collection is an in vitro collection of triple-indexed accessions to maintain disease-free stock. The germplasm serves as a genetic resource for continued conventional breeding as well as biotechnology research in both institutions.

Exploring Photoperiod Regulation and Breeding of *Lilium* × *formolongi*.

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Lilium × *formolongi* is an important bulb flower which can blossom in one year from seeds. The seedlings require of a long-day condition for flowering induction and significantly regulated by the photoperiodic flowering pathway. To identify the different development stages during flowering initiation in *Lilium* × *formolongi* seedlings, the morphological characters, anatomical structure of the shoot apex meristem (SAM) and the circadian rhythm expression patterns of *CONSTANS*(CO) and *FLOWERING LOCUS T* (FT) were investigated in long days. The morphological characters included the numbers of the rosette leaves and internodes. The CO ortholog *LfCOL9* (KJ744206) and FT ortholog *LfFT1* (KJ744207) have been cloned from *Lilium* × *formolongi*. cv. Raizen 3. The results indicated that the juvenile stage was defined from the seeds germination to sprout out 5-6 rosette leaves, when the morphology of the SAM exhibited hemispheric vegetative shape and the mRNA accumulation of *LfCOL9* and *LfFT1* did not show a diurnal rhythmic expression pattern for three days. As the seedlings grew to 9-10 rosette leaves, the expression of *LfCOL9* and *LfFT1* started to display an ambiguous circadian rhythm and low amplitude, which indicated that the seedlings were entering into the photoperiod-sensitive stage. When the seedlings began to bolting, and had 1-2 internodes, the

morphology of the SAM remained vegetative status, but the expression of LfCOL9 and LfFT1 showed a distinct and strong circadian rhythm pattern for three days. Therefore the stage of 1-2 internodes was identified as flowering induction stage. When the seedlings had 6 average internodes, the paraffin section results showed that the morphology of the SAM appeared to be elongated and broaden, which meant the SAM turned into the morphological transition stage from vegetative to flowering, and identified as flowering transition stage. When the average internodes of the seedlings reached 10, the SAM was concaved and developed into inflorescence primordium, which was defined as floral differentiation stage. In conclusion, the conformation of the different development stages during flowering initiation in *Lilium* × *formolongi* seedlings applied the numbers of rosette leaves and internodes as the morphological markers, which will be served as the foundation to understand the molecular regulatory mechanism of flowering initiation and early flowering characteristic of *Lilium* × *formolongi* in the future. Further it will be helpful for the cultivation and breeding of seed-propagated, non-vernalization-requiring lily hybrids. Project supported by the National Natural Science Foundation of China (Grant No.31470106). Corresponding author: Guixia Jia. E-mail: gxjia@bjfu.edu.cn.

Key Factors Affecting Conservation in Vitro and Rapid Propagation of Wild Ornamental *Gentiana*.

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The aim of this study is to explore the key technologies to conserve wild *Gentiana* with ornamental value and establish a rapid propagation system for *Gentiana* with excellent ornamental traits, which will lay a foundation for breeding new varieties. **【Methodology】** Wild *Gentiana rhodantha*, *Gentiana arethusae*, *Gentiana rubicunda*. and *Gentiana duclouxii* with high ornamental value discovered and collected in low and middle-altitude regions were chosen as subjects, and the suitable explants for sterile material' s establishment and the best concentrations of hormone (1.0~2.5 mg/L 6-BA, 0~0.2 mg/L NAA), and hormone combination on adventitious bud induction and rooting as well as the influence of pH on the growth of *Gentiana* was explored. **【Findings】** The best explant for *G. rhodantha* and *G. rubicunda* is stem with axillary buds or apical bud; the best explant for *G. arethusae* is rootstock; the best explant for *G. duclouxii* is immature seed. The optimal medium for propagation is: MS+2.0mg/L 6-BA+0.10mg/L NAA for *G. rhodantha*, *G. rubicunda* and *G. duclouxii*, MS+2.0mg/L 6-BA+0.20mg/L for *G. arethusae*;; the optimal medium for strengthening young plants is: MS+1.0mg/L 6-BA+0.10mg/L NAA, and the optimal medium for rooting is: MS+0.1mg/L NAA+0.2g/L activated carbon. pH 5.5 in medium is good for *Gentiana*, and too high or too low will disturb its growth obviously. **【Conclusions】** The suitable explants are different for different *Gentiana*, and the use of suitable explants is essential for sterile material' s establishment. The skills to prevent water lose and the suitable media are the key factors for culture in vitro and rapid propagation of the wild ornamental *Gentiana*.

Applications of Modern Technology

Tissue Culture as A Tool for Mass Propagation and Research of Ornamental Germplasm

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Plant tissue culture, as a tool for micropropagation and research of plant species, can be efficiently used not only for mass propagation and conservation of rare and endangered species, but also for genetic transformation and breeding of various ornamental and medicinal plant species. The techniques can play an important role in the clonal propagation and qualitative improvement of many important plants. Direct adventitious organogenesis is preferred as it enables to retain clonal fidelity, since many plant species are propagated for one or more unique features. Clonal propagation through somatic embryogenesis has also become an essential method for mass propagation and improvement of important plants. Direct embryogenesis reduces the time required for mass propagation, which may be beneficial to minimize culture-induced genetic changes. The success in regeneration of adventitious organs varies depending upon plant species and a number of endogenous and exogenous factors, among which hormonal balance has a primary role. In particular, the auxin-cytokinin ratio appears to be the most important factor in channeling regeneration responses toward a specific *in vitro* morphogenic process. Efficient protocols were developed for *in vitro* mass propagation of many plants including *Ajuga multiflora*, *Campanula punctata*, *Cotoneaster wilsonii*, *Crocus vernus*, *Dendranthema grandiflorum*, *Dianthus caryophyllus*, *Hedera helix*, *Jeffersonia dubia*, *Paeonia lactiflora*, *Rhododendron keoskei* var. *hypoglaucum*, and *Senecio cruentus*. Efficient protocols were developed also for genetic transformation of *Dendranthema grandiflorum* and *Rosa hybrida* for silicon transporter genes *Lsi1* and *Lsi2*. Methods of suppressing hyperhydricity in micropropagated plantlets such as carnations have also been studied. This study was carried out with the support of ‘Cooperative Research Program for Agriculture Science & Technology Development (Project No. 01090805)’, Rural Development Administration, Republic of Korea.

