VII International Symposium on Rose Research and Cultivation

July 2-7, 2017
Angers (France)

Abstract book
Dear congress participants, dear colleagues,

In the name of the organizing committee, I am very pleased to welcome you in Angers for the VII International Symposium on Rose Research and Cultivation. We are around 130 people from more than 20 countries.

We have organized this meeting with the objective to gather breeders, producers and researchers working on roses from all over the world. The symposium will cover all areas of rose research with updates on the most recent developments in all fields: agronomy, physiology, genetics, genomics… The meeting is organized around 7 scientific sessions and a round table. There will be 36 oral presentations and 70 posters presented during the symposium. I am sure that you will have interesting and passionate discussions that will be the beginning of fruitful collaborations.

The symposium will also be the opportunity to discover beautiful rose gardens around Angers: the Loubert rose garden (Les Rosiers sur Loire) with more than 3000 different varieties with a large collection of botanical roses and the international rose garden of the city of Nantes (Roseraie Paul Plantiveau, La Beaujoire) with around 1600 varieties with a specialization on perfume roses. You will also have the opportunity to visit different rose nurseries in the area of Doué en Anjou, the first region of garden rose production in France.

There are not only roses in Angers! We hope that during this meeting you can visit this charming city with its historical center. History but also future, with our visit of “Terra Botanica”, a park dedicated to plant: beautiful gardens and also amusement for children and adults. During the post-congress tour, we will also visit the beautiful city of Nantes, with the recent development of the area ‘Ile de Nantes’

This symposium would not have been possible without the precious help of the members of the organizing committee. I would like to thank Patricia and Pierre for their help concerning the administrative management, Nathalie and Etienne for the website management and abstract book, Sandrine for the blooming of the symposium, Nathalie and Gaëtan for their help at Agrocampus-Ouest and all the members of the organizing committee for their help in the organization of this meeting. Thanks very much to Sandrine, Rachid, Annie, Jérémy, Laurent, Agnès, Vincent, Latifa, Laurence, Lydie, Julien, Nathalie, Lucie, Valéry, Vanessa and Tatiana.

I would also like to thank the different institutions that support financially this meeting: the University of Angers, Agrocampus Ouest, INRA (Plant Breeding and Biology department and Environment and Agronomy department), Angers Loire Métropole, the region “Pays de la Loire and the competitive cluster “Végépolys”.

So enjoy science during the meeting and also enjoy the French way of life.

Have a very nice and exciting meeting.

For the organizing committee,
Fabrice FOUCHER
### Committees

#### Convener

| Fabrice Foucher, INRA |

#### Local organizing committee

| Sandrine Balzergue, INRA | Laurence Hibrand-Saint Oyan, INRA |
| Rachid Boumaza, Agrocampus Ouest | Julien Jeaffre, INRA |
| Annie Chastellier, INRA | Pierre Langlais, INRA |
| Jérémy Clotault, University of Angers | Nathalie Leduc, University of Angers |
| Laurent Crespel, Agrocampus Ouest | Nathalie Mansion, INRA |
| Sabine Demotes-Mainard, INRA | Alix Pernet INRA |
| Fabrice Foucher, INRA | Soulaiman Sakr, Agrocampus Ouest |
| Agnès Grapin, Agrocampus Ouest | Vanessa Soufflet-Freslon, Agrocampus Ouest |
| Vincent Guérin, INRA | Tatiana Thouroude, INRA |
| Lydie Huché-Thélier, INRA | Patricia Vandaele, INRA |

#### Scientific committee

| Sylvie Baudino, BvPAM, St Etienne, France |
| David Byrne, Texas & AM, College Station, TX, USA |
| Thomas Debener, Univ. Hanover, Hanover, Germany |
| Fabrice Foucher, INRA, Angers, France |
| Junping Gao, CAAS, Beijing, China |
| Johan van Huylenbroeck, ILVO, Melle, Belgium |
| Alain Meilland, Meilland, Cannet des Maures, France |
| Hilde Nybom, Swedish Univ. of Agri. Sci., Kristianstad, Sweden |
| Niu Genhua, AgriLife Research and Extension Center, El Paso, TX, USA |
| Brent Pemberton, Texas & AM, College Station, TX, USA |
| Soulaiman Sakr, Agrocampus-Ouest, Angers, France |
| René Smulders, Wageningen UR, Wageningen, Netherland |
| Yoshihiro Ueda, Gifu International Aca. Hort., Gifu, Japan |
Access Map to Agrocampus Ouest

By car:
From Paris: A11 - Take the exit n°15 direction Angers, continue along the river "Maine" (D323).
Take the exit "Université-Angers Technopole".
Follow the direction "Angers Technopole".
Continue on the "Boulevard Victor Beaussier", cross 2 fires. In the traffic circle (intersection SuperU/ESSCA),
take to the left "Boulevard Lakanal" then in the face of the "Maison de la Technopole", take to the right "Rue André Le Nôtre".

By bus:
Ligne 1 (direction Belle-Beille) - final stop
(Maison de la Technopole / Belle-Beille)
Line 4 is not serving the stop "Belle-Beille" during the symposium.
ISHS ROSE
18h15 - 20h15 :
Angers (14 rue du Musée, Angers).

Angers Map

Agrocampus Ouest - 2 rue André Le Nôtre - Angers - tél : 02 41 22 54 54

Terra Botanica - Route d’Épinard - Angers - tél : 02 41 25 00 00

Train Station - 1 esplanade de la gare - Angers - tél : 0 892 35 35 35

Musée des Beaux-Arts - 14 Rue du Musée - Angers - tél : 02 41 05 38 00
Sunday 2nd
Angers, (Musée des Beaux-Arts)

18h15 - 20h15: Registration and welcome reception at the Museum des Beaux-Arts in the historical center of Angers (14 rue du Musée, Angers).
### Scientific sessions 1: Rose genetics and breeding

**Chairpersons:** Jérémy Clotault & Johan Van Huylenbroeck  

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>9.30</td>
<td>S1_K1</td>
<td>High-density SNP maps for genetics and genomics in tetraploid rose</td>
<td>René Smulders</td>
</tr>
<tr>
<td>10.05</td>
<td>S1_1</td>
<td>Genetic dissection of shoot organogenesis in roses</td>
<td>Thi Hong Nhung Nguyen</td>
</tr>
<tr>
<td>10.25</td>
<td>S2_2</td>
<td>Heritability of markers for plant architecture in diploid roses</td>
<td>Ellen Roundey</td>
</tr>
<tr>
<td>10.45</td>
<td></td>
<td>COFFEE BREAK</td>
<td></td>
</tr>
<tr>
<td>11.15</td>
<td>S1_3</td>
<td>Control and selection of blooming seasonality in rose</td>
<td>Fabrice Foucher</td>
</tr>
<tr>
<td>11.35</td>
<td>S1_4</td>
<td><em>Rosa arvensis</em> as a possible genetic model</td>
<td>Pascal Heitzler</td>
</tr>
<tr>
<td>11.55</td>
<td>S1_5</td>
<td>SNP Markers linked to gender in dioecous <em>Rosa setigera</em> Michx.</td>
<td>David C. Zlesak</td>
</tr>
<tr>
<td>12.15</td>
<td></td>
<td>LUNCH</td>
<td></td>
</tr>
<tr>
<td>13.20</td>
<td></td>
<td>POSTER SESSION</td>
<td></td>
</tr>
<tr>
<td>14.20</td>
<td>S1_6</td>
<td><em>Rosa palustris</em> and <em>Rosa setigera</em>: breeding challenges</td>
<td>Ellen Roundey</td>
</tr>
<tr>
<td>14.40</td>
<td>S1_7</td>
<td>breeding for beautiful strong and chemical-free roses</td>
<td>Ping Lim</td>
</tr>
<tr>
<td>15.00</td>
<td>S1_8</td>
<td>Fieldbook app: use in data collection in rose breeding</td>
<td>Jeekin Lau</td>
</tr>
<tr>
<td>15.20</td>
<td></td>
<td>COFFEE BREAK</td>
<td></td>
</tr>
</tbody>
</table>

### Scientific session 2: Secondary metabolites

**Chairpersons:** Junping Gao & Jean-Claude Caissard  

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>15.50</td>
<td>S2_K1</td>
<td>Biosynthesis of scent compounds in rose</td>
<td>Sylvie Baudino</td>
</tr>
<tr>
<td>16.25</td>
<td>S2_1</td>
<td>Bioactive compounds content and antioxidant activity of leaf and hip extracts from four Sicilian Rose species</td>
<td>Giancarlo Fascella</td>
</tr>
</tbody>
</table>

### Round Table :

**Chairperson:** Dave Byrne & Mike Shoup  

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Participants</th>
</tr>
</thead>
<tbody>
<tr>
<td>16.50</td>
<td>How research can be useful for breeders, producers, rose keepers and rosarians ?</td>
<td>François Felix (president of the FNPHP), Alain Meilland (Rose Breeder), David Zlesak (Rose breeder), Silvia Fineshi (manager of the family's rose garden), Henrieann de Briey (vice-president of the WFRS)</td>
</tr>
</tbody>
</table>
# Tuesday July 4th
Agrocampus Ouest (Amphitheatre Pisani)

## Scientific session 3: Rose physiology

**Chairpersons:** Nathalie Leduc & Marie-Christine Van Labeke

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Speaker</th>
</tr>
</thead>
<tbody>
<tr>
<td>9.00</td>
<td>S3_K1</td>
<td>Role of ethylene in petal growth and senescence of roses</td>
<td>Junping Gao</td>
</tr>
<tr>
<td>9.35</td>
<td>S3_1</td>
<td>Digital image analysis to assess flower productivity and foliage retention in garden roses throughout the season</td>
<td>David Byrne</td>
</tr>
<tr>
<td>9.55</td>
<td>S3_2</td>
<td>Light use efficiency of a rose crop as influenced by the spectrum of the artificial light</td>
<td>Victoria Nieves Garcia</td>
</tr>
<tr>
<td>10.15</td>
<td>S3_3</td>
<td>Effects of Some Preservative Solutions on the Vase Life of Cut Rose Flowers</td>
<td>Soner Kazaz</td>
</tr>
<tr>
<td>10.35</td>
<td></td>
<td><strong>COFFEE BREAK</strong></td>
<td></td>
</tr>
</tbody>
</table>

## Scientific session 4: Rose genomics

**Chairpersons:** René Smulder & Dietmar Schultz

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Speaker</th>
</tr>
</thead>
<tbody>
<tr>
<td>11.05</td>
<td>S4_K1</td>
<td>Rose genome sequencing initiative</td>
<td>Fabrice Foucher</td>
</tr>
<tr>
<td>11.40</td>
<td>S4_1</td>
<td>Genome structure of <em>Rosa multiflora</em> an ancestral wild rose of cultivated roses</td>
<td>Yoshikazu Tanaka</td>
</tr>
<tr>
<td>12.00</td>
<td>S4_2</td>
<td>The draft genome of <em>Rosa gigantea</em></td>
<td>Shubin Li</td>
</tr>
<tr>
<td>12.20</td>
<td></td>
<td><strong>LUNCH</strong></td>
<td></td>
</tr>
<tr>
<td>13.40</td>
<td>S4_3</td>
<td>Transcriptome of the floral transition in <em>Rosa chinensis</em> 'Old Blush'</td>
<td>Xuelian Guo</td>
</tr>
<tr>
<td>14.00</td>
<td>S4_4</td>
<td>A genotype-driven comparative informatics approach to discover useful disease resistance genes for rose improvement”</td>
<td>James Bradeen</td>
</tr>
<tr>
<td>14.20</td>
<td>S4_5</td>
<td>The development of a dense SNP-based consensus map and QTL detection for black spot resistance in three diploid rose populations</td>
<td>Patricia Klein</td>
</tr>
<tr>
<td>14.40</td>
<td></td>
<td><strong>POSTER SESSION</strong></td>
<td></td>
</tr>
</tbody>
</table>

### VISIT TERRA-BOTANICA AND GALA DINNER

- 15.45: Departure by bus for “Terra Botanica”
- 16.10: Guided and free visit of “Terra Botanica”, a park dedicated to plants
- 19.00: Gala dinner at “Terra Botanica”
  (Return to the hotel by tramway, the last tramway is at 0.30 am).
Wednesday July 5th
Agrocampus Ouest (Amphitheatre Pisani)

Scientific session 4: Rose genomics
Chairpersons: René Smulder & Dietmar Schultz

9.00 : S4_6 Association studies in roses reveal robust markers for flower traits Dietmar Schulz
9.20 : S4_7 Preliminary study on molecular mechanism of phyllody phenotype in Rosa chinensis cv. Viridiflora Huijun Yan

Scientific session 5: Abiotic stress
Chairpersons: David Byrne & Dik de Vries

9.40 : S5_K1 Salt tolerance in garden roses Genhua Niu
10.15 : S5_1 Light targets cytokinins as early signaling vectors to control bud outgrowth in Rose Nathalie Leduc
10.35 : S5_2 Evaluating landscape rose performance on reduced irrigation Karrie Reid
10.55 : S5_3 Seasonal changes in cold hardiness of garden roses Lin Ouyang

Technical symposium tour

11.30 : Bus to the Loubert rose garden (Les Rosiers-sur-Loire)
12.30 : Visit of the Loubert rose garden and picnic.
15.00 : Bus to rose nurseries
15.30 : Visit of rose producers in the area of Doué la Fontaine
    - Rose nursery "Loubert" J.Chéné
    - Rose nursery "La Saulaie" C.Travers
    - Rose nursery "Chastel" P.Chastel
17.30 : Bus to "Les écuries Foullon" (Doué en Anjou)
18.00 : Welcome reception by the city of Doué en Anjou and presentation of the association "Rose producers around Doué" and Regional Innovative platform on rose production (Association and Chamber of Agriculture)
19.15 : Bus to the restaurant "La cathédrales de la Saulaie".
19.30 : Dinner with "Fouée" in a troglodyte restaurant ("Les cathédrales", Doué en Anjou)
22.30 : Bus to Angers center (train station, castle and Agrocampus Ouest)
# Scientific session 6: Social sciences and humanities