Comparative Analysis of Anthocyanin Biosynthesis Pathway in Different Cultivars of *Senecio cruentus* Based on Transcriptomics

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There are three anthocyanin biosynthesis pathways in flavonoid metabolic flux included cyanidin, pelargonidin and delphinidin pathways which are responsible for red, orange and blue flower colors respectively. Different species evolved multiple regulation mechanism of these branches formation. In the present study, using the five cultivars of *Senecio cruentus* with different colors as materials, we found that there is no anthocyanin accumulation in the white and yellow cultivars, and the main anthocyanin in the blue, pink and carmine cultivars are Dp, Pg and Cy. Totally 43 unigenes encoding the anthocyanin biosynthesis genes were isolated by transcriptome sequence in blue cultivar, According to a combination of chemical analysis and transcriptome analysis, the major metabolic pathways related to the different series of *S. cruentus* flower pigmentation were investigated, the mutation of ScbHLH17 and ScCHI1/2 genes were responsible for the formation of white and yellow cultivars, the competition of ScF3'H1, ScF3'5'H and ScDFR1/2 for naringenin determined the different branches metabolic flux to the Cy, Dp and Pg, respectively. All the above works provide new insights of the anthocyanin branches regulation and would provide effective gene resources for plant molecular breeding of flower color modification.

Flower Color Chimera May Regulated by circRNA in *Prunus mume*

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One class of non-coding RNA, circular RNA (or circRNA), was easily abandoned during the classical separate process and often ignored by scientists because of its particular structure. It was generated by the way of back-splicing with covalently closed 3' end and 5' end that is quite different from normal linear RNA. CircRNA was identified in many eukaryotes with the development of next-generation sequencing and bioinformatics, and recent attention has been focused on circRNA's "sponge" functions, interacting with the miRNA. By utilizing RNA-seq data and bioinformatics tools, we totally found 2268 circRNAs and revealed the general features of these circRNAs in different color petals tissue from one genotype of *Prunus mume* in the early blooming period. Based on information of white petals tissue, we identified 1533 circRNAs. Based on information of red petals tissue, we identified 1584 circRNAs. They were mainly composed by middle exon and usually contain multiple exons. Differential analysis displayed that 849 circRNAs were shared by the two petals samples. GO and KEGG enrichment analysis

on differential circRNA origin genes indicated that these genes took part in pathways of carotenoid biosynthesis, etc, which suggested that circRNA may have an active function in controlling flower color.

Development and Characterization of EST-SSR Markers by Transcriptome Sequencing in *Rhododendron*

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Rhododendron latoucheae, fragrant evergreen specie of *Rhododendron* that originates from China, is a well-known landscape tree with important medicinal value. Up to now, there were no molecular biology studies and genetic database resource of *Rhododendron latoucheae*, which brings great difficulties in molecular biology of *Rhododendron latoucheae*. We use illumina RNA-seq technology for the leaves and flowers of *Rhododendron latoucheae* and have assembled almost 7.77 GB database, containing 80660 unigenes. In the gene expression profiling analysis, the number of transcripts with GO annotation was 26,212, all unigenes are involved in 3 categories: biological process, cellular component and molecular function and 58 GO-terms, in which, the dominated terms were ‘metabolic process’ (12,314, 46.97% of 26,212), ‘cellular process,’ (12,604, 48.08% of 26,212), and ‘binding’ (13,052, 49.79% of 26,212). 10290 unigenes mapped to 273 biological pathways in the Kyoto Encyclopedia of Genes and Genomes pathway database, in which, unigenes involved in lipid metabolism, biosynthesis of plant hormones, biosynthesis of phenylpropanoids, terpenoids and steroids, Flavone and flavonol, Isoflavonoid were annotated. Based on the physiological characteristics of *Rhododendron latoucheae*, this paper preliminarily analyzed the unigene involved in fragrance, pigments and alkaloid in the secondary metabolites biosynthesis. These data represent abundant messages about transcripts and provided valuable genome data sources in molecular biology of *Rhododendron latoucheae*.

Construction of a Genetic Linkage Map and QTLs Analysis for Phenotypic Traits in Tetraploid Roses

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Roses (*Rosa* sp.), which belong to the family Rosaceae, are one of the most important ornamental flowers in terms of economy and cultural history of humankind, due to their beauty, attractiveness and different usage areas. In recent years inter-qualities have become increasingly important. Compared with traditional breeding method that is regarded as higher degree of uncertainty of unpredictability, molecular marker assisted selection is supposed to be a more efficient way to enhance and accelerate the breeding process. Genetic maps provide a framework of the chromosomal organization and can be used to identify genetic linkage between markers and desirable traits, to locate single genes, for QTL analyses and serve as starting point for map-based cloning of genes etc. Currently, related research are mainly focused on diploid level, while in this genus polyploidy occurs frequently in wild as well as in cultivated roses. The majority of the wild species are diploid, whereas most cultivated roses are tetraploid or triploid. QTLs are difficult to select for in a highly heterozygous tetraploid genome like that of the cultivated rose. Thus, a better understanding of a genetic linkage map with a tetraploid population and important genes that contribute to desired phenotypes will lead to improved rose cultivars. The main results were shown as follows: 1). The present work contains a genetic linkage map for tetraploid roses that was constructed from an F1 segregation population using AFLP and SSR markers on 189 individuals. The preliminary ‘Yunzheng Xiawei’ and ‘Sun City’ maps consisted of 298 and 255 loci arranged into 26 and 32 linkage groups respectively. 2). The recombinant parental maps covered 737 cM and 752 cM of the genome respectively. The final integrated linkage map was aligned with seven integrated linkage groups, which had a calculated total length of 874 cM and 295 polymorphic markers, and it had a mean intermarker distance of 2.9 cM. 3). A set of newly developed EST-SSR markers that are distributed evenly throughout the mapping population were released. On the final integrated map, 108 pairs of newly developed EST-SSR markers provided 149 polymorphic loci, accounting for approximate 50% of the loci. Common SSRs were distributed within the different linkage groups in the present study, and these can be used as anchoring points in the future, while the newly developed EST-SSRs complement them well.

De Novo Transcriptome Assembly and Analysis of *Clarkia* Petal

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Pigmentation patterns, in particular petal spots, are widespread in plants; yet we know little about how they form and diversify. There are over 40 species are currently classified in genus *Clarkia*, which is with in the flowering plant family Onagraceae and found mostly in western North America, and it boasts an immense diversity in floral pigmentation patterns. Particularly distinctive are the dark, large spots found in the petals of some species. The information associated with genes and genetic markers for petal spots formation is very limited. In order to

identify new genes and to develop genetic markers, we performed a transcriptome analysis (RNA-Seq) of *Clarkia gracilis*. Spots and non-spots region of *C. gracilis* petal were harvested for total RNA extraction. Trinity transcriptome assembler were applied for RNA-Seq de novo transcriptome assembly. TransDecoder identified possible coding regions in assembled transcripts. This study provides transcriptome data for petal spots formation.