**Chairpersons:** Fabrice Foucher & Deborah Golino

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Author(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>9.00</td>
<td>S6_K1 Roses in the horticultural context of 19th century in France. Questioning the diversity in historical sources</td>
<td>Cristiana Pavie</td>
</tr>
<tr>
<td>9.35</td>
<td>S6_1 The great leap forward towards Chinese genetic background: Impact of practices of French breeders from the nineteenth century on the evolution of the diversity of garden rose</td>
<td>Jérémy Clotault</td>
</tr>
<tr>
<td>9.55</td>
<td>S6_2 Legacies of Robert Basye and Ralph Moore: historical perspective</td>
<td>David Byrne</td>
</tr>
<tr>
<td>10.15</td>
<td>S6_3 The rise and decline of the ‘Scots Rose’ phenomenon c.1800-1860</td>
<td>Peter D. A. Boyd</td>
</tr>
<tr>
<td>10.35</td>
<td>COFFEE BREAK</td>
<td></td>
</tr>
<tr>
<td>11.05</td>
<td>S6_4 Survey of the rose community: desired rose traits and research issues</td>
<td>David Byrne</td>
</tr>
<tr>
<td>11.25</td>
<td>S6_5 American Rose Trials for Sustainability® (A.R.T.S.): A new united states rose trialing program for identifying and promoting regionally adapted roses</td>
<td>Gaye Hammond</td>
</tr>
<tr>
<td>11.45</td>
<td>S6_6 Neuromarketing a novel approach to determine the consumer preferences and willingness-to-pay for Rose attributes</td>
<td>David Byrne</td>
</tr>
<tr>
<td>12.05</td>
<td>LUNCH</td>
<td></td>
</tr>
</tbody>
</table>

# Scientific session 7: Biotic stress

**Chairpersons:** Thomas Debener & Stan Hokanson

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Author(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>13.15</td>
<td>S7_K1 Combating Rose rosette disease US national project</td>
<td>David Byrne</td>
</tr>
<tr>
<td>13.50</td>
<td>S7_1 Development of tools to study rose resistance to black spot</td>
<td>Vanessa Soufflet-Freslon</td>
</tr>
<tr>
<td>14.10</td>
<td>S7_2 Resistance of garden roses to Cercospora leaf spot</td>
<td>Stella Kang</td>
</tr>
<tr>
<td>14.30</td>
<td>S7_3 Testing EDNA-ROSE: a novel <em>in silico</em> approach for detection of rose viruses combining next generation sequencing and bioinformatics</td>
<td>Lizbeth Pena-Zuniga</td>
</tr>
<tr>
<td>14.50</td>
<td>COFFEE BREAK</td>
<td></td>
</tr>
<tr>
<td>15.20</td>
<td>CLOSING REMARKS</td>
<td></td>
</tr>
<tr>
<td>16:30</td>
<td>End</td>
<td></td>
</tr>
</tbody>
</table>
Friday July 7th
Post-Congress tour in Nantes

8.00: Departure by bus to Nantes (Departure in front of the train station)

9.30-11.30: Visit of the IRSTV and a garden

12.00-13.45: Visit of the rose garden of the city of Nantes (Beaujoire) and picnic.

14.15-15.45: Plants and urbanism in the "île de Nantes".

15.50-17.50: Visit of "Les machines de l'île"

18.00-20.00: Return to Angers (Castle and train station)

* Possibility to stay in Nantes in order to reach the Nantes Airport.

* Time of arriving in Angers is approximate and will depend of the traffic on the highway.
<table>
<thead>
<tr>
<th>Poster ID</th>
<th>Title</th>
<th>Author(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>S1_P01</td>
<td>A Study of Morphological Variation and Palynomorphology of Rosa laxa Retz. (Rosaceae) in Xinjiang, China</td>
<td>Xuelian Guo</td>
</tr>
<tr>
<td>S1_P02</td>
<td>Field evaluation of species and modern garden roses for black spot and landscape performance in Texas</td>
<td>Brent Pemberton</td>
</tr>
<tr>
<td>S1_P03</td>
<td>A decorative value estimation of hybrid tea roses for use in greening of the Southern Russian cities.</td>
<td>Svetlana Plugatar</td>
</tr>
<tr>
<td>S1_P04</td>
<td>The main directions of a rose selection in the South of Russia.</td>
<td>Zinaida Klymenko</td>
</tr>
<tr>
<td>S1_P05</td>
<td>Palynological Features Comparison of Compatible and Incompatible <em>Rosa hybrida</em> L. cultivars in Korea</td>
<td>Gyung Ran Do</td>
</tr>
<tr>
<td>S1_P06</td>
<td>Heritability of flower size and heat stress in diploid roses</td>
<td>Lau Jeekin</td>
</tr>
<tr>
<td>S1_P07</td>
<td>Field evaluation of rose cultivars to black spot in Southern Ontario</td>
<td>Parminderjit Sandhu</td>
</tr>
<tr>
<td>S1_P08</td>
<td>RosBREED2 - Combining disease resistance with horticultural quality in new rosaceous cultivars including rose!</td>
<td>Stan C. Hokanson</td>
</tr>
<tr>
<td>S1_P09</td>
<td>Characterization of Rosa 'Harison's Yharisonellow' clones using SNP Markers</td>
<td>David Zlesak</td>
</tr>
<tr>
<td>S1_P10</td>
<td>Rose parental characterization and population development for the identification of novel rose black spot resistance genes</td>
<td>David Zlesak</td>
</tr>
<tr>
<td>S1_P11</td>
<td>Screening and identification of proteins interacting with RhMLO1 and RhMLO2 in rose</td>
<td>Xianqin Qiu</td>
</tr>
<tr>
<td>S1_P12</td>
<td>Breeding of posterity crossing between cut rose cultivar ‘PEKcougel’ and tetraploid <em>Rosa multiflora</em>.</td>
<td>Masaki Ochiai</td>
</tr>
<tr>
<td>S1_P13</td>
<td>Isolation of candidate genes for self-incompatibility in rose</td>
<td>Koji Kawamura</td>
</tr>
<tr>
<td>S1_P15</td>
<td>40 years of results of in situ disease resistance selection</td>
<td>Guillaume Beaugey</td>
</tr>
<tr>
<td>S1_P16</td>
<td>Rose genetic resources preservation: which criteria for determining core collections?</td>
<td>Alix Pernet</td>
</tr>
<tr>
<td>S1_P17</td>
<td><em>In vitro</em> propagation of three wild rose species grown in Sicily (south Italy)</td>
<td>Fascella Giancarlo</td>
</tr>
<tr>
<td>S1_P18</td>
<td>3D Phenotyping and QTL analysis of a complex character: rose bush architecture</td>
<td>Laurent Crespel</td>
</tr>
<tr>
<td>S1_P19</td>
<td>Taxonomic diversity of the genus <em>Rosa</em> in the collection of the botanical garden of Maria Curie-Sklodowka University of Lublin</td>
<td>Krystyna Rysiak</td>
</tr>
<tr>
<td>S1_P20</td>
<td>Evaluation, innovation and application of wild rose species in Xinjiang, Northwest China</td>
<td>Shu-Hua Yang</td>
</tr>
<tr>
<td>Session 2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-----------------</td>
<td>-----------------</td>
<td></td>
</tr>
<tr>
<td>S2_P01</td>
<td>Evolution of the NUDX1 gene in wild roses</td>
<td>Baptiste Nairaud</td>
</tr>
<tr>
<td>S2_P02</td>
<td>Prolonged Post-harvest Handling of the Oil Rose (Rosa damascena Mill.) flowers</td>
<td>Nima Ahmadi</td>
</tr>
<tr>
<td>S2_P03</td>
<td>Characteristics of floral scent of rose cultivars evaluated from cut flowers</td>
<td>Naomi Oyama-Okubo</td>
</tr>
<tr>
<td>S2_P04</td>
<td>Effects of sugars and methyl jasmonate treatment on vase life and scent emission in cut rose flowers</td>
<td>Hiromi Ikeura</td>
</tr>
</tbody>
</table>

| Session 3 |
|-----------------|-----------------|
| S3_P01 | Rhizogenesis and contents of polyphenolic acids in cuttings harvested in different phenological phases from the once-blooming shrub roses and treated with the rooting stimulants | Marta Monder |
| S3_P02 | Optimum pH value for extended vase life of cut Rosa Cv. Tereasa | Nermeen Shanan |
| S3_P03 | Indolebutyric acid on cut rose seedling production by bench grafting on different rootstocks | Kathia Fernandes Lopes Pivetta |
| S3_P04 | Performance of ‘Tineke’ rose cultivar grafted on nine rootstocks | Kathia Fernandes Lopes Pivetta |
| S3_P05 | Changes in Flower Quality and Plant Growth Substances of Rose cv. ‘Dolce Vita’ in Response to Different Nitrogen Sources in Soilless Culture | Mehdi Hosseini Farahi |
| S3_P06 | Changes in vase life and postharvest quality of cut rose (Rosa hybrida cv. Angelina) flowers by application of cumin uminum cyminum L. essential oil and 8-hydroxyquinoline sulfate | Yousef Payro |
| S3_P07 | Effect of polyamines on vegetative characteristics mineral absorption and endogenous hormones in hydroponic grown rose cv. ‘Dolce Vita’ | Mehdi Hosseini Farahi |
| S3_P08 | Influence of Polyamines and CaSO4 on mineral nutrient absorption of cut rose flower (Rosa hybrida) cv. ‘Dolce Vita’ in hydroponic culture | Mehdi Hosseini Farahi |
| S3_P09 | The Effect of different media cultures and salicylic acid on qualitative and quantitative characteristics of cut rose flower in soilless culture | Mehdi Hosseini Farahi |
| S3_P10 | Changes in carbohydrate metabolism in incurved malformed flowers of fragrant cut rose variety ‘Yves Piaget’ | Rei Kaneeda |
| S3_P11 | Evaluation of the ethylene effect on display quality and expression of some senescence related enzymes in potted Miniature rose | Nima Ahmadi |
| S3_P12 | Scientific collaboration to solve some thorny™ problems? | Richard Boyle |
| S3_P13 | Effects of some antimicrobial compounds on the vase Life of cut rose flower | Soner Kazaz |
| S3_P14 | Effects of Different Rootstocks on the Yield and Quality of Some Cut Rose Varieties propagated by Stenting | Soner Kazaz |
| S3_P15 | Asparagine and sugars are both required to trigger bud outgrowth and secondary axis elongation in Rosa hybrida | Marie-Anne Lemoigne |

<p>| Session 4 |
|-----------------|-----------------|
| S4_P01 | Bent-neck in roses - understanding the underlying causes | Bianca Lear |
| S4_P02 | Sequence and copy number variation of Ty1/copia retrotransposon RoRE1 in the rose genome | Shungo Otagaki |</p>
<table>
<thead>
<tr>
<th>Session 5</th>
<th>Session 6</th>
<th>Session 7</th>
</tr>
</thead>
<tbody>
<tr>
<td>S5_P01</td>
<td>S5_P02</td>
<td>S7_P01</td>
</tr>
<tr>
<td>Heat tolerance in garden roses</td>
<td>Irrigation of Oil-Bearing Rose (<em>Rosa damascena</em> Mill.) in Turkey</td>
<td>Rdr1 provides broad spectrum black spot resistance in various genetic backgrounds</td>
</tr>
<tr>
<td>S5_P02</td>
<td>S5_P03</td>
<td>S7_P02</td>
</tr>
<tr>
<td>Does ploidy level affects the response to drought stress in roses?</td>
<td>Quantitative factors influencing leaf spot diseases in roses</td>
<td>Towards an MLO mediated powdery mildew resistance in tetraploid roses</td>
</tr>
<tr>
<td>S5_P03</td>
<td>S5_P04</td>
<td>S7_P03</td>
</tr>
<tr>
<td>What are the contributions of cytokinins abscisic acid and sugars in bud outgrowth regulation by light intensity in rose?</td>
<td>Transcriptome analysis of the defense response of roses in the interaction with <em>diplocarpon rosae</em> and <em>podosphaera pannosa</em> using the MACE technique</td>
<td>Quantitative factors influencing leaf spot diseases in roses</td>
</tr>
<tr>
<td>S5_P04</td>
<td>S5_P05</td>
<td>S7_P04</td>
</tr>
<tr>
<td>S5_P05</td>
<td>S5_P06</td>
<td>S7_P05</td>
</tr>
<tr>
<td>S5_P06</td>
<td>S5_P07</td>
<td>S7_P06</td>
</tr>
<tr>
<td>S5_P07</td>
<td>S5_P08</td>
<td>S7_P07</td>
</tr>
<tr>
<td>S5_P08</td>
<td>S5_P09</td>
<td>S7_P08</td>
</tr>
<tr>
<td>S5_P09</td>
<td>S5_P10</td>
<td>S7_P09</td>
</tr>
<tr>
<td>S5_P10</td>
<td>S5_P11</td>
<td>S7_P10</td>
</tr>
<tr>
<td>S5_P11</td>
<td>S5_P12</td>
<td>S7_P11</td>
</tr>
<tr>
<td>S5_P12</td>
<td>S5_P13</td>
<td>S7_P12</td>
</tr>
<tr>
<td>S5_P13</td>
<td>S5_P14</td>
<td>S7_P13</td>
</tr>
<tr>
<td>S5_P14</td>
<td>S5_P15</td>
<td>S7_P14</td>
</tr>
<tr>
<td>S5_P15</td>
<td>S5_P16</td>
<td>S7_P15</td>
</tr>
</tbody>
</table>

**SESSION 4**

<table>
<thead>
<tr>
<th>S4_P03</th>
<th>S4_P04</th>
<th>S4_P05</th>
</tr>
</thead>
<tbody>
<tr>
<td>Development of a complete process of <em>in vitro</em> culture and Agrobacterium <em>tumefaciens</em>-mediated genetic transformation of Rose cultivars</td>
<td>Search for polymorphism in <em>Rosa chloroplast</em> genomes</td>
<td>Genome assembly in <em>Rosa wichurana</em> using cytogenetic and sequencing tools</td>
</tr>
</tbody>
</table>

**SESSION 6**

<table>
<thead>
<tr>
<th>S6_P01</th>
<th>S6_P02</th>
<th>S6_P03</th>
</tr>
</thead>
<tbody>
<tr>
<td>The american hand in rose hybridization</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**SESSION 7**

<table>
<thead>
<tr>
<th>S7_P01</th>
<th>S7_P02</th>
<th>S7_P03</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rdr1 provides broad spectrum black spot resistance in various genetic backgrounds</td>
<td>Towards an MLO mediated powdery mildew resistance in tetraploid roses</td>
<td>Quantitative factors influencing leaf spot diseases in roses</td>
</tr>
<tr>
<td>S7_P03</td>
<td>S7_P04</td>
<td>S7_P05</td>
</tr>
<tr>
<td>Transcriptome analysis of the defense response of roses in the interaction with <em>diplocarpon rosae</em> and <em>podosphaera pannosa</em> using the MACE technique</td>
<td></td>
<td>Rose rosette disease: It all started with a tiny mite</td>
</tr>
<tr>
<td>S7_P05</td>
<td>S7_P06</td>
<td>S7_P07</td>
</tr>
<tr>
<td></td>
<td>A simplified technique for counting eriophyid mites on roses that are endangered by rose rosette disease</td>
<td>Black spot and cercospora leaf spot resistance in cultivated roses</td>
</tr>
<tr>
<td>S7_P07</td>
<td>S7_P08</td>
<td>S7_P09</td>
</tr>
<tr>
<td></td>
<td>Controlling rose rosette disease with cultural and chemical methods</td>
<td>Eriophyid mite populations found on different rosa species</td>
</tr>
<tr>
<td>S7_P09</td>
<td>S7_P10</td>
<td>S7_P11</td>
</tr>
<tr>
<td></td>
<td>Evaluation of rose cultivars for resistance to rose rosette disease</td>
<td>National clean clant network for roses</td>
</tr>
<tr>
<td>S7_P11</td>
<td>S7_P12</td>
<td>S7_P13</td>
</tr>
<tr>
<td></td>
<td>Categorization of garden roses for field growth response to black spot disease</td>
<td>Virus Elimination of rose viruses using microshoot tip tissue culture</td>
</tr>
<tr>
<td>S7_P13</td>
<td>S7_P14</td>
<td>S7_P15</td>
</tr>
<tr>
<td></td>
<td>Combating rose rosette disease: exploring development of accurate rapid efficient easy-to-use and affordable virus diagnostic tools</td>
<td>Thrips management program for ornamental plants</td>
</tr>
</tbody>
</table>
Session 1
Rose genetics and breeding
High-density SNP maps for genetics and genomics in tetraploid rose

M.J.M. Smulders*, P.M. Bourke, P. Arens, R.E. Voorrips, C. Maliepaard

*Plant Breeding, Wageningen University & Research, Wageningen, The Netherlands.
*email: rene.smulders@wur.nl

Session: Rose Genetics and Breeding

Development and effective application of markers in breeding of polyploid crops used to lag behind. Most frequently marker development and the construction of a linkage map were carried out on the diploid level, such as diploid rose species. Translating this knowledge back to the tetraploid level was done only to a limited extent, as it was generally expected to be complicated.

Thanks to developments in sequencing technology, in marker detection (SNP arrays), and in software for linkage mapping in tetraploids, this situation has changed recently. Sequencing of e.g. transcriptomes of a few genotypes makes it possible to generate thousands of potential SNP markers. Software has been developed to enable dosage scoring of SNPs and to map and phase markers in tetraploids and construct an integrated linkage map across all homologous chromosomes. Software to perform QTL analysis for tetraploids has been improved.

The 68K WagRhSNP array was based on transcriptome-derived SNPs from several genotypes of cut and garden roses, making it very versatile for use in rose genomics. It is available for the research community through Affymetrix. The SNP loci are all published so custom arrays or detection of selected markers with other technologies is also possible. We used the array to genotype a tetraploid cut rose population and to construct an ultra-high density linkage map of 25,695 SNP markers across all homologs of the seven rose chromosomes. Using it, we studied meiotic behaviour of the chromosomes in both parents. Our results suggest that pairing affinities vary along chromosome arms. We mapped many markers per bin as the dense map is also intended to assist in assembly of the rose genome. The rose array has also been used for genome-wide association studies in garden roses. QTLs have been mapped for a range of traits in biparental tetraploid cut rose and garden rose populations.

A comparison of the rose maps with the Fragaria vesca genome sequence provided a detailed picture of the synteny between rose and strawberry genomes.

In conclusion, the methods and tools developed extend the possibilities for genetic research as well as enable efficient marker-assisted breeding in tetraploid rose. In the future, array-based studies will likely be complemented or even replaced by sequencing-based approaches, which offer the possibility of identifying specific haplotypes directly, lending greater power to linkage and association studies as well as improving the transferability of results from populations into wider germplasm.
Genetic dissection of shoot organogenesis in roses

Thi Hong Nhung Nguyen¹, Traud Winkelmann², Thomas Debener¹

¹Leibniz Universität Hannover, Institute of Plant Genetics, Hannover, Germany
²Leibniz Universität Hannover, Institute of Horticultural Production Systems, Hannover, Germany

debener@genetik.uni-hannover.de

Floral Shoot organogenesis is an essential step for genetic engineering and the study of developmental processes in roses. Several adventitious shoot regeneration protocols have been established, but the number of responding cultivars is very limited. Furthermore, large differences for regeneration capacity between genotypes were reported rendering many cultivars as recalcitrant for shoot regeneration. Therefore, knowledge about the genetic complexity of the capacity for adventitious shoot regeneration and genes influencing this trait would be helpful for optimising regeneration protocols. Here we present first results of a survey conducted in our association panel of 96 genotypes. Data on in vitro shoot regeneration from petioles was collected in two repetitions consisting of 60 explants each. The percentage of shoot forming explants (shoot regeneration rate) and the mean number of shoots formed per explant were recorded. A number of trait-marker-associations that give first evidence of loci and candidate genes associated to this trait is introduced.
Heritability of and Markers for Plant Architecture in Diploid Roses

Ellen Roundey*, Xuan Wu*, Shuyin Liang*, Muqing Yan*, Patricia Klein*, David Byrne*

*Department of Horticultural Sciences, Texas A&M University, College Station, TX
*ellenlouise@tamu.edu

Session: Rose Genetics and Breeding

Plant architecture, which is the result of both the plant organization and the interaction between the plant and the environment, affects the ornamental value and flower productivity of roses. Thus, it is helpful to understand the genetic basis of plant architecture so that breeding efforts can be directed towards improved architecture. To this end, six rose architectural traits (plant height, number and length of primary shoots, number of nodes on primary shoot, number of secondary/tertiary shoots per primary shoot) were evaluated in May and December of 2015 in College Station, TX for 13 interrelated diploid rose populations segregating for plant architecture types. Three of the traits (number of primary shoots, length of primary shoots, and number of nodes on primary shoot) exhibited low to moderate narrow sense heritability but moderately high to high broad sense heritability, indicating an important non-additive genetic component. The number of nodes on the primary shoots and the number of secondary and tertiary shoots per primary shoot displayed a large genotype by environment interaction. A comparison of desirable and undesirable plant growth types indicated that desirable growth types have more than 30 primary shoots with multiple secondary/tertiary shoots. The 13 rose populations were genotyped for single nucleotide polymorphisms (SNPs) using digital genotyping and a consensus map was developed using JoinMap 4.1. The next step will be to perform a quantitative trait loci (QTL) analysis using FlexQTL to identify markers for high numbers of primary shoots and plant height.
Control and selection of blooming seasonality in rose.

Vanessa Soufflet-Freslon¹, Marie Randoux¹, Jérémy Clotault¹, Emilie Araoux¹, Alix Pernet¹, Tatiana Thouroude¹, Gilles Michel¹, Julien Jeauffre¹, Sandrine Pierre¹, Hikaru Iwata¹, Koji Kawamura², Jean Michel Davière³, Cristiana Oghina-Pavie⁴, Laurence Hibrand-Saint Oyant¹, Fabrice Foucher¹

¹ Genetic and Diversity of Ornamentals team, Institut de Recherche en Horticulture et Semences (INRA, Agrocampus Ouest, Université d’Angers), SFR 4207 QUASAV, BP 60057, 49071 Beaucouzé Cedex, France
² Department of Environmental Engineering, Osaka Institute of Technology, Omiya, Osaka 535-8585, Japan
³ Institut de Biologie Moléculaire des Plantes, CNRS, Unité Propre de Recherche 2357, Conventionné avec l’Université de Strasbourg, 12 rue du Général Zimmer, 67084 Strasbourg Cedex, France
⁴ UMR CERHIO (Centre de Recherche Historique de l’Ouest), University of Angers, Angers, France
fabrice.foucher@inra.fr

Session: Rose genetics and Breeding

Rose is one of the most successful plants in the ornamental sector for gardens, cutting flowers and flowerpots. The tremendous success can be partially explained by selection of roses that can flower continuously. Rose, genus *Rosa*, is a good model to study seasonality of blooming, a developmental process which is poorly understood. We have previously demonstrated that continuous flowering in rose was due to a mutation of a gene encoded a floral repressor, *RoKSN*, a *TFL1* (*TERMINAL FLOWER 1*) homologue. In continuous-flowering roses, the insertion of *copia* retrotransposon in *RoKSN* gene completely blocked the transcript accumulation. Our objectives were to understand the mode of action of this floral repressor and its selection during the process of human breeding.

We have studied the function of *RoKSN* in Arabidopsis and in rose. We have demonstrated that *RoKSN* is a floral inhibitor. In Arabidopsis, we have complemented *tfl1* mutant with the *RoKSN* gene. In rose, its ectopic expression in a continuous-flowering rose completely block blooming. By yeast-two-hybrid FLIM-FRET method, we have shown *RoKSN* was able to interact with a transcription factor, *RoFD*, to inhibit blooming. *RoKSN* is competing with *RoFT*, a floral activator, for the inhibition of *RoFD*. *RoFT* belongs to the same gene family than *RoKSN*. By genetic approach, we have shown that *RoFT* co-localized with a strong QTL for the precocity, suggesting a role of *RoFT* in floral induction in rose.

In collaboration with historians, we studied the process of rose selection during the 18th and 19th centuries, an important period for rose breeding in France. During this period, more and more recurrent roses were selected. By genotyping and sequencing *RoKSN* on a large collection of roses from this period, we showed a progressive selection of the *copia* allele (bringing continuous flowering). Furthermore, we detected a new allele that can be responsible for intermediate phenotype (occasionally-reblooming). This new allele at the *RoKSN* locus encodes a functional RoKSN but the transcript accumulation is weaker. These results open new way to finely control blooming in rose and more generally in perennial plants.
Rosa arvensis as a possible genetic model

Pascal Heitzler*

Institut de Biologie Moléculaire des Plantes (IBMP), 67084 Strasbourg

*pascal.heitzler@ibmp-cnrs.unistra.fr

Session: Rose genetics and Breeding

Despite long-range breeding tradition in Europe, the rose remains poorly investigated at the level of formal genetics. In particular, a genetic model is missing that uses the advantages of reliable advanced wild type pedigree and natural variants from European species. Diploid species are more suitable for developing and understanding genetics in roses. When performed with accuracy, such studies can be extrapolated to tetraploid garden roses. R. arvensis, a common hardy rose from the synstylae group, is the only one diploid species to be broadly distributed in Europe. Here I will summarize 20 years of investigations and preliminary results to explore R. arvensis as a genetic model.

R. arvensis was first used as a model to explore physiological aspects of achene germination and hip development at the University College of North Wales, Bangor, UK. These studies have been published in the journal ‘Nature’ in 1959 (Prosser & Jackson) and 1965 (Jackson & Blundell). In the wild, R. arvensis has distinctive traits, with no or little variability at first glance. However, many natural variants, mutants and hybrids, that deviate from standard descriptions, were described by past French and Belgian taxonomists. Unfortunately, today, many competences and plants disappear with the past naturalists. I nevertheless decide to found an experimental and conservatory garden to restore and maintain R. arvensis biodiversity and to investigate the species genetically. I sampled from several regions of France, natural occurring mutants or variants affecting growth habit, leaf serration or the hip shape. Some variants fit with earlier descriptions, among others, ‘biserrata’, ‘grandidentata’, ‘elipsoidea’, ‘gallicoides’, ‘inermis’ or ‘majus’, a lost giant form, whereas some others, including several ‘pumila’ dwarf forms, or mutants with distinct pattern of glandulous hairs, are unrecorded from both science and horticulture. I found also kleptons that clearly indicate that R. arvensis is involved in gene reticulation together with either R. canina or R. gallica. Altogether, this work reconstitutes most of the lost intra-specific biodiversity that was recorded mainly between 1800 and 1940.