Molecular Cloning and Expression Analysis of a Monoterpene Synthase Gene Involved in Floral Scent Production from Lily (*Lilium* ‘Siberia’)

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Lilium ‘Siberia’ has a strong floral scent, of which monoterpene is the main volatile component. Using a homology-based PCR strategy, we cloned a monoterpene synthase, named LiTPS, from the petals of *Lilium* ‘Siberia’. The gene had an open reading frame of 1,761 nucleotides and encoded a protein of 587 amino acids with a calculated molecular mass of 67.7 kDa. The deduced amino acid sequence contained a highly conserved DDxxD domain in the C-terminus and RRx8W motifs in the N-terminus, which were both characteristic features of terpene synthase genes. It was showed that mostly 40% to 50% similarity to known monoterpene synthases in other plants, and contained shared domains of terpene synthases, Terpene_synth and Terpene_synth_C. Phylogenetic analysis of LiTPS positioned it in the TPS-b terpene synthase subfamily. LiTPS was predicted to contain an organelle targeting peptide and function as monoterpene synthases in the plastid. Subsequently, it is guessed that LiTPS belonged to class III of terpene synthases according to the analysis of genome structure of LiTPS. Tissue analysis showed that LiTPS expression was petal-specific; it was highly expressed in the petals but barely detectable in stamen, style and leaves. During the flower development of *Lilium* ‘Siberia’, LiTPS was present in mature flower buds; its level peaked on the fourth day after anthesis, when the flower was fully opened, and then decreased slowly. To our knowledge, this is the first time that a terpene synthase gene from *Lilium* has been cloned, and there was a positive correlation between the expression level of LiTPS gene and floral release rate. It provides a theoretical basis for further research into the possible roles of the LiTPS gene.

Graduate Student Oral Competition

Hybrid Analysis of Somatic Fused Lilac (*Syringa* spp.)

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Typical selection and cross-pollination schemes within the tree lilacs (*Syringa* spp.) have revealed few inherent variations for flower color throughout the long history of cultivation. Interspecies crosses have repeatedly failed between the two groups. Somatic hybridization is an *in vitro* technique in plant improvement that has demonstrated the ability to overcome the barriers of sexual incompatibility across species and familial divides. Depending on the success of the protoplast fusion technique many individual hybridization events occur simultaneously leading to a diverse population of polyploid cells mandating the application of marker-assisted selection. Indeed, a large volume of interspecific lilac somatic fusions were produced within several of the tested fusion parameters. Differential protoplast staining procedures aimed at identifying heterokaryons for fluorescent microscopy identification or fluorescence assisted cell sorting (FACS) have conflicted with previous reports. To differentiate heterokaryons from allopolyploids we employed low-copy nuclear genes utilized in phylogenetic studies to identify molecular markers. In the development of a suite of informative markers we targeted four genes within the flavanol and anthocyanin biosynthetic pathways. Intron flanking degenerate primers were designed based on the BLAST consensus sequence alignments from members within the core eudicots. Preliminary screenings revealed the highest consistency and information content when exonic primers spanning intron 2 of a putative dihydroflavonol 4-reductase (DFR) gene were tested. Primers were redesigned to provide greater exon context and assessed across the breeding panel. Amplicon sequencing revealed consistent 8-25 base pair indels consistent and unique to each tested taxonomic *Syringa* series. Somatic fusion tests produce, as found in many other studies, a low heterokaryon yield envisaging opportunities for improvement. Mesophyll derived protoplasts give rise to a number of differences in protoplasts size and plastids aiding in the obscurity of optimal electroporation settings and early heterokaryon analysis. Results indicate that accumulation of fluorochromes with non-destructive viability indicators will yield a high quality visual selection mechanism for early heterokaryon analysis and provide other opportunities for improving the heterokaryon yield.

Comprehensive Evaluation of Landscape Application Potential for Wild Ornamental Plants in Hubei, China

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Hubei province is located in the middle reach of Yangtze River in the center of China, and it belongs to the middle latitude monsoon area. There exists unique natural conditions with rich plant resources, and has more than 3800 plant species. Thus, it has long been concerned by botanists and gardeners from all over the world. Wild plants would have great application potentialities for enriching landscape and garden plant by introduction and domestication. In this study, 1000 local wild plants with ornamental traits were selected firstly as the evaluation objectives based on the preliminary habitat investigation and classification. They were divided into nine categories in terms of application forms and plant ecotypes, which are arbors, shrubs, vines, annuals and biennials, perennials, bulbous, petrophifles, aquatic plants, ornamental grass and ground covers. Secondly, index systems and weights were established according to the application form of ornamental plants in landscape and gardens. The index system of ornamental characters were involved in color, ornamental part, the effect of each other, implication of artistic conception, sound, fragrance, seasonal performance, overall texture and plant morphology. The risk assessment factors were rare and endangered degree, harmony, natural diffusion and use frequency. For the evaluation of ecological habits, we used the parameters of altitude, soil condition, moisture condition, temperature and light condition. By integrated evaluation systems above combined with the preliminary introduction and domestication test, we put forward a hierarchical strategy for rational exploitation and application of wild plant resources. Five grades for the 1000 wild local species were suggested to recommend uses in different levels: (1) direct use, which plants have the highest ornamental values and widest ecological range. 100 of 1000 species were selected with highest potential, and used directly in landscape greening and gardens, including 5 species of ferns, 38 species of trees, 11 species of vines, and 46 species of herbs. For other four grades, we also divided them into different classes: (2) selective use, which plants have higher ornamental value and wider ecological range (3) improved use, which plants have normal ornamental value and low environmental adaptability or use by cultivation and breeding means. (4) controlled use, which plants have lower ornamental value and narrow ecological range, (5) difficult to use, which plants have the lowest ornamental value and narrowest ecological range. This work was carried out the evaluation system of landscape plant application, it is not only an important theoretical guidance for gardeners and landscape designers, but also have a practical significance to speeding up the process of the introduction and domestication of wild plants, to enrich the urban landscape plants species.

Keywords: Hubei; ornamental plants; evaluation system; comprehensive evaluation."

Exponential Growth of Gladiolus ‘Glamini’ under the Influence of Plant Growth Regulators

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Gladiolus xhybridus is a perennial monocot in the Iridaceae. Gladiolus is top ten major cut flowers sold in the USA. In commercial production, gladioli corms produce 1-2 inflorescences per shoot, each of which produce multiple flowers. However, gladioli have the ability to generate multiple shoots, which could influence the flowering timing and floral traits of gladiolus in addition to cormel production. Our objectives are to analyze the influence of plant growth regulators (gibberellic acid 3, GA3; 6-benzyladenin, BA) on the number of shoots, number of inflorescences/shoot, flower timing, plant and flower height, weight and number of corms and cormels produced. BA treatments significantly increased the generation of multiple shoots (vegetative, floral): 6.0 vs. 1.2 (BA vs. control and GA3, respectively). Also in week 7, GA3 and the control treatments resulted in significantly taller vegetative shoots than BA. However, in week 13 and beyond the BA treatment overcame this foliage height difference. BA treatments utilized the energy in gladiolus corms to enhance the generation of stalks as a tradeoff of foliage height; yet over time the multiple vegetative shoots were able to support the energy demands, resulting in an exponential growth pattern.

Poster Session (Outside of Valdosta Room)

Assessment of Genetic Diversity and Phylogenetic Relationship of Dianthus caryophyllus Germplasm Using ISSR and RAPD Molecular Markers

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Carnation (*Dianthus caryophyllus*) is a well-known cut flower or potted plants cultivated worldwide for its ornamental values. The information of genetic relationship and phylogenetic pedigree among different cultivars of carnation can greatly aid in the development of efficient germplasm-management and utilization strategies. Moreover, the importance of genetic variations can be demonstrated by molecular markers-based DNA fingerprinting approaches. In the present study, the genetic diversity among 40 carnation cultivars bred in Korea was assessed using random amplified polymorphic DNA (RAPD) fingerprinting and inter simple sequence repeats (ISSR). For the polymorphism analysis, a total of 20 RAPD decamers and 10 ISSR

molecular markers were employed. The consensus phylogenetic tree was constructed using the binary data obtained from the banding pattern generated by the individual markers. Further, the cluster analysis using Jaccard's similarity coefficient based on Un-weighted Pair Group Method with Arithmetic mean (UPGMA) revealed the genetic similarity between the cultivars. Thus, an efficient and highly reliable method for the identification polymorphism in carnation cultivars using dual-marker system was established. In addition, the results can be further utilized for the enhancement of breeding of carnations. This research was supported by Cooperative Research Program for Agriculture Science and Technology Development (Project No. 01090805), Rural Development Administration, Republic of Korea. Abinaya Manivannan and Prabhakaran Soundararajan were supported by a scholarship from the Brain Korea 21 Plus (BK21 plus) Program, Ministry of Education, Korea."

Gene Expression and Functional Analysis in *Chrysanthemum lavandulifolium* Provides Clues to Understand the Mechanism of Plant Flowering Time Responds to

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Many wild species could be used not only as good gene resources to improve its relative closed cultivated crops but also as good model to understand agronomic traits. *Chrysanthemum lavandulifolium* (Fisch. ex Trautv.) Makino is a diploid in the genus and closely to *chrysanthemum* (*Chrysanthemum ×morifolium* Ramat), which is a typical obligate short-day plant (SDP). Its flowering characters give us clues to understand the flowering mechanism of *chrysanthemum* cultivars that are not only polyploidy but also hybrid-complex. According to recent studies on the molecular mechanism in flowering plants responds to day length, circadian clock genes can sense the day-length signal and transfer such signal into flower signal. We isolated circadian clock, CO and FT homologous based on the transcriptome and digital gene expression database, and then checked the expression patterns of these genes in different photoperiod conditions, combining the functional analysis of key genes. The results showed that the circadian clock genes maintain their rhythm under the alternation of day and night condition and the peak expression levels of CIGIs genes at the beginning of light period could activate the expression of CICAL4/5, CIFT1 and CIFKF1 itself or the synchronous expression of CIFKF1 and CIGIs could repress the expression of CIFT2 gene when the length of dark period beyond the critical night length. When the expression levels of CIFT1 exceed the levels of CIFT2, the flower transition could be completed. Such conclusion not only lay out foundation for understanding the molecular mechanism of plant flowering responds to light period but also provide the new idea to modify flowering time by manipulating the circadian clock and its downstream flower time genes.

De novo transcriptome Sequence Assembly and Characterization of *Paeonia lactiflora* ‘Dafugui’ Buds Under the Natural Low Temperature by RNA-seq

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Herbaceous peonies (*Paeonia lactiflora*) is one of the six famous flowers in ancient china ,which has been cultivated for nearly 4000 years as an ornamental plants owing to its attractive flowers and good moral. Bud dormancy of herbaceous peonies manipulated by the low temperature is a critical developmental process to survive winter conditions in north temperate zone before they break and begin to grow, which is also a major obstacle to the forcing culture. However little is known about the mechanism regulating the bud dormancy in *P. lactiflora*. Here we performed a comprehensive transcriptomics study to identify the global and differentially expressed genes for the underground renewal buds of *Paeonia lactiflora* ‘Dafugui’ using the Illumina RNA-seq system. More than 20 Gb high-quality clean reads were generated after trimming, and assembled into 93,881 unigenes (mean length = 763.80 bp) with a N50 of 1,481 bp. A total of 41,337 (44.03%) unigenes were annotated in at least one of the seven public protein databases

(COG,GO,KEGG, KOG , Pfam ,Swiss-Prot, nr) with a BLAST and HMMER cut-off E-value above 10⁻⁵ and 10⁻¹⁰ , respectively. To investigate changes in gene expression profile among bud dormancy stages, differential expressed genes (DEGs) were identified by pairwise comparisons of the four time-points by applying cut-off of FDR < 0.05 , all 6,224 DEGs were identified twenty co-expression clusters with distinctive patterns, and we found that there were 2,501, 1,979 and 1,984 genes were differentially expressed between dormancy induction and endodormancy, endodormancy and ecodormancy ,and ecodormancy and germination, respectively. Further,we characterized the functional properties of the DEGs by GO function and KEGG pathway enrichment analysis to captures the relevant biological functions.Furthermore, the genes (such as the gene involved in temperature response, hormone metabolism ,water metabolism, energy metabolism, signal transduction ,and so on) ,which may plays an important role in maintenance and breaking of bud dormancy, were also analyzed. The results will increase our knowledge of endo-dormancy release in *Paeonia lactiflora*. The transcriptome data for the species lacking the genomic information currently, will provide valuable resources to better understand the molecular and biological mechanisms regulating its bud dormancy. And will also give a reference to the study of the forcing culture in other non-model perennial horticultural crops.