R. arvensis was never explored genetically. I choose a standard plant ‘Osenbuhr’, originated from a wild-collected sample, as reference genotype for several strategies of breeding programmes. First, I made controlled consanguineous crosses between ‘Osenbuhr’ and two other standard wild-type clones of R. arvensis, in order to establish inbred semi-compatible lines. Second, I cross ‘Osenbuhr’ with the wild-collected variants, in order to explore the nature of the inheritance of the new traits. Third, I reconstitute a historic core-collection of diploid R. x hybrida cultivars, representing the pedigree network that recapitulates the main base of many European horticultural lines. I cross ‘Osenbuhr’ with most of these historic lines, to explore disregarded or subtle horticultural traits. Altogether, from this long-range experience, I will discuss whether R. arvensis would be suitable as a genetic model to investigate specialized metabolisms in roses.
SNP Markers Linked to Gender in Dioecous *Rosa setigera* Michx.

Session: Rose Genetics and Breeding

*David C. Zlesak*\(^a\), Kathy Zuze\(^b\), Megan Melcher\(^c\), Stan C. Hokanson\(^d\), Jacqueline Van Schaick\(^a\), Anthony Varghese\(^b\), Chondra Carlson\(^e\), and Farhad Ghavami\(^e\)

\(^a\)University of Wisconsin-River Falls, 410 S. 3\(^{rd}\) Street, River Falls, WI 54022 USA

\(^b\)39920 Trulson Road, North Branch, MN 55056 USA

\(^c\)Greenwood High School, 306 West Central Ave., Greenwood, WI 54437 USA

\(^d\)University of Minnesota, Department of Horticultural Science, 1970 Folwell Ave., St. Paul, MN 55108 USA

\(^e\)Eurofins Biodiagnostics, 507 Highland Dr., River Falls, WI 54022 USA

\(^*\)david.zlesak@uwrf.edu

*Rosa setigera* is the only dioecious rose species and displays cryptic dioecy; flowers have both gender organs, but only one gender is functional per individual genotype. There is increased interest by rose breeders to use *R. setigera* in breeding programs due to its resistance to rose rosette disease, a lethal viral disease spread by eriophyid mites. Expanded understanding the reproductive biology of this species can help breeders overcome crossing barriers and more efficiently generate interspecific hybrids and introgress disease resistance and other desirable traits from *R. setigera* into cultivated roses. We previously reported that gender in *R. setigera* is controlled by a single gene with males being heterozygous and females homozygous recessive. In 2008, a male genotype (19670317-2) unexpectedly produced a very limited crop of undersized fruit containing one to a few seeds each that resulted in 20 seedlings. Seedlings segregated 16 males:4 females, consistent with a 3:1 male:female ratio expected from crossing two males (males possess at least one dominant allele). Previous ISSR and RAPD marker analyses suggest 19 of the 20 seedlings were from self-fertilization and the remaining seedling was sired by the neighboring male *R. setigera* (19670317-1). The parents (19670317-1 and 19670317-2), 20 seedlings, and two additional females were analyzed using the WagRhSNP Axiom\(^\text{®}\) rose SNP array in order to find markers that segregate with gender. Thirteen markers were identified that fit the single gene genetic model and were identified by females being homozygous for one of the two SNP alleles and the males being either homozygous for the other allele or heterozygous. Candidate SNP markers with their flanking sequences were BLAST searched and none were in the database. Ten of the SNP markers revealed the same six male seedlings as homozygous for the male associated allele and suggest these plants may be supermales; homozygous dominant for the male gender. Test crosses of putative supermales onto female *R. setigera* will be pursued to confirm if they are homozygous dominant for the male allele. Future work will focus on mapping this gender gene and understanding its function.
**Rosa palustris** and **Rosa setigera**: Breeding Challenges


**Department of Horticultural Sciences, Texas A&M University, College Station, TX**
**Weeks Roses, Pomona, CA**
**Star Roses and Plants, Westgrove, PA**
**University of Wisconsin River Falls, River Falls, WI**
**ellenlouise@tamu.edu**

Session: Rose Genetics and Breeding

*Rosa palustris* Marshall (section *Carolinae*) and *Rosa setigera* Michaux (section *Systylae*, formerly *Synstylae*) are diploid rose species native to North America known as the swamp rose and the prairie rose, respectively. Neither has been used extensively in breeding: approximately forty first-generation *R. setigera* hybrids and fewer than ten first-generation *R. palustris* hybrids were at some point available in commerce. Thus, little is known regarding their behavior and usefulness as breeding parents. These two species, however, are now of great interest for breeding due to their apparent resistance to rose rosette disease (RRD), a lethal viral disease of roses in North America. Therefore, in 2015 and 2016 the species were crossed with breeding lines developed at Texas A&M University as well as with standard cultivars. Pollen from both species was also assessed through the hanging drop pollen assay. *R. palustris* was found to have low hip set and seed production both as a male and as a female, though it generally performed better as the former. Through the hanging drop pollen assay, several *R. palustris* accessions were found to have nonfunctional pollen and were not used in breeding. In contrast, *R. setigera* had high hip set and seed production. *R. setigera*, however, is cryptically dioecious, and determining the gender of some accessions proved challenging: gender is determined by the hanging drop pollen assay, but (presumably) heat-damaged pollen can fail to germinate and cause the plant to be identified as a female. Both *R. palustris* and *R. setigera*, therefore, have various challenges, but they are not insurmountable. *R. palustris*’s low fertility can be compensated for by increasing the number of pollinations, and through careful work *R. setigera*’s gender can be correctly determined. Both species will continue to be used for breeding for resistance to RRD.
Breeding for Beautiful, strong, and chemical-free roses

Ping Lim*

plim@altmanplants.com

Session: Rose genetic and breeding

Abstract

With the increasing concerns over global climate change and the impact of synthetic chemicals in our environment, natural beauty on this planet may seem like a fading dream. But modern rose breeders are making strong progress in developing roses that can withstand these stresses and beautify the planet without harm.

In this 30-minute presentation, Ping Lim will be discussing few obstacles from his past 25 years expeditions in rose breeding research through his limited budget and resource, this effort has resulted of 3 AARS awards and 30 (Easy Elegance Rose Collection) commercially released in USA and Europe including Russia and Arctic circle nations.

To explore the challenges facts of his breeding program that withstands the environmental stresses and some of the hottest new varieties that are beautiful, strong, hardy, chemical-free and easy to grow.

*Ping Lim

Director of Ornamental Plant Research for Altman Plants, USA

Tel: 670. 272. 5570

Email: plim@altmanplants.com

Breeding Rose since 1992, hybridization efforts focus on ‘Eco friendly’ with less energy used for stress resistance to combine fragrance, grand petals, lasting color, compact form and quick blooming cycle.

- Twenty Easy Elegance Roses were patented.
- Three times AARS Award: ‘Love and Peace’™, ‘DayDream’™, and ‘Rainbow Sorbet’™
- Four 911 Roses: Forty Heroes, The Finest, Patriot’s Dream and Survivors
- Two emblem Roses: “Macy’s Pride” and “Centennial“ (St. Paul, Minnesota)
- Two Biltmore International Rose Trial Award: “FlyingKiss” and “Double 10”
- Nine Portland Best Roses Awards since 2005
- Rose Hill International Rose Trial Award: Goldmine (2016)
- ARTS All-Star winner: Double 10 (2017)

Website: www.rosesbyping.com
Youtube: http://www.youtube.com/user/u2ac
FaceBook: https://www.facebook.com/RosesByPing
Fieldbook app: Use in data collection in rose breeding

Jeekin Lau*, Ellen Roundey*, Natalie Anderson* and David Byrne*

*Department of Horticultural Sciences, Texas A&M University, College Station, TX, USA
*jzl0026@tamu.edu

Session: Rose genetics and Breeding

Phenotypic evaluation of genotypes has traditionally been done by plant breeders using a pen and paper. Most breeding programs record data on paper then later enter it into spreadsheets. However, this traditional method permits more mistakes in data entry and delays the accessibility of the data to the breeder for analysis. Previous attempts at data collection directly into spreadsheets has proved cumbersome and ineffective at replacing the antiquated methods of pen and paper. Fieldbook, an open source Android software developed for the collection of phenotypic data of wheat germplasm by Trevor Rife and Jesse Poland at Kansas State University, has been successfully adopted for phenotypic data collection in the Texas A&M Rose Breeding and Genetics Program. The software loaded on an Android powered tablet or a phone is used to collect monthly data of garden roses looking at traits of flower intensity, disease severity [black spot (Diplocarpon rosae), cercospora (Cercospora rosicola), and powdery mildew (Podosphaera pannosa)], defoliation, flower rating, flower cleaning, overall landscape ranking, along with any additional breeder notes associated with disease and/or growth patterns. Furthermore, pictures taken are automatically associated with the plant being evaluated. The use of Fieldbook has saved time and has avoided transcription errors by exporting the data directly to spreadsheets bringing phenotypic data collection fully into the computer age. This talk will showcase the types of phenotypic data that can be collected, show examples of the spreadsheet output, and discuss the advantages and hurdles when adopting this system of data collection.
A Study of Morphological Variation and Palynomorphology of Rosa laxa Retz. (Rosaceae) in Xinjiang, China

Le Luo¹, Xuelian Guo¹, Chao Yu, Huitang Pan, Qixiang Zhang*

Beijing Key Laboratory of Ornamental Plants Germplasm Innovation & Molecular Breeding, National Engineering Research Center for Floriculture, Beijing Laboratory of Urban and Rural Ecological Environment, Key Laboratory of Genetics and Breeding in Forest Trees and Ornamental Plants of Ministry of Education, School of Landscape Architecture, Beijing Forestry University, Beijing, 100083, China.

Corresponding author: zqxbjfu@126.com

Session: Rose genetics and breeding

Rosa laxa Retz., widely distributed in the Xinjiang Uygur Autonomous Region of China, has strong adaptability and rich variations. This study investigated the morphology, habitats and palynomorphology of R. laxa Retz. varieties in Xinjiang. And the results confirmed that, besides R. laxa var. laxa, there were three other varieties of R. laxa Retz. growing in southern Xinjiang, including R. laxa var. mollis, R. laxa var. kaschgarica and R. laxa var. tomerepis. The four varieties demonstrated morphological variations mainly in terms of prickle, glandular trichome and flower color. The pollen grains of R. laxa Retz. varieties, all medium in size (21.77µm-48.39µm), came in three shapes which are perprolate, prolate and subsphaeroidal. Their pollen exine sculptures were characterized by either striate-perforation pattern or striate pattern, but perforation varied obviously in diameter and density as striae did in depth and density. The palynomorphologic study results showed that three types of evolution, i.e. primitive, transitive and evolutionary, were present in R. laxa Retz. varieties, and pollen dimorphism was observed in the same variety. The perprolate pollen with dense striate pattern was the most evolutionary. Based on morphological and palynomorphologic studies, R. laxa var. tomerepis was considered to be most evolutionary among the studied varieties.

Key words: Rosa laxa Retz., variation, evolution, morphology, palynomorphology
Field Evaluation of Species and Modern Garden Roses for Black Spot and Landscape Performance in Texas


Texas A&M AgriLife Research and Extension Center, Texas A&M System, Overton, TX, USA
Department of Horticultural Sciences, Texas A&M University, College Station, TX USA

Session: Rose Genetics and Breeding

During early summer and fall of 2015 and late winter of 2016, plants of almost 300 garden rose entries were field planted in Overton and College Station, Texas USA for evaluation of disease development and landscape characteristics. The entries included species and modern roses from several hybrid groups including hybrid tea, hybrid rugosa, and traditional and modern shrub type roses. Plants were planted in a randomized complete block design and evaluated monthly during the 2016 growing season for disease incidence of black spot (Diplocarpon rosae) and landscape performance. During the growing season at Overton, overall black spot incidence varied from 4.2 in April to 3.0 in June and July to 4.9 in October using a rating scale of 0 to 9 with 0 representing a total lack of disease and 9 denoting all foliage infected with heavy defoliation and reduced plant vigor. In College Station, black spot incidence varied from 4.0 in May to 2.6 in July to 3.4 in October. Considering season long averages of black spot ratings, many species roses such as Rosa roxburghii exhibited ratings of less than 1 and hybrids such as Sir Thomas Lipton and Miracle on the Hudson exhibited ratings of less than 2 at both locations. Ratings of over 5 were given to mainly hybrids such as Cherry Parfait and Julia Child. Not surprisingly, there were positive correlations between black spot and defoliation (rated on a scale of 0 to 9; 0% to >90%) and black spot and landscape performance (rated on a scale of 1 to 5 with 1 the best and 5 the worst). There was a negative correlation between black spot incidence and cercospora leaf spot (Cercospora rosicola) rated using the same scale as black spot at both locations.
A decorative value estimation of hybrid tea roses for use in greening of the Southern Russian cities.

Yu.V. Plugatar *, Z.K. Klymenko b, S.A. Plugatar c, V.K. Zykova d

* Dr. of Agricultural Sciences, Director Nikita Botanical Gardens – National Scientific Centre, Head of the Department of Dendrology and Floriculture and Landscape Architecture, Russia
b Dr. of Biological Sciences, professor, Principal research fellow, Russian Federation
c Scientific Researcher at the Laboratory of Floriculture, Russia
d Cand. of Biological Sciences, Scientific Researcher at the Laboratory of Floriculture, Russia
* E-mail: plugatar.y@mail.ru

The Nikita botanical gardens – National scientific center, Yalta, Russia, 298648

Session: Rose genetics and Breeding

The introduction of garden roses in the South of Russia was started in nineteenth century in the Nikita Botanical Gardens, which is situated at the Southern Coast of the Crimea. The very first director Christian Steven started an introduction research of roses in 1812, and a second director Nickolay Gartvis continued it in 1824 and he also started a breeding work. As the result of it the richest Eastern European collection of garden roses has been created for the period. The first sorts of hybrid tea roses were delivered to the Nikita Botanical Gardens in 1900. Later on the sorts of hybrid tea roses in the Nikita Botanical Gardens collection took the leading positions, made up to 54% of its total volume.