Key words: *Paeonia lactiflora* ‘Dafugui’; RNA-seq; low temperature; dormancy; DEGs

Advance in Transcriptome-based Analyses of Cold Response and Signaling Pathways of Plant Cold Resistance

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Low temperature is one of the most important environment factors limiting plant's growth, development and distribution. Moreover, Cold stress can always lead to impaired growth, maldevelopment or even physiological imbalance in plant. On the brighter side, plants have evolved a number of adaptive mechanisms to resist cold depending upon the activation of molecular networks involved in stress perception, signal transcription and transduction, expression of specific stress-related genes and physiological reaction of tolerance. Up to now, researches related to plant cold response performed over last few years have made significant achievements in molecular, physiology and phenology aspects. Genome-wide analyses have dramatically improved the efficiency of gene discovery. With the development of omics-based technology including transcriptome and protein mass spectrometry, large scale transcriptome data became available in both model and non-model species these days. The present lecture uses the research transcriptome-based analyses of cold response and signaling pathways in *Lilium lancifolium* as an example and combines with latest studies in other plants, focuses on the molecular aspects of cold stress adaptive mechanism, attempts to highlight the major findings in response to cold stress factors from transcriptome-based analyses, and offers the tentative signaling regulatory pathway and preliminary perspectives on the need for integrated omics approaches facing the realistic field-level studies of stresses .

Rose (*Rosa hybrida*) NAC Transcription Factor gene, RhNAC3, improves dehydration tolerance through regulating ABA and osmotic stress-related genes

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Rose (*Rosa hybrida*) is an important ornamental crops with its highly ornamental values and is widely used in cut flower markets all over the world. However, cut roses are often influenced by dehydration stress, which reduced the production and quality of cut rose flowers. Plant transcription factors play pivotal roles in regulating downstream genes, and less transcription factors were found in cut rose flowers. In this paper, A stress-associated NAC gene from rose (*Rosa hybrida*), RhNAC3, was cloned and functional analyzed in rose petals. RhNAC3 were induced by dehydration, wounding, and exogenous ethylene and abscisic acid treatments. Its full length and carboxyl-terminal domain has transactivation activity in yeast and Arabidopsis

protoplasts. Silencing RhNAC3 in rose petals by virus-induced gene silencing significantly decreased the cell expansion of rose petals under rehydration conditions. In total, 24 out of 27 osmotic stress-related genes were downregulated in RhNAC3-silenced rose petals. In addition, we isolated 1,447 bp of RhNAC3 promoter region and analyzed the upstream regulatory sequence of above. We found that many stress-related cis-elements, including ABRE motifs, MYB motifs and MYC motifs were existed. Overexpression of RhNAC3 in *Arabidopsis thaliana* resulted in ABA hypersensitivity during seed germination and promoted leaf stomata closure after ABA or drought treatments. Additionally, the expression of 11 ABA-responsive genes was induced to a greater degree by dehydration in the transgenic plants overexpressing RhNAC3 than control lines. Taken together, we propose that the rose positive regulator RhNAC3 protein mediate ABA signaling and confers dehydration tolerance through regulating ABA and osmotic stress-related genes.

Key words: NAC transcription factor, dehydration tolerance transcriptional regulation, rose flower

Immature Embryo Germination Revealed Polyembryonic *Viburnum setigerum* Hance

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Viburnum setigerum Hance (tea viburnum) is an upright vase shaped shrub with loaded white flowers, abundant red fruits, and brilliant red fall foliage. It is a great germplasm resource for *Viburnum* breeding. To shorten the breeding cycle, immature embryo germination was investigated. Embryos at globular, heart-shaped or early cotyledonary stages were isolated and cultured on MS medium (0.65% agar, PH 5.7) with various treatments on sucrose concentration, MS strength, as well as collecting time. Results concluded that *Viburnum setigerum* was a polyembryonic plant with 2-9 embryos per seed. Embryos started to germinate in 2 weeks after culture and reached 92% in the 5th week. Reduced MS strength had positive effect on immature embryo germination, mean number of embryos per seed on MS, $\frac{1}{2}$ MS, $\frac{1}{4}$ MS were 3, 6, and 5, respectively. Sucrose concentration at 2% resulted in the highest germination rate at 98% (91% and 92% for 1% and 3% sucrose). Immature embryo could be isolated from Mid-June to early September. This immature embryo germination protocol on *Viburnum setigerum* could speed up its breeding cycles at least 1-2 years and we should carefully exam the hybrid seedlings from apomixis seedlings.

Genetic Diversity of American and Chinese Pepper Cultivars using ISSR

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Genetic diversity of 37 American and 8 Chinese chili pepper cultivars was analyzed using ISSR markers. A total of 100 random primers were screened and 15 ISSR primers (UBC807, UBC808, UBC816, UBC825, UBC826, UBC835, UBC856, UBC857, UBC864, UBC881, UBC886, UBC887, UBC889, UBC895, UBC899) were selected for PCR amplification. As a result, 149 bands were produced, among which 89 bands were polymorphic, accounting for 59.7%. The average Shannon's information index and Nei's genetic diversity index were 0.3410 and 0.2316, respectively. Cluster analysis of Unweighted Pair Group With Arithmetic Average showed that the genetic similarity coefficient of the 45 chili pepper cultivars ranged from 0.6577 to 0.9262. All 45 chili pepper cultivars could be classified into five groups. Group I contained only 'Hot Ornament Sangria' chili pepper with cherry-shaped purple fruits. Group II was also comprised of 'Danshenrui' only with finger-shaped green fruits. Similarly, Group III possesses a single variety, say "Whitney", with cone-shaped yellow fruits. Group IV consists of two varieties, "Duyun Line pepper" and "089", both of which have thin linear, prone, green fruits. The remaining 40 pepper varieties make up Group V, in which the most members are characteristic of small conical, acute apexes, fascicled, upturned, yellow or purple fruits, with some exception of green fruits. Group V also contains some linear and Capsicum varieties. The results of molecular markers will guide the selection of parents in cross breeding.

Plant Genome Editing Made Efficient And Easy: Targeted Mutagenesis Using The CRISPR/Cas System

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Genome editing is one of the most classical plant breeding and transgenic methods to reveal gene function and improve characters. CRISPR/Cas9, a convenient, precise and efficient genome editing technology, was developed rapidly recently, which is a specific gene structure found in the genome of bacteria and archaea, and is the immune system of bacteria and archaea involved in destroying phage and exogenous plasmids. These sequence-specific nucleases can recognize and cleave the specific sequence at target loci to generate double-strand breaks (DSBs), which are repaired by two mechanisms: homologous recombination (HR) and non-homologous end joining (NHEJ). This system has been successfully used in rice, wheat, maize, sorghum,

Arabidopsis, tobacco, sweet orange and tomato using transient expression assays including protoplast transformation and leaf agroinfiltration, according to the recent studies reported. But, there is no any reports suggests CRISPR/Cas9 is an useful tool for targeted mutagenesis of the ornamental plants genome. In this view, we summarize and discuss the advantages and further improvement aspects of this technology in recent applications of CRISPR/Cas in plants, in order to provide some references for the genome editing of ornamental plants.

Effect of Plant Growth Regulator on Induce and Proliferation of *Camellia oleifera* in Vitro

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To investigate the effect of different growth regulator on *Camellia Oleifera* induction and shoots proliferation. “yu liangyouA1” new buds were used as materials. The optimum combination of plant growth regulators in 1/2MS culture medium for plant regeneration was established by orthogonal test. The results revealed zeatin promoted buds induction ratio, the most effective medium was 1/2MS+2.5mg/L-1 IBA+2.5mg/L-16-BA+7mg/L-1ZT+600mg/L-1CH. ABT-6 rooting powder had effective on shoots proliferation, the most effective medium was 1/2MS+4mg/L-1ABT-6+1mg/L-1IBA+1 mg/L-1KT.

Cross Talk Between Hormones and Sugar Metabolism Pathways During Floral Transition in *Rosa chinensis* ‘Old Blush’

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Rosa chinensis ‘Old Blush’ can flower year-round in favorable conditions, and contributes the valuable trait, recurrent flowering, to modern roses. Physiological and molecular studies have demonstrated that vegetative-to-reproductive transition is not only regulated by exogenous cues, but are also regulated by endogenous signals such as plant hormones and sugar metabolism. Hormones, sugar and starch content showed a fluctuated change and their biosynthesis and metabolism genes displayed an interactive network, in which AGPase, a starch synthesis enzyme, showed a positive relation with sugar, IAA, ABA. YUC1, GA2ox8, SCL13 were related to sugar

metabolism. HXK2 was simultaneously related to GAs, IAA, ABA. Additionally, bZIP60 was connected collectively with ABA and sugar metabolism and transport. Overall, the interactive network between hormones and sugar metabolism provide useful approach to study the molecular mechanism underlying floral transition in *R. chinensis* ‘Old Blush’.

Identification and Characterization of CYC2 Clade Genes in Regulation of Ray Flower Development in *Chrysanthemum morifolium*

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Chrysanthemum morifolium, one of the most economically important ornamental crops worldwide, is well-known for the elaborate and complex inflorescence which is composed of both bilaterally symmetrical ray flowers and radially symmetrical disc flowers. Despite continuing efforts, the molecular mechanisms underlying regulation of the two flower types are still unclear so far. Proteins of the CYCLOIDEA2 (CYC2) clade have been shown to control flower symmetry or regulate flower-type identity in several angiosperm plant lineages. In this study, we conducted comparative analysis of the CmCYC2 genes in two hexaploid chrysanthemum cultivars and their F1 progenies with various whorls of ray flowers. Six CmCYC2 genes were identified and sequenced, all of which were grouped into CYC2 clade. All the six CmCYC2 genes were predominantly expressed in reproductive organs, and in particular in the corolla of ray flowers. Of these genes, the transcription level of CmCYC2c was highly upregulated in ray florets of the double-ray flowered heads (with multiple whorls of ray flowers). In addition, the result that CmCYC2c was highly expressed at stage IIa and stage IV suggests it may function in regulating petal development at both early and late stages. Gene expression analysis demonstrated that all the six CmCYC2 genes were predominantly expressed in reproductive organs, and in particular in the corolla of ray flowers. In addition, CmCYC2c may play an important role in regulating petal development at both early and late stages. Furthermore, overexpression of CmCYC2c in *C. lavandulifolium*, one of the original species of *C. morifolium*, led to significant increase in flower numbers and petal ligule length of ray flowers. Besides CmCYC2c, the expression of CmCYC2f was also significantly upregulated in transgenic lines, implying a possible role in regulating development of ray flowers. Both results of expression patterns and transgenic phenotypes suggest that CmCYC2c is involved in regulating ray flower identity in the chrysanthemum. This study will be useful for genetic manipulation of flower shape in chrysanthemum and hence promote the process of molecular breeding.

Variation in tissue Na⁺ content and the activity of SOS1 genes among two species and two related genera of Chrysanthemum

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Chrysanthemum, a leading ornamental species, does not tolerate salinity stress, although some of its related species do. The current level of understanding regarding the mechanisms underlying salinity tolerance in this botanical group is still limited. A comparison of the physiological responses to salinity stress was made between *Chrysanthemum morifolium* ‘Jinba’ and its more tolerant relatives *Crossostephium chinense*, *Artemisia japonica* and *Chrysanthemum crassum*. The stress induced a higher accumulation of Na⁺ and more reduction of K⁺ in *C. morifolium* than in *C. chinense*, *C. crassum* and *A. japonica*, which also showed higher K⁺/Na⁺ ratio. Homologs of an Na⁺/H⁺ antiporter (SOS1) were isolated from each species. The gene carried by the tolerant plants were more strongly induced by salt stress than those carried by the non-tolerant ones. When expressed heterologously, they also conferred a greater degree of tolerance to a yeast mutant lacking Na⁺-pumping ATPase and plasma membrane Na⁺/H⁺ antiporter activity. The data suggested that the products of AjSOS1, CrcSOS1 and CcSOS1 functioned more effectively as Na⁺ excluders than those of CmSOS1. Over expression of four SOS1s improves the salinity tolerance of transgenic plants and SOS1s from salt tolerant plants were more tolerant than SOS1s from salt sensitive plants. In addition, the importance of certain AjSOS1 residues for effective ion transport activity and salinity tolerance was established by site-directed mutagenesis and heterologous expression in yeast. AjSOS1, CrcSOS1 and CcSOS1 have potential as transgenes for enhancing salinity tolerance. Some of the mutations identified here may offer opportunities to better understand the mechanistic basis of salinity tolerance in the chrysanthemum complex.