The creation of hybrid tea roses home assortment has been started since 1939, and it has come to over 100 sorts up to now. It has been found out that the sorts of hybrid tea roses have a very long –term and remontant flowering in the climatic conditions of the Southern Coast of the Crimea: some sorts of hybrid tea roses from the Nikita Botanical Gardens collection blossom totally over 200 days a year and have high decorative qualities.

We have worked out the 100-grade scale of a decorative value estimation of hybrid tea roses to select the most decorative assortment for use in greening of the Russian South. The scale includes the flower characteristics such as a coloration stability, proportion, a half – open form, a full – open form, terry, aroma, stability to a higher humidity, a petal stability to a sun scorching, a petal stability to a tripes' damage (Thysanoptera Haliday), and it also takes into account a bush habitus, its foliage, a flower-carrying shoot durability, if there is “mass flowering” phase during the fourth (autumn) flowering period, a flowering longevity during the season, a sort originality. Each of characteristics has its own transfer coefficient, which shows its significance for a total sort décor.

According to the scale, the decorative value estimation of hybrid tea roses sorts from the Nikita Botanical Gardens collection has been done. As the result of it 45 highly prospective sorts with the grade of from 85 to 100 points, 33 prospective sorts with the grade of from 75 to 84 points, 16 less prospective sorts with the grade of from 65 to 74 points and 6 dead-end sorts with the grade of less than 65 points have been discovered.

To sum up the decorative value estimation of hybrid tea roses' sorts from the Nikita Botanical Gardens collection 78 sorts have been recommended for greening of the South of
The main directions of a rose selection in the South of Russia.

Yu.V. Plugatar *a, Z.K. Klymenko b, S.A. Plugatar c, V.K. Zykova d

*a Dr. of Agricultural Sciences, Director Nikita Botanical Gardens – National Scientific Centre, Head of the Department of Dendrology and Floriculture and Landscape Architecture, Russia

b Dr. of Biological Sciences, professor, Principal research fellow, Russia

c Scientific Researcher at the Laboratory of Floriculture, Russia

d Cand. of Biological Sciences, Scientific Researcher at the Laboratory of Floriculture, Russia

* E-mail: plugatar.y@mail.ru

The Nikita botanical gardens – National scientific center, Yalta, Russia, 298648

Session: Rose genetics and Breeding

The garden roses’ introduction work was first started in Russia by the Nikita botanical gardens in 1812, and the breeding one was started in 1828. Different methods of hybridization are used during the creating of a new sort (e.g. interspecific, next related, distant), a clonal breeding and an experimental mutagenesis. The introduction testing of more than 6,000 sorts has been done and over 300 sorts have been created un the Nikita botanical gardens up to the present moment. The introduction testing let define the influence of the Russian South specific climatic conditions on ornamentality and physiological peculiarities of garden roses. In connection with a higher soil and air temperature and lower air humidity during a summer – autumn season there is a growth and blossoming suspension as to a rose sorts’ majority, and its common duration is shortened. The ornamental quality of the plants is also lowered thanks to a color fading, upshriveling and a petals’ deformation. The main fungous deceases of roses in the South of Russia are a powder dew (Sphaerotheca pannosa Lev. var rosae Woronich) and rust (Phragmidium disciflorum James, Ph. Tuberculatum Mull.), that make lower ornamentality of sorts during their cultivation. A long vegetative period and absence of strong winter conditions allow to widen the number of garden rose groups and work to increase a created sorts’ blossoming duration. To sum it up, the main task of a breeding work with garden roses in the South of Russia is to create of the sorts with a long blossoming period, a higher ornamentality and resilient to a powder dew and rust.

According to the task the sorts that have valuable signs in the conditions of the South of Russia as well as the complex of those signs have been created..

During the work of creating the sorts that do not have a color fading and upshriveling in the sun, such sorts as e.g. ‘Klimentina’, ‘Crimean Torch’, ‘YCL Fire’, 'Major Gagarin' etc. have been created.

It has been studied that the most creating resultant method that is resilient to a powder dew and rust is a distant hybridization, as well as use in breeding a garden group of Kordes rose. Used the methods 14 sorts have been created..

A breeding work with the garden groups of the most heatloving little- and big flowers’ plaited roses has been done. They are the most promising ones for a region greening. 20 sorts of the those groups have been created.

During the breeding at the sign of a repeated long blossoming 20 sorts have been created. They blossom over 200 days during a year. They are ‘Blagovest’, 'Feodossia beauty', ‘Selena’, 'Beautiful Tavrida', etc.

To sum it up, 4 main specific tasks for a breeding work with garden roses in the South of Russia have been discovered, and 55 sorts met the tasks have been created. The study was funded by the research grant N 14-50-00079 of the Russian Science Foundation.
Palynological Features Comparison of Compatible and Incompatible *Rosa hybrida* L. cultivars in Korea

Gyung Ran Do\(^a\), Ki Young Park\(^a\), Jeom Hwa Han\(^a\), Hyun Hee Han\(^a\), Jae Hoon Jeong\(^a\), Su hyun Ryu\(^a\), Yong Hee Kwon\(^a\), and In Myung Choi\(^a\)

\(^a\)National Institute of Horticultural and Herbal Science, RDA, Wanju, 55365, Rep. of Korea

*micredo@korea.kr

Session: Rose genetics and Breeding

The sterility of male gametophyte is an interesting subject because it provides a potential use for hybrid seed production. Unfortunately, in spite of relatively low crossing efficiency in roses, pollen sterility in conventional breeding of roses has been overlooked by breeders that have been crossing with well-known fertile pollen. For improvement of crossing efficiency in roses, we first carried out morphological approach by comparing compatible and incompatible pollen grains with microscopy techniques including histochemical analysis (P.A.S. method). The results of pollen morphological investigations of compatible *Rosa hybrida* L. cultivars (‘Michel’ and ‘Aladin’) and incompatible *Rosa hybrida* L. cultivars (‘Duet’ and ‘Tineke’) have been presented in this article. All the pollen grains of the studied cultivars showed the similar shape and type of pollen aperture, which were small circular, isopolar, radially symmetrical, and tricolporate with rather long furrows tapering to pointed poles. The sculpture of pollen exine has been presented the striate pattern with the ridges varying from short to long and from straight to curved form. But the features of ridges and perforations were not markedly different among the cultivars. Pollen morphological structure descriptions of the examined cultivars reflected no discrimination related with fertility. Neither did the histochemical analysis for comparing pollen grains of the above mentioned cultivars before anther dehiscence. Therefore, the results of this study suggest supplementary further research about interaction between pollen and female gametophyte, stigma by using cytochemistry. We hope that those contribute to the breeding of roses by increasing the understanding of male gametophyte, pollen morphology.
Heritability of flower size and heat stress in diploid roses

Jeekin Lau\textsuperscript{a}, Shuyin Liang\textsuperscript{a}, Xuan Wu\textsuperscript{a}, Muqing Yan\textsuperscript{a}, Patricia Klein\textsuperscript{a}, Ellen Roundey\textsuperscript{a}, and David Byrne\textsuperscript{a}

\textsuperscript{a}Department of Horticultural Sciences, Texas A&M University, College Station, TX, USA
\textsuperscript{*}jzl0026@tamu.edu

Session: Rose genetics and Breeding

Heat stress on roses (\textit{Rosa x hybrida}) negatively affects rose performance and reduces the market value of the crop. The effect of heat on flower size was assessed with a heat shock treatment (44°C for 1 hour) and in the field during the cool (~20°C) and warm (~30°C) seasons of the year for 10 and 9 interrelated diploid rose populations respectively. The elevated temperature caused a decrease in flower size under both conditions for flower diameter (~16-18%), petal number (~23-17%), and flower weight (~17-32%). Flower size showed low to moderate (flower diameter, 0.24-0.38; petal number, 0.12-0.26; flower weight, 0.34-0.53) narrow and moderate (flower diameter, 0.62-0.70; petal number, 0.74-0.91; flower weight, 0.76-0.88) broad sense heritability inferring a major non additive genetic component for flower size. Differences in heat tolerance would indicate that roses respond differentially to the environment (heat stress). Thus in a genetic variance analysis, a high GxE variance would indicate genetic differences in heat stress. Among the three size parameters, flower diameter showed the largest GxE genetic variance. However, the GxE variance for flower diameter in the heat shock experiment explained less (6.3%) genetic variance as compared to the field experiment (37%) indicating that selection would be more effective under field conditions. We are now investigating the use of FlexQTL to analyze the phenotypic and genotypic data from these interrelated populations to identify important QTLs conditioning the changes in flower size and heat tolerance.
Field evaluation of rose cultivars to black spot in Southern Ontario

Sandhu P*, Ghosh A*, Pacelli F, Morimoto E, Batenburg J

* Vineland Research and Innovation Centre, Department of Applied Genomics
4890 Victoria Ave. N., Box 4000, Vineland Station, ON, L0R 2E0 Canada
* parminderjit.sandhu@vinelandresearch.com

Black spot caused by Diplocarpon rosae Wolf. is the most destructive disease to roses throughout the world. The disease appears as black fringed spots on rose foliage followed by the induction of leaf chlorosis and severe defoliation. There are thousands of rose cultivars on the market but only a small amount have broad resistance to geographically different races of black spot. It is very important to know the disease tolerance of any genotype before including it in a breeding program aimed at the development of new disease resistant cultivars. Rose breeding is one of the major ongoing research projects at Vineland Research and Innovation Centre (Vineland) in Southern Ontario, Canada. The Vineland rose breeding program is focused on introducing black spot resistant, cold hardy landscape roses, which possess characteristics that are desirable to consumers. Before including germplasm in the breeding program, it is first evaluated in the field for agronomic performance. No fertilizers or fungicides are used in this rigorous field screening. In June 2014, 220 rose cultivars, consisting primarily of grandiflora, floribunda, hybrid tea and a few climbers, were planted in the field at Vineland for evaluation. Each cultivar was planted as a replicate of three plants and were grafted on multiflora rootstock. Prior to planting the cultivars for evaluation, the test plot had held existing rose breeding lines that were planted in 2012. In 2013, the breeding lines were inoculated in the field with a mixture of black spot inoculum to establish disease pressure in the test plot. The disease inoculum used was collected from four different locations in Canada – residential roses in Brampton, Ontario, a rose nursery in St. Catharines, Ontario, the Montreal Botanical Garden, Quebec and a rose nursery in British Columbia. Since 2014, we have seen high black spot pressure across the entire test field and plants were overhead irrigated each year to keep the disease pressure high. In 2015 and 2016, all the cultivars were evaluated for disease tolerance twice a year. During these two years, the average temperature ranged between 17 °C and 24 °C, and the total precipitation varied between 211 mm and 321 mm. Cultivars with more than 30% of their foliage infected with black spot were rated as susceptible, those with 21-30% as less susceptible, 11-20% as tolerant, up to 10% as moderately resistant and those with no black spot were rated as resistant. The typical growing season for outdoor roses in Southern Ontario ranges from May through September/ October. The cultivars evaluated varied in their tolerance to black spot with the advance of the growing season. A few cultivars were very susceptible to black spot early in the season, while a large collection of cultivars showed susceptibility later in the season, depending on the precipitation level and temperature. From the two years of evaluation data, we found that among all the 220 cultivars included in this study, only 21 had less than 10% of their foliage infected with black spot throughout the growing season in both years. Parallel pathology research at Vineland is studying the presence of most prevalent black spot races in the Vineland field. Further work will be undertaken on testing cultivars that displayed less than 30% black spot infection in the field, in a detached leaf assay, in order to identify genes that convey race specific resistance to the predominant black spot races in the Vineland field.
RosBREED2 – Combining Disease Resistance with Horticultural Quality in New Rosaceous Cultivars, Including Rose!

Stan C. Hokanson\textsuperscript{a*}, David Byrne\textsuperscript{b}, Patricia Klein\textsuperscript{b}, Muqing Yan\textsuperscript{b}, David C. Zlesak\textsuperscript{c}, Sarah Kummeth\textsuperscript{c}, James M. Bradeen\textsuperscript{d}, Amy Iezzoni\textsuperscript{e}, Cameron Peace\textsuperscript{f}

\textsuperscript{a}Department of Horticultural Science, University of Minnesota, Saint Paul, MN, USA
\textsuperscript{b}Department of Horticultural Science, Texas A&M University, College Station, TX, USA
\textsuperscript{c}Department of Plant & Earth Science, University of Wisconsin-River Falls, River Falls, WI, USA
\textsuperscript{d}Department of Plant Pathology, University of Minnesota, Saint Paul, MN, USA
\textsuperscript{e}Department of Horticulture, Michigan State University, East Lansing, MI, USA
\textsuperscript{f}Department of Horticulture & Landscape Architecture, Washington State University, Pullman, WA, USA
\textsuperscript{*}hokan017@umn.edu

Session: Rose Genetics and Breeding

There has long existed a gap between the accumulating fundamental knowledge concerning genetics and genomes of plants and the practical application of such knowledge in plant breeding programs. This is certainly the case in regards to the Rosaceae family, which includes some of our most important fruit, nut, and ornamental crops. The list of problems faced by growers of rosaceous crops is outstripping the capacity for breeders using traditional breeding techniques to solve. Recognizing the dilemma, in 2009, twenty-eight university, USDA, and private-sector scientists received $7.2M in federal funds for a four-year USDA Specialty Crop Research Initiative grant to designed to enable marker-assisted breeding (MAB) in rosaceous crops. The research effort was highly successful in developing a pipeline of genetic tools and resources that allowed MAB and marker assisted selection (MAS) to become a reality for important rosaceous crops including apple, peach, strawberry, and cherry. In 2014, RosBREED2 was built on the shoulders of the previous project and was awarded nearly $10M for five years. The goal of the RosBREED2 project is to standardize phenotyping and genetic/genomic tools and approaches in order to develop disease resistant, horticulturally superior rosaceous cultivars. The project involves eight rosaceous crops; apple, peach, strawberry, cherry, pear, blackberry, peach/cherry rootstocks and notably, rose. The project is carried forth by 35 scientists from 14 U.S. institutions and several international cooperators. The primary goal for the rose effort within the project involves the development of tools and approaches to breed durable resistance to rose black spot disease, which is incited by the fungal pathogen Diplocarpon rosae Wolf. Two teams are involved in the rose research. At Texas A&M University, effort is directed towards identifying QTLs in diploid rose populations and associating molecular markers with those QTLs for use in MAB/MAS breeding. At the University of Minnesota, efforts are focused on identifying major gene resistance to the disease in 3x and 4x commercial germplasm and developing markers linked to the genes which can be used in MAB approaches.
Characterization of *Rosa* ‘Harison’s Yellow’ clones using SNP Markers

Session: Rose Genetics and Breeding or Social Sciences and Humanities

*Peter Harris*\(^a\), *David C. Zlesak*\(^{ab}\), *Chondra Carlson*\(^c\), and *Farhad Ghavami*\(^c\)

\(^a\)Rose Hybridizers Association, 541 Anderson Heights Road, Charleston, WV 25314
\(^b\)University of Wisconsin-River Falls, 410 S. 3\(^{rd}\) Street, River Falls, WI 54022 USA
\(^c\)Eurofins Biodiagnostics, 507 Highland Dr., River Falls, WI 54022 USA

*Rosa* ‘Harison’s Yellow’ is a historic old garden rose that originated in the United States c. 1824. It is believed to have been a chance seedling in the rose garden of George Folliott Harison in New York City and was introduced by William Prince Nursery and other local nurserymen by 1830. Its unique attributes include its bright yellow, loosely double blooms borne for approximately a month in spring, its strong ability to reproduce by rhizomes and root suckers, and its tolerance to a wide range of climatic conditions (temperature extremes and drought). Its phenotype suggests it is a hybrid involving *R. spinosissima* (similar prickles and growth habit) and *R. foetida* (bright yellow blooms that resist fading). This rose can be found persisting on old United States farmsteads and along routes taken by settlers as they traveled West and Southwest. It is especially common along the Oregon Trail and in parts of Texas (an alternative name is The Yellow Rose of Texas). Nine clones of ‘Harison’s Yellow’ were obtained for comparison and were supplied by: botanical gardens (Brooklyn Botanical Garden and the University of Minnesota Landscape Arboretum), commercial nurseries (Bailey Nurseries and Greenmantle Nursery), and multiple individuals, some of whom have had the rose in their family for generations. The sample about which the greatest information is known was planted in Cheyenne, Wyoming in 1937. Chromosome counts were conducted using root tip squashes on those six plants received as own-root plants (versus grafted), and all were triploid. Triploidy is consistent with the relatively low fruit and seed set and generally poor seed germination rates of ‘Harison’s Yellow’. Phenotypic characteristics of all the plants were very similar. The nine clones were analyzed using the WagRhSNP Axiom® rose SNP array in order to learn if they were the same genotype or if there were enough divergence between some samples to suggest they are of seedling origin. Out of the 24,512 SNPs scored, only 167 SNPs were polymorphic and the distribution of those polymorphisms was relatively dispersed among the nine samples. *Rosa foetida* ‘Austrian Copper’ was included as a control, and 4,466 polymorphic SNPs separated it from the ‘Harison’s Yellow’ roses. The SNP data are consistent enough to suggest that these nine ‘Harison’s Yellow’ samples are the same genotype, with minor detectable mutations that have accumulated over the nearly two centuries since 1824.
Rose Parental Characterization and Population Development for the Identification of Novel Rose Black Spot Resistance Genes

Session: Rose Genetics and Breeding

David C. Zlesak\textsuperscript{a}, James Bradeen\textsuperscript{b}, Sarah Kummeth\textsuperscript{a}, Nahla Bassil\textsuperscript{c}, Jason D. Zurn\textsuperscript{c}, and Stan C. Hokanson\textsuperscript{d},

\textsuperscript{a}University of Wisconsin-River Falls, 410 S. 3\textsuperscript{rd} Street, River Falls, WI 54022

\textsuperscript{b}University of Minnesota, Department of Plant Pathology, 1991 Upper Buford Circle, St. Paul, MN USA 55108

\textsuperscript{c}USDA-ARS National Clonal Germplasm Repository, 33447 Peoria Road, Corvallis, OR 97333

\textsuperscript{d}University of Minnesota, Department of Horticultural Science, 1970 Folwell Ave., St. Paul, MN USA 55108

* david.zlesak@uwrf.edu

Rose black spot disease, caused by the pathogen \textit{Diplocarpon rosae} Wolf, is one of the most widespread and serious diseases of outdoor-grown roses worldwide. Defoliation caused by the disease compromises ornamental value, and repeated defoliation events weakens plants and can lead to plant death. Both race-specific and horizontal resistances to rose black spot have been documented in \textit{Rosa} spp. and are valuable to pursue for the purpose of developing new resistant cultivars. Having molecular markers tightly linked to race-specific resistance genes is of great value to breeders for use in screening germplasm and working towards stacking multiple race-specific resistances. To date only three black spot resistance genes have been characterized, and tightly linked markers have only been reported for one gene, \textit{Rdr1}. More resistance genes need to be characterized and tightly linked markers identified. Eleven races of \textit{D. rosae} preserved in the international \textit{D. rosae} race collection at the University of Minnesota were successfully cultured after ten years in cryopreservation and used to characterize six rose cultivars for resistance that would be used as parents (Brite Eyes\textsuperscript{TM}, ‘George Vancouver’, High Voltage\textsuperscript{TM}, Lemon Fizz\textsuperscript{TM}, ‘Morden Blush’, and Yellow Submarine\textsuperscript{TM}). Four populations of at least 120 offspring were generated (High Voltage\textsuperscript{TM} x Lemon Fizz\textsuperscript{TM}, ‘Morden Blush’ x Brite Eyes\textsuperscript{TM}, ‘Morden Blush’ x ‘George Vancouver’, and ‘Morden Blush’ x Yellow Submarine\textsuperscript{TM}) based on parental resistance patterns. To date, two populations (High Voltage\textsuperscript{TM} x Lemon Fizz\textsuperscript{TM} and ‘Morden Blush’ x Brite Eyes\textsuperscript{TM}) have been challenged with eight and two races, respectively, using detached leaf assays. Individual seedlings of both populations were either susceptible or resistant to all races with which they were challenged and resistant:susceptible seedlings segregated 1:1. Segregation patterns are consistent with a single race-specific gene in simplex in each of the resistant parents (Brite Eyes\textsuperscript{TM} and Lemon Fizz\textsuperscript{TM}). Continued work to complete the phenotyping of all four populations is underway. The WagRhSNP Axiom\textsuperscript{®} rose SNP array is being utilized to genotype the seedlings in each population in order to map the gene(s) and identify markers associated with resistance.
Screening and identification of proteins interacting with RhMLO1 and RhMLO2 in rose

Xianqin Qiu, Hao Zhang, Huijun Yan, Shubin Li, Ningning Zhou, Kaixue Tang*

*corresponding author: kxtang163@163.com
Session: Rose genetics and breeding

Powdery mildew caused by *Podospora pannosa* was the most common disease in cut rose production globally. It is also one of the main diseases of garden roses and pot roses. China is one of the distribution centers of wild roses in the world, and it is also one of the main cut rose producing areas in the world. Mildew resistance locus o (*MLO*) genes are new type of disease resistance. In dicots such as arabidopsis, pea, and tomato, loss-of-function mutations in *MLO* genes confer high levels of broad-spectrum resistance in powdery mildew. We got *RhMLO1* and *RhMLO2* genes from rose in our previous research. Our purpose is to screen and identify the proteins interacting with RhMLO1 and RhMLO2 in rose in this study. The complex interacting with RhMLO1 and RhMLO2 was extracted by co-immunoprecipitation, and separated by SDS-PAGE. The differential bands were cut by enzyme trypsin. The peptide segments were separated by liquid chromatography, and then analyzed and identified by electrospray ionization mass spectrometry.

Protein profiling interacting with RhMLO1 and RhMLO2 was obtained. Five proteins, transcription factor b3, elongation factor 1-alpha, BHLH transcriptional factor AN1 homolog, TIR-NBS-LRR resistance protein muRdr1A and muRdr1C were verified by co-immunoprecipitation, mass spectrometry and Western blot. Our findings may provide useful information for our further study of mechanisms of powdery mildew susceptibility in rose and other plants.
Breeding of posterity crossing between cut rose cultivar ‘PEKcougel’ and tetraploid *Rosa. multiflora*.

Masaki Ochiai **a**, Wu Weijun **b**, Shingo Funahashi **a**, Hiroki Sugimoto **a** and Hirokazu Fukui **a**

* Corresponding author: mochiai@gifu-u.ac.jp

**a** Laboratory of Horticulture, Faculty of Applied Biological Sciences, 1-1 Yanagido, Gifu 501-1193, Japan

**b** United Graduate School of Agricultural Science, Gifu University, 1-1 Yanagido, Gifu 501-1193, Japan

Session: Rose genetics and Breeding

The cut rose cultivar ‘PEKcougel’ and *R. multiflora* have resistant against crown gall disease by *R. radiobacter* and root rot disease by *P. helicoides* respectively, and these resistant characters were inherited to progeny. So we attempted to develop the combined resistance stock to crown gall and root rot disease by crossing with *R. ‘PEKcougel’* and tetraploid *R. multiflora*. 121 of torpedo-shaped embryo in ‘PEKcougel’ x ‘Matsushima No.3’ were cultured. 97 plantlets were died as the case of seed germination because of browning of hypocotyl, and 18 plantlets were died after true leaves expansion by browning of shoot apex. Six plantlets evaded browning and were acclimated finally. The six plants acclimated (No. 1-6) were tetraploid. From the result of identification of hybrids of ‘PEKcougel’ x ‘Matsushima No.3’ using SCAK16583 marker which was species-specific DNA marker of *R. multiflora*, it was decided that No. 1, No. 5 and No. 6 were progenies of ‘PEKcougel’ x ‘Matsushima No.3’, and No. 2, No. 3 and No. 4 were self-fertilization posterities of ‘PEKcougel’ resulting from failure of artificial crossing. These three F1 plants (No. 1, No. 5 and No. 6) have resistance to crown gall and root rot disease. And these were self-compatible, and backcrossing with ‘PEKcougel’ or ‘Matsushima No.3’ was also easy for them.

Around 450 words or 3000 characters
Isolation of Candidate Genes for Self-incompatibility in Rose

Koji Kawamura*a, Shungo Otagaki*b, Hibrand-Saint Oyant*c, Fabrice Foucher*c, Shogo Matsumoto*b

*a Department of Environmental Engineering, Osaka Institute of Technology, Japan
*b Graduate School of Bioagricultural Sciences, Nagoya University, Japan
*c UMR 1345 IRHS, Genetic and Diversity of Ornamentals, SFR4207 Quasav, France

* koji.kawamura@oit.ac.jp

Session: Rose genetics and Breeding

Diploid roses (Rosa sp.) are self-incompatible species belonging to the Rosaceae and cannot produce viable seeds by self-pollen. The molecular basis of self-incompatibility in rose has not been elucidated, whereas it is very important for development of effective breeding program and understanding of rose genetics. We aim to isolate candidate genes controlling the self-incompatibility in rose.

A RNAseq database in rose and the genome database of Fragaria vesca was used to identify candidate genes. In Fragaria species, two self-incompatibility loci S and T were mapped by a previous work on FvLG6 and FvLG1, respectively, although the responsible genes have not been identified. In Prunus and Malus species, however, the genes controlling self-incompatibility have been identified as a S-RNase gene expressed in pistil and F-box genes expressed in pollen. The S-RNase gene is tightly linked with multiple F-box genes in the locus controlling self-incompatibility. Therefore, we first performed BLAST search on Fragaria genome linkage group FvLG6 and FvLG1 in order to identify S-RNase genes homologous to the Prunus and Malus S-RNase. We then performed BLAST search on rose RNAseq database using Fragaria S-RNase as a query. The candidate S-RNase gene was then isolated from a diploid species Rosa multiflora and mapped by using a diploid F1 hybrid population (FW). The surrounding genomic region of the S-RNase gene was also sequenced by a genome walking kit to isolate F-box genes linked to the S-RNase.