Conservation and Sustainability

Genetic Diversity, Population Structure, and Conservation Implications of Endangered Endemic *Paeonia jishanensis* in China

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Paeonia jishanensis, one of the most important ancestral species of cultivated tree peonies, is an endangered ornamental and medicinal plant endemic to China. A total of 236 individuals of *P. jishanensis* from 10 extant populations were analyzed using 21 EST-SSR markers to assess the genetic diversity and population structure. Moderate genetic diversity levels ($HE=0.340$) and high genetic differentiation among populations ($F_{ST} = 0.335$) were revealed. Combined with the results of the STRUCTURE, PCoA and neighbor-joining analyses, 10 populations were divided into four genetic groups significantly related to the geographical origins, which was further supported by the hierarchical AMOVA with the highest variation of 17.9% among groups. The Mantel test showed a significant positive correlation between the genetic distance and geographic distance among populations ($r = 0.873$, $P < 0.0001$). The genetic structure of *P. jishanensis* may be due to the limited gene flow hindered by vicariance and the breeding system of the facultative vegetative reproduction. This study provides significant implications for the conservation and utilization of this endangered species.

Key words: conservation; EST-SSR; genetic diversity; *Paeonia jishanensis*; population structure; tree peony.

Investigation on Mechanisms of Embryo Abortion During Chrysanthemum Distant Hybridization

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The chrysanthemum (*Chrysanthemum morifolium*) is the second most important flower in the world and plays a vital role in the flower production industry. However, a challenge exists in chrysanthemum cultivation: most chrysanthemum cultivars are less resistant to biotic and abiotic stresses. To improve chrysanthemum resistance, breeders often carry out wide crosses between chrysanthemum cultivars and wild chrysanthemum species that display strong tolerances to biotic and abiotic stresses. However, reproductive barriers often exist in these crosses, and as a

consequence, breeding efficiency is considerably reduced. Our previous investigation indicated that embryo abortion is the main cause of failure in chrysanthemum cross breeding, but the cellular and molecular mechanisms associated with embryo abortion are poorly understood. Thus, we applied fluorescence and electron microscopy, RNA sequencing, isobaric tags for relative and absolute quantitation (iTRAQ), 5'RNA Ligase-Mediated Rapid Amplification of cDNA Ends (RLM-RACE) to analyze mechanisms of embryo abortion. We found that embryo abortion mainly occurred during stage of globular embryo. In addition, abortive embryos had higher activity of three key executioner caspase-like enzymes, LEVDase, VEIDase and LEHDase, than the normal embryos. Furthermore, genes and proteins associated with cell death, protein degradation, reactive oxygen species scavenging, and stress-response transcriptional factors were significantly up-regulated in abortive embryos relative to normal embryos. These results indicate that chrysanthemum embryo abortion is likely a result of programmed cell death (PCD), and several senescence- or death-associated genes contributing to embryo abortion. Taken together, this study highlights our understanding of mechanisms related to chrysanthemum embryo abortion, and will be useful in the future for overcoming embryo abortion during cross breeding of chrysanthemum and other crops.

Breeding Fragrant Crape Myrtles Using *Lagerstroemia caudata*, A Native Germplasm to China

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Lagerstroemia indica (crape myrtle) is known as a worldwide ornamental woody plant with 80-100 days flowering but lack of fragrance. Though few cultivars were recorded with a faint fragrance, real or strong fragrant crape myrtle still seems impossible. *L. caudata* is one of the excellent germplasm resources endemic to China, which leads to a profound impact on its tea like fragrance and early flowering. However, small flower size and white flower color limit its direct commercial application. Therefore, reciprocal hybridizations with larger flower and bright color crape myrtles may breed new cultivars with excellent fragrance and commercial characters. In this study, we used *L. caudata* as core parent to cross with bright color and /or larger flower size crape myrtles. Hybrid seed data were evaluated to select the best crossing match. Morphological and SSR comparisons were made to verify the authenticity of hybrid offspring. HS-SPME sampling and GC/MS analysis were used to analyse the volatile components of parents and crossing progenies, even seek for genetic behaviour of flower fragrance. *L. caudata* showed quite compatibility with crape myrtle cultivars, especially when as the maternal parent. The bagged set-seed percentage of cross, backcross and three way cross ranged from 12.6% to 81.7%. Reciprocal hybrids, which were verified with 8 SSRs, were intermediate in appearance

between parents, but variability in leaf, flower size and flower color existed among the hybrids. The main difference of volatile component between parents was monoterpene derivatives such as geraniol, neral and citral. Myrcene was the only mutual ingredient among *L. caudata* and its hybrids, of which the relative contents were not high [0.69%, 3.16% (F1), 0.51% (F2) and 0.75% (BC1)] respectively. The main aroma components of F1 progenies were fatty acid, while terpenoids were the main aroma components of F2 and BC1. The data generated in this study testify the feasibility of *L. caudata* as an important breeding material for aromatic cultivars and document the first step in an effort to combine desirable ornamental features from *L. caudata* and *L. indica*.

The Resources Evaluation and Landscape Application of *Hosta* Cultivars

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Hosta is one of the world famous ornamental groundcovers for its colored leaves, various leaf shapes and flower shapes. In order to resolve the problem about lack of *hosta* resources in Beijing landscape greening, the introduction, breeding and application of *hosta* cultivars has been implemented since 2000 in Beijing Botanical Garden. Based on years of *hosta* morphological observation and biological characteristics, selected 50 *hosta* cultivars were evaluated according to their ornamental characteristics, resistance and propagation ability. Better 26 *hosta* cultivars were screened, such as 'Blue Boy', 'Nigresence', 'Knock Out', 'June' and so on. These screened *hosta* cultivars have been applied to perennial Garden, *hosta* Garden, edge of forests in Beijing Botanical Garden with better ornamental characteristics and resistance. The research results enriched plant materials for groundcovers under forests in Beijing landscape greening and improved landscape level.

Key Words: *Hosta*; Resources Evaluation; Landscape Application"

Collecting Horticulturally-useful Traits in the Wild Methodology to Maximize Genetic Gain and Minimize Risk

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The potential value to be found in collecting wild species of ornamental crop relatives is immensely proportional to the careful planning of collection trips, integration of local experts, serendipity in finding mutant genotypes, and risk management both during collection and thereafter in the breeding, domestication and selection process. Objectives of this research were



to demonstrate the value of well-planned collecting trips to maximize genetic gain in future breeding and minimize risks in collected plant materials. More than 30 years of plant collecting experience throughout the world (S. Africa, Europe, N. America) and testing these findings with undergraduate students in a plant production course for new crop development are the basis for this research. Essential collection procedures include creating a crop ideotype to identify which traits are of importance in the new germplasm; these traits will direct the timing of when to collect, the best location of populations to maximize trait expression in wild populations, and existence of natural hybrids, rather than collecting only when seed are produced and implementing targeted (centers of origin, diversity) vs. random collections. Methods of population sampling to maximize genetic diversity, the numbers of genotypes to collect, and minimizing invasion risk also influence potential genetic gain.