Two candidate S-RNase genes were isolated in rose. One S-RNase gene was mapped on rose LG3, which is homologous to FvLG6. In the rose LG3, horticulturally important traits, such as continuous-flowering, double-flower, prickless have been mapped by previous works. Distorted segregations of these traits have suggested the presence of a self-incompatibility locus in the LG3. The S-RNase gene we isolated is a good candidate gene for the self-incompatibility locus in LG3. A 16kbp genome walking surrounding the S-RNase gene identified two F-box genes. We have also mapped another S-RNase gene in rose LG2, which is homologous to FvLG1. The S-RNase gene was also tightly linked with a F-box gene. Therefore, we have successfully isolated two candidate genomic regions controlling self-incompatibility in rose. Validation of the candidate genes is going to be conducted by tissue-specific gene expression analyses, and results will be included in presentation.
Cryopreservation of ex vitro-grown Rosa buds using droplet-vitrification: Importance of a genotype effect

Marie-Magdelaine J.\textsuperscript{a}, Belin J.\textsuperscript{a}, Gachenot M.\textsuperscript{a}, Chameau J.\textsuperscript{a}, Pernet A.\textsuperscript{a}, Grapin A.\textsuperscript{b}\textsuperscript{*}

\textsuperscript{a} Institut de Recherche en Horticulture et Semences - UMR 1345, INRA, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France

\textsuperscript{b} Institut de Recherche en Horticulture et Semences - UMR 1345, AgrocampusOuest, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France

* Agnes.Grapin@agrocampus-ouest.fr

Session: Rose genetics and Breeding

The genus Rosa comprises about 200 wild species and a huge diversity of cultivars created by repetitive interspecific hybridizations. Commonly, Rosa genetic resources are conserved in field collections (mostly rose gardens), which is a rather risky solution due to disease and climatic hazards and possible conflicts in land use. Cryopreservation could be a complementary strategy of choice for long-term germplasm conservation, especially if the protocol does not require prior introduction and maintenance of plant material \textit{in vitro}. In the past years, we successfully set up a droplet-vitrification protocol using buds from \textit{ex vitro}-grown \textit{Rosa chinensis} ‘Old Blush’ (Le Bras \textit{et al.}, 2014). The next step was to apply this protocol established on ‘Old Blush’ to a large sample of \textit{Rosa} genotypes and to study the variability of response.

This was done in the frame of the FloRHiGe project, a multidisciplinary project, combining history and genetics, which aimed to study the evolution of the diversity of rosebushes selected in France during the 18\textsuperscript{th} and 19\textsuperscript{th} centuries. In this project, a sample of 1228 varieties, including 940 European varieties from this period, was collected and genotyped with 32 microsatellite primer pairs (Liorzou \textit{et al.}, 2016), leading to a genetic structuration in 16 groups. A sub-sample of 26 accessions was determined representing 11 genetic groups and different ploidy levels (2x, 3x, 4x, 5x, 6x). It included 17 European varieties from the 18\textsuperscript{th} and 19\textsuperscript{th} centuries, two varieties from the 20\textsuperscript{th} century and seven botanical accessions of different \textit{Rosa} species. Plants of each accession were cultivated in a greenhouse. Axillary buds were directly introduced \textit{in vitro} without cryopreservation (as controls) or submitted to the droplet-vitrification protocol (20 min LS, 15 min PVS2 before transfer to LN\textsubscript{2} and rewarming) and then \textit{in vitro} cultivated. For each accession, the results were based on three repetitions with at least a total of 36 explants per treatment (control / cryopreservation). Results were expressed as the percentage of surviving explants and the percentage of regrowth. The results were highly influenced by the genotype. The percentage of regrowth after cryopreservation ranged from 3\% to 89\%. The influence of some characteristics (genetic group, ploidy level...) on the results were evaluated.
40 years of results of *in situ* disease resistance selection

Guillaume BEAUGEY*, Matthias MEILLAND*, Sonja MEILLAND-GUIBERT*, Alain MEILLAND*

*MEILLAND INTERNATIONAL, Domaine de Saint André, 83340 Le Cannet des Maures, France

*g.beaugey@meilland.com

Session : Rose Genetics and Breeding

Disease resistance is one of the major criteria in Rose selection nowadays with pressure of states and associations to use less and less phytosanitary products. Since the late 70’s, MEILLAND INTERNATIONAL R&D team decided to test all varieties *in situ*, in “0 spray” fields – No Fungicide, No Insecticide – in different pedoclimatic conditions. MEILLAND INTERNATIONAL started to test cultivars in “0 spray zone” in Le Cannet des Maures, 43° North. The first result of these trials was the variety MEIdomonac, Bonica® 82, which was granted ADR and AARS in 1987 and a WFRS All of Fame in 2003.

Due to the diversity of diseases and disease strains in the world, one “0 spray zone” is not enough to breed for stable, horizontal and vertical disease resistance. So MEILLAND INTERNATIONAL tests all its varieties in 5 main “0 spray test fields”: 2 in France, 1 in Germany and 2 in USA, in Pennsylvania and California, plus other fields in all continents.

Results of this breeding & selection strategy are validated by state funded projects like BELAROSA, which shows breakthrough disease resistance comparing to other historical and commercial varieties.
Rose genetic resources preservation: which criteria for determining core collections?

Pernet A.\(^a\), Marie-Magdelaine J.\(^a\), Oghina-Pavie C.\(^b\), Grapin A.\(^c\)

\(^a\) Institut de Recherche en Horticulture et Semences - UMR 1345, INRA, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France

\(^b\) UMR CNRS 6258 CERHIO, Centre de recherches historiques de l'Ouest, Université d'Angers, 5 bis Bd Lavoisier 49045 Angers, France

\(^c\) Institut de Recherche en Horticulture et Semences - UMR 1345, AgrocampusOuest, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France

* Alix.Pernet@inra.fr

Session: Rose genetics and Breeding

Sustainability of the preservation of the cultivated genetic resources is a major problem for a lot of collection managers whose mission is to preserve, to characterize and to distribute these resources. Indeed, preservation areas, financial and human means are limited. To address this problem, one first solution is to build networks of collections of the same species or the same group of species. This solution promoted by the French national office of the genetic resources is still underway. This solution allows managers to mutualize the efforts and to secure the preservation of a large number of entries. Another complementary solution consists in implementing the concept of "core-collection" (Brown, 1989). In this concept, a subset of entries representing at best the total present diversity in the collection is chosen among all the preserved genetic resources. On this subset will be carried out the efforts of characterization, and possibly long-term preservation, by, for example, a strategy of cryopreservation.

Then comes the question on how to determine this subset. There are diverse strategies which can be implemented with various types of data. Developing core collections was mainly made, until now, thanks to genetic data (molecular characterization) and/or to phenotypic data (various traits, with a qualitative or quantitative variation). For managers of rosebush collections, other types of data are particularly important: data of historic nature, as well as data that permit an estimation of the patrimonial value of each variety.

By taking as model of study the rosebush, we will present different ways of elaborating core-collections. Effects of various types of data and strategies will be evaluated and the obtained collections will be compared by various methods. We will discuss the respective interest of the various types of data for the elaboration of core-collections according to different objectives.
In vitro propagation of three wild Rose species grown in Sicily (south Italy)

Giancarlo Fascella*, Francesca D’Angiolillo, Gaetano Giardina, Michele Massimo Mammano

Consiglio per la Ricerca in Agricoltura e l'Analisi dell’Economia Agraria - Unità di Ricerca per il recupero e la valorizzazione delle Specie Floricole Mediterranee, Bagheria (Palermo), Italy.

*giancarlo.fascella@crea.gov.it

Session: Rose genetics and breeding/Propagation

Micropropagation of Rose species has received considerable attention in the last decades because traditional methods do not ensure production of healthy plants, and influences of the season and slow multiplication rates are the major limiting factors. Though numerous studies on in vitro culture of cultivated rose species and varieties are available in literature, few researches about micropropagation of wild roses of different world areas have been actually reported. Therefore, an in vitro culture assay of three Sicilian spontaneous rose species was established in order to define an efficient mass propagation protocol of genotypes with high ornamental and functional value.

Microcuttings of wild *Rosa canina* L., *R. micrantha* Borrer ex Sm, and *R. sempervirens* L. plants grown in Sicily were initially sterilized and placed on a Murashige & Skoog (MS) basal medium without using any plant growth regulators. For the multiplication phase, four 6-benzyladenine (BA) concentrations (0, 1.1, 2.2 and 3.3 µM) were successively added to a MS medium in order to induce adventitious shoots emission. For the rooting phase, three 3-indolacetic acid (IAA) concentrations (0, 1.7 and 3.4 µM) were added on a MS medium to induce root formation. Rooted plantlets were transferred to greenhouse and grown into plastic pots containing a mixture of brown peat and perlite (1:1, v/v) under mist system for the ex-vitro acclimatization. Adventitious shoots proliferation was influenced both by genotype and by BA level: *R. canina* was the most effective whereas *R. micrantha* showed lowest values (1.6 and 0.7 shoots/explant, respectively); multiplication rates increased (from 0.1 to 1.6 shoots/explant) as BA concentrations increased. In vitro rooting was also affected by genotype as well as by IAA concentration as higher number of rooted microshoots was obtained with IAA 3.4 µM for *R. canina* (68.5%), and with IAA 0 µM for *R. sempervirens* (98.1%). IAA concentration had no influence on the number of roots/microshoot but only on root length. Ex-vitro acclimatization of rooted plantlets significantly varied with the species studied as higher rates were observed in *R. canina* and *R. sempervirens* (86.1 and 79.2%, respectively).

Presentation preference: poster
3D Phenotyping and QTL analysis of a complex character: rose bush architecture

Li-Marchetti C\textsuperscript{a}, Le Bras C\textsuperscript{b}, Chastellier A\textsuperscript{c}, Relion D\textsuperscript{b}, Morel P\textsuperscript{c}, Sakr S\textsuperscript{b}, Hibrand-Saint Oyant L\textsuperscript{c}, Crespel L\textsuperscript{b*}

\textsuperscript{a}ASTREDHOR – Institut Technique de l’Horticulture, Paris, France
\textsuperscript{b}Institut de Recherche en Horticulture et Semences - UMR 1345, Agrocampus Ouest, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France
\textsuperscript{c}Institut de Recherche en Horticulture et Semences - UMR 1345, INRA, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France

\textsuperscript{*}laurent.crespel@agrocampus-ouest.fr

Session: Rose genetics and Breeding
Poster

Abstract

Plant shape, and thereby plant architecture, is a major component of the visual quality of ornamental plants. We have been developing a new method for analyzing the entire plant architecture by 3D digitalization that allows an almost exhaustive description of rose bush architecture and generates a large number of variables, many of them inaccessible manually. We carried out a QTL analysis using this original phenotyping method. In order to evaluate a broader allelic variability as well as the effect of the genetic background on QTL detection, we used two connected, segregating, recurrent blooming populations. Out of 41 variables generated, we selected six variables (i.e. the most explanatory variable of the variability observed and the least correlated between them). Five had never been analyzed genetically. Their broad-sense heritability was moderate to high. The number of QTLs per variable varied from four for the length of long axes (LLA) to seven for the branching angle of order 2 long axes (AngLA2), the two populations taken together. Most major and stable QTLs were located on LG2 in the proximity of RoMAX2, a gene involved in the strigolactone pathway. Five new QTLs, located on LGs 2, 6 and 7, were detected for the branching angle of axes, and the QTL located on LG7 co-located with RhBRC1, a branching repressor. Branching and stem elongation QTLs also co-located with RhBRC1, suggesting its pleiotropic nature.

QTLxYear interactions were also revealed, that explained the GenotypexYear interactions observed for the length of order 4 short axes (LSA4) and AngLA2 from a genetic point of view; they involved more particularly QTLs located on LGs 5 and 6. We also evidenced an effect of the genetic background on QTL detection.

This new knowledge should help to better reason the genetic improvement programs for rose bush architecture, and therefore rose bush shape.
Taxonomic diversity of the genus ROSA in the collection of the Botanical Garden of Maria Curie-Skłodowska University in Lublin

Krystyna Rysiak*, Grażyna Szymczak

Botanical Garden of Maria Curie-Skłodowska University, Lublin, Poland

ul. Sławinska 3,20-810 Lublin

*rysiakk@hektor.umcs.lublin.pl

Session: Rose genetics and Breeding

The collections of the Botanical Garden of Maria Curie-Skłodowska University in Lublin covering an area of over 21 ha have gathered over 6500 species and varieties of plants native to different continents and climate zones. The plants are displayed in separate thematic sections and collections.

The collection of the genus *Rosa* comprised approximately 250 taxa. It occupies a mild slope located in the proximity to a picturesque linden alley leading to the yard of the historic Kościuszko Manor House.

The first rose shrubs were planted in the Garden in 1972. They represented approximately 115 varieties produced by members of the Polish Society of Friends of Roses and producers of roses from Kutno and Końskowola. To date, nearly 30% of the varieties have survived since the planting time.

The current collection shows the diversity of the varieties in terms of the flower shape, colour, and decorative value as well as the mode of propagation and frost resistance. It comprises representatives of all groups of roses distinguished based on the cultivated forms, i.e. park, climbing, grandiflora, multiflora, ground cover, and miniature rose species. There are also wild *Rosa* species and representatives of old and latest varieties. The multiflora roses are characterized by a rich palette of colours from snow-white 'Schneewitchen', orange-yellow-red 'Samba', 'Rumba' to different shades of red 'Pustsa', 'Montana', or 'Lilli Marleen'. The most numerous group in the Garden collection is represented by grandiflora roses (approximately 70 varieties), e.g. 'Allegro', 'Ambasadour', Baronne E. Rotschlidn', 'Berolina', 'Burgund', 'Mainzer Fastnacht', 'Peace', 'Primaballerina', 'Sonia', 'Traviata' or 'Vivaldi'. The group of park roses comprises e.g. varieties *R.* moyesii 'Nevada' and 'Marguerite Hilling', *R.* spinosissima 'Maigold', Fruhligsgold', Fruhlingsmorn', 'Fruhlingsduft', 'Aicha', and 'Hispida'.

The Garden collection of roses also has Polish varieties such as *Rosa rugosa* 'Adam Chodun' (A. Chodun), 'Alinka' (J. Byczkowski), 'Chopin', 'Jarocin', 'Mercury 2000', 'Św. Tereska z Lisieux', 'Venrosa', 'Weneda' (S. Żyła), 'Irena' (Z. Wituszyński), *R. rugosa* 'Kórnik' (produced in Kórnik Arboretum), 'Magda' (L. Kurowski), 'Mazowsze', or 'Poznań' (L. Grąbczewski).