International Conference on Germplasm of Ornamentals



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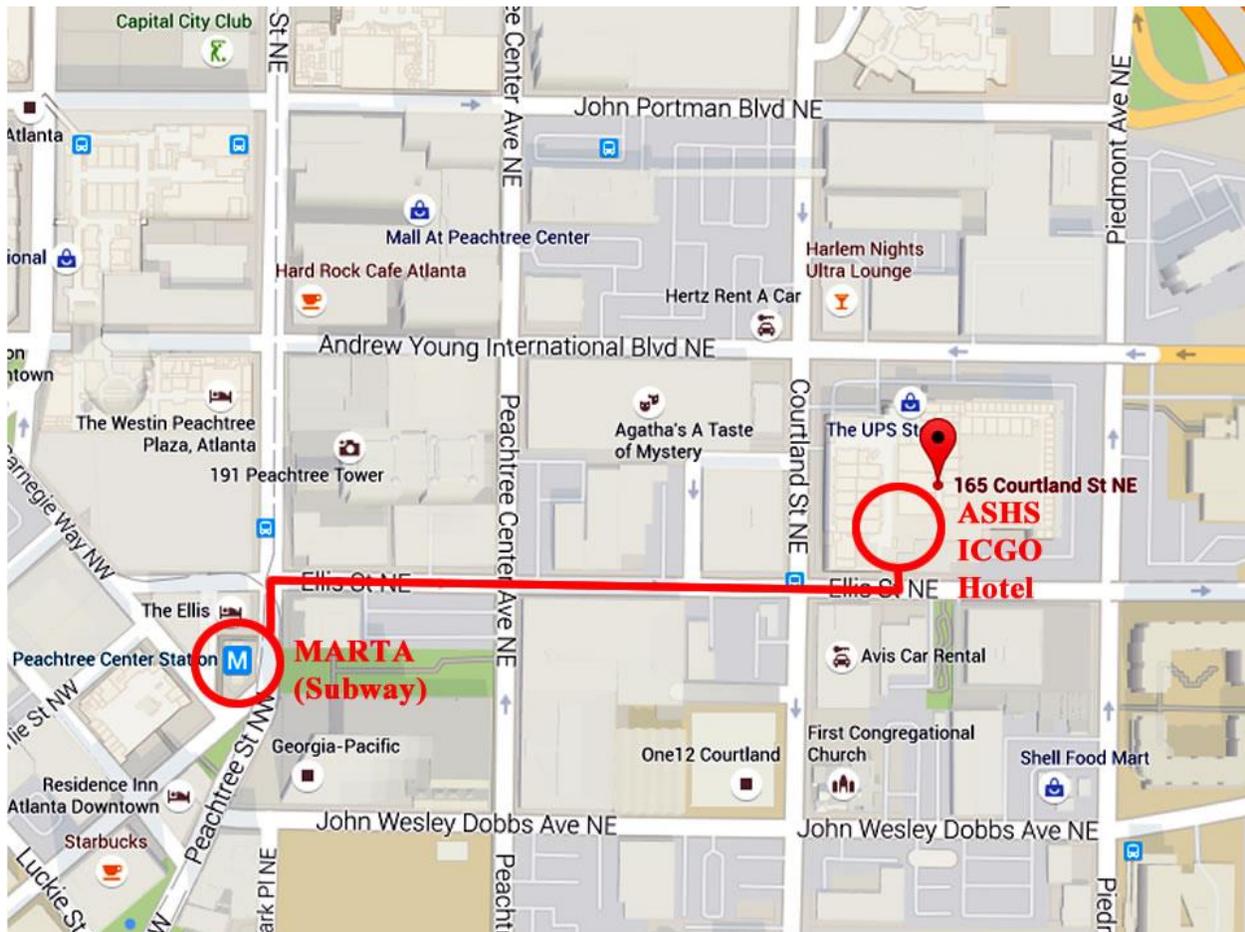


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Editor-in-Chief
Prof. Dr. Donglin Zhang



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Programs and Tours

Day 1 (August 7, 2016): Registration (all day)
(www.ashs.org).

Day 2-3 (August 8-9, 2016): Join the ASHS Scientific Program
(www.ashs.org).

Day 4 (August 10, 2016):

8:00am: Welcome and Open Remarks.
8:30-10:00am: Oral Presentation --- New Ornamental Plants.
10:00-10:30am: Break and Poster Session.
10:30-12:00 noon: Oral Presentation --- Selection and Breeding.
12:00-1:00pm: Box lunch will be provided
1:00-2:30pm: Visit Pike Nursery / Garden Center.
4:30-8:00pm: Visit Atlanta Botanical Garden (ABG) in Gainesville, GA.
Welcome dinner and keynote speech at ABG.
9:30pm: Return to Sheraton Atlanta.

Day 5 (August 11, 2016):

8:00-9:45am: Oral Presentation --- Germplasm Resources.
9:45-10:30am: Break and Poster Session.
10:30-12:00noon: Oral Presentation --- Ornamental

Exploration and Utilization.

12:00-1:00pm: Lunch on your own.
1:00-2:30pm: Oral Presentation --- Applications of Modern Technology.
2:30-3:15pm: Break and Poster Session.
3:15-4:45pm: Oral Presentation --- Conservation and Sustainability.
4:45-6:00pm: Closing Remarks.
6:00-7:00pm: Committee meeting
7:00pm: Sponsor's Dinner

Day 6 (August 12, 2016):

8:00am: Load on the bus and visit Angel Creek Nursery and Southeastern Growers
12:00-2:00pm: Box lunch (provided) and question and answers.
2:00-4:00pm: University of Georgia (UGA) Horticulture Farm & Trial Gardens
4:00-6:00pm: Farewell Dinner at Georgia Center (UGA), Student Awards.
7:45pm: Arrive the hotel and the symposium adjourn!

Day 7 (August 13, 2016): Departure

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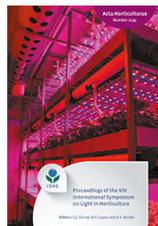
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