An interesting taxon in the collection is *Rosa sericea* subsp. *omeiensis* f. *pteracantha* - a four-petal rose, and a distinguished rose is 'Marie Curie' dedicated to the patron of the University in Lublin.

The flowers of the roses decorate the Garden from early summer to the first frost. The autumn decoration is provided by their variegated fruits and colourful leaves of e.g. *R. x rugotida* 'Dart’s Defender' and the shining rose *R. nitida* with red shoots.
Evaluation, innovation and application of wild rose species in

Xinjiang, Northwest China

Yang Shu-Hua\textsuperscript{a}, Ge Hong\textsuperscript{a}, Huang Shan-Wu\textsuperscript{a}

\textsuperscript{a}Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, 100081
\textsuperscript{a}yangshuhua@caas.cn

Session: Rose genetics and breeding

Rose is one of the most important ornamentals that more than 24,000 varieties were registered. The genus \textit{Rosa} L. contains over 150 species world-wide but only about 10–15 species are in the background of the most varieties, leaving the vast untapped resources. A good practice for the introgression of wild roses into the current varieties was the application of wild species in Northwest China for the interspecific hybridization.

We’ve introduced \textit{R. beggeriana} from Xinjiang, Northwest China to Beijing and carried out the hybridization with the modern roses since 1980’s. During the decades, many new shrub rose varieties with the extreme cold resistance were successfully released. Moreover, a yellow-leaf mutant of \textit{R. beggeriana} had been obtained by using \textit{γ}-ray irradiation. The morphological and physiological studies showed that the leaf mutant should be associated with the chlorophyll decline. A transcriptome analysis and genetic mapping had been currently conducted for deciphering this yellow-leaf mutant.

On the other hand, the investigation and evaluation of wild species had been initiated in the origins of Northwest China since 2006. The genetic diversity of three species of \textit{R. beggeriana}, \textit{R. laxa} and \textit{R. platyacantha} was analyzed carefully by using the morphological, karyotypic and molecular markers, respectively. Moreover, \textit{R. platyacantha} had been firstly successfully introduced to Beijing. The effect of altitude on the photosynthetic adaptation had been analyzed among the different populations of \textit{R. platyacantha}. In summary, the current goal of our research group is to evaluate, innovate and utilize the wild species in Northwest China for the rose breeding.
Session 2
Secondary metabolites
Biosynthesis of scent compounds in rose

S. Baudino*\textsuperscript{a}, P. Sun\textsuperscript{a,b}, J-C. Caissard\textsuperscript{a}, B. Nairaud\textsuperscript{a}, S. Moja\textsuperscript{a}, J-L. Magnard\textsuperscript{a}, A. Bony\textsuperscript{a}, A. Roccia\textsuperscript{a,c}, F. Nicolè\textsuperscript{a}, F. Jullien\textsuperscript{a}, P. Vergne\textsuperscript{c}, A. Dubois\textsuperscript{c}, O. Raymond\textsuperscript{c}, M. Bendahmane\textsuperscript{e}, L. Hibrand-Saint Oyant\textsuperscript{d}, J. Jeaffre\textsuperscript{d}, T. Thouroude\textsuperscript{d}, F. Foucher\textsuperscript{d}, R. Baltenweck\textsuperscript{e}, S. Meyer\textsuperscript{e}, P. Claudel\textsuperscript{e}, P. Huguene\textsuperscript{e}, C. Tisné\textsuperscript{f}, S. Réty\textsuperscript{g}, M. Rohmer\textsuperscript{h}, R. C. Schuurink\textsuperscript{b}

\textsuperscript{a}. Université de Lyon, UJM-Saint-Étienne, CNRS, BPam FRE3727, F-42023 Saint-Étienne, France.
\textsuperscript{b}. Department of Plant Physiology, Swammerdam Institute for Life Sciences, University of Amsterdam, Science Park 904, 1098 XH, Amsterdam, The Netherlands
\textsuperscript{c}. Laboratoire Reproduction et Développement des Plantes UMR INRA-CNRS, Université Lyon 1-ENSL, IFR128 BioSciences-Gerland Lyon sud, Ecole Normale Supérieure, 46 allée d’Italie 69364 Lyon Cedex 07, France.
\textsuperscript{d}. Institut de Recherche en Horticulture et Semences (INRA, AGROCAMPUS-OUEST, Université d’Angers), SFR 4207 QUASAV, BP 60057, 49071 Beaucouzé Cedex, France.
\textsuperscript{e}. INRA, Université de Strasbourg, UMR 1131 Santé de la Vigne et Qualité du Vin, 28 rue de Herrlisheim, F-68000 Colmar, France.
\textsuperscript{f}. Laboratoire de Cristallographie et RMN Biologiques, UMR, CNRS 8015, Université Paris Descartes, Faculté de Pharmacie, Sorbonne Paris Cité, 75006 Paris, France
\textsuperscript{g}. Institut de Biologie Physico-chimique, CNRS, UMR 8261 CNRS/Université Paris Diderot, 13 rue Pierre et Marie Curie, Paris 75005
\textsuperscript{h}. Université de Strasbourg – CNRS, UMR 7177, Institut Le Bel, 4 rue Blaise Pascal, 67070 Strasbourg Cedex, France.

* sylvie.baudino@univ-st-etienne.fr

The rose is the queen of flowers and is widely used as garden plants and for the cut flower market. Roses are also used for the production of essential oil for the cosmetic and perfume industries. A lot of botanical roses are scented and use their perfume to attract pollinators. Fragrances in garden roses are very diverse and scent has always been an important character in the selection process. Breeders have recently tried to introduce new fragrances, for instance reminiscent of fruit or spice odors. But despite their efforts, some roses on the market are not very fragrant, especially the ones bred for the cut flower market. The cause of this lack of scent is not known. In spite of numerous chemical studies, the biosynthetic pathways of many rose scent compounds are unknown. Terpenoids, especially monoterpenoids, are major floral constituents of rose flowers, mostly responsible for the typical rose scent. Generally, terpenoids biosynthesis in plants is achieved by various terpene synthases. However, with a combination of transcriptomic and genetic approaches, our group recently discovered a terpene synthase-independent pathway. A key enzyme of this pathway is RhNUDX1, belonging to the nudix protein family. It has geranyl diphosphate diphosphohydrolase activity \textit{in vitro}. A positive correlation was found between the expression levels of RhNUDX1 and the production of geraniol, indicating the essential role of this protein in scent production in roses. New results on this unusual scent biosynthetic pathway will be presented, in particular its evolution in the genus \textit{Rosa}.

Magnard et al., 2015: Biosynthesis of monoterpenoid scent compounds in roses. Science 349, 6243.
Bioactive compounds content and antioxidant activity of leaf extracts from four Sicilian Rose species

Francesca D’Angiolillo, Michele Massimo Mammano, Giancarlo Fascella*

Consiglio per la Ricerca in Agricoltura e l'Analisi dell'Economia Agraria - Unità di Ricerca per il recupero e la valorizzazione delle Specie Floricole Mediterranee, Bagheria (Palermo), Italy.

*giancarlo.fascella@crea.gov.it

Session: Secondary metabolites

Recently there is an increasing interest in spontaneous plant species, such as wild roses, which can be used as promising sources of healthy compounds. Rose extracts have been used in several countries as a traditional medicine for their antioxidant and antimicrobial properties associated with the content of secondary metabolites (phenols, carotenoids, essential oils, flavonoids, tannins) which are particularly common in leaves and flowers. It is well known that content of leaf extracts can be affected by the genotypes and climate and therefore by the collection time. Some species of the genus Rosa are widespread in Sicily (south Italy) but no report on the characterization of metabolites extracted from leaves of Sicilian wild roses has been found in literature. Leaf methanolic extracts of four Rose species (Rosa canina L., R. corymbifera Borkh, R. micrantha Borrer ex Sm and R. sempervirens L.) grown in Sicily were analysed in order to evaluate the possibility to use them as a source of bioactive compounds and natural antioxidants. The leaves were harvested during two different periods (June and October) corresponding to different phenological phases (blooming and fruits ripening). Leaf morphological characteristics and the concentration of pigments as chlorophylls ("a" and "b"), carotenoids and anthocyanins, flavonoids, polyphenols content (Folin–Ciocalteu method) and the antioxidant activity (DPPH method) were determined. Leaf photosynthetic pigments content was not affected by the species but only by the harvest period as total chlorophylls and carotenoids were higher (0.92 and 26.6 mg g⁻¹ fresh weight, respectively) in leaves harvested in June, with limited differences recorded among Rose species. Leaf anthocyanins content was influenced by the genotypes and by the harvesting periods as higher content was measured in R. micrantha and R. corymbifera leaves harvested in October (14.4 and 12.7 mg 100 g⁻¹ FW, respectively). Polyphenols content was affected both by the species and by the harvest time as higher values were recorded in R. micrantha plants (67.5 mg 100 g⁻¹ FW) and, generally, when leaves of all species were harvested in October. No difference in the flavonoids content were recorded among the species as well as between the two harvest periods. The DPPH radical scavenging activity was high in leaf extracts of all species in both periods, mainly in leaves harvested in June from R. micrantha plants (147.1 µg FW ml⁻¹), confirming the assessment that some spontaneous Sicilian roses can be used as sources of natural antioxidants.

Presentation preference: oral
Evolution of the *NUDX1* gene in wild roses

NAIRAUD Baptiste, MOJA Sandrine, PULU Sun, HUGUENETY Philippe, BONY Aurélie, BAUDINO Sylvie, CAISSARD Jean-Claude

Recently, a new enzyme involved in geraniol biosynthesis has been characterised in modern roses. This enzyme, named NUDX1, does not belong to terpene synthases but to Nudix hydrolases (Magnard et al. 2015 Science 349, 81-83). In other organisms like *Escherichia coli*, *Arabidopsis thaliana* and *Homo sapiens*, NUDX1 homologs are involved in cellular sanitization, hydrolysing 8-oxo-dGTP to avoid mutations. In modern roses, it hydrolysies geranyl diphosphate into geranyl monophosphate. This compound is then probably hydrolysed into geraniol by an unknown enzyme. To gain knowledge about this new function of NUDX1 and its evolution, we have begun the characterisation of *NUDX1* gene orthologs in wild species of roses and in other Rosaceae. We would like to know whether this function has appeared during domestication (30,000 cultivars created by growers since the XVIIth century), during evolution of the genus *Rosa* (120 species all around the world), or during the evolution of Rosaceae and closed families.
Prolonged Post-harvest Handling of the Oil Rose (*Rosa damascena* Mill.) flowers

Maryam Mirzaei, Nima Ahmadi, Fatemeh Sefidkon, Abdolali Shojaeiyan, Rassul Mohammadi, Hossein Hosseini

Graduated Ph.D students, Tarbiat Modares University, Tehran, Iran; 

Department of Horticultural Sciences, Tarbiat Modares University, Tehran, Iran; 

Research Institute of Forests and Rangelands, Tehran, Iran; 

R & D Department, Barij Essence pharmaceutical Co., Kashan

Damask rose (*Rosa damascena* Mill.), an economically important species of the Rosaceae family, mainly used for rose oil and rose water production that is obtained from fresh gathered Damask rose flowers. Due to gathering huge amount of fresh flower before oil extraction, postharvest handling of flowers prior to distillation process is considered as a key issue in rose essential oil production. Evaluating the effects of different prolonged handling conditions of Damask rose on the yield and quality of the extracted essential oils by distillation, petals were stored in poly-film (PET/EVOH/LDPE) bags under frozen storage (−20°C); active and passive modified atmosphere packaging (MAP) at 4±1°C as well as room temperature conditions for 7, 14 and 21 days. With the storage of petals under MAP conditions, the results elucidated that active MAP conditions had no significant impact on maintaining the oil content comparing passive MAP. Furthermore, Frozen-stored petals qualified for the higher essential oil contents for all the durations of the prolonged storage. In this respect, the values from petals stored for 7–14 days under frozen condition were not significantly different from freshly-harvested petals (0.069 V/W %). The results provide a reference material for interested groups such as producers, consumers who are concerned about rose oil production.

**Key words:** Modified Atmosphere Packaging, Oil Rose, PET Poly-Film Bags, Prolonged Handling
Characteristics of floral scent of rose cultivars evaluated from cut flowers

Naomi Oyama-Okubo

Institute of Vegetable and Floriculture Science, NARO
Tsukuba, Ibaraki 305-0852 Japan
namisea1@affrc.go.jp

Session: Secondary Metabolites

Floral scent, the characteristic fragrance that emanates from roses, enhances their charm, and is an important quality of roses. Rose scents are generally classified into the following 7 types: Damask classic, damask modern, blue, fruity, spicy, anise (myrrh) and tea, and each of these scent types are imparted by specific compounds. Interestingly, some modern day cultivars have novel scents that do not belong to any of the existing classifications. In this research, I analyzed scent compounds emitted by 62 of cut flower cultivars, which included both new and old cultivars.

Cut flowers of 62 rose cultivars with excellent fragrance (including ‘Yves Piaget’ and ‘Papa Meilland’ as standard cultivars) were placed in an environmental controlled room maintained at 21 ± 2 ºC and under a 12-h photoperiod at a light intensity of about 10 µmol/m²/s. Emitted scent compounds were collected in Tenax-TA tubes by dynamic headspace method. The collected samples were directly introduced into GC-MS using a thermal desorption system.

Here I again classified these rose cultivars into 6 groups according to the composition of scent components and using sensory assessment: Glamorous rose-like scent group whose major compounds are β-citronellol, geraniol, nerol and 2-phenylethanol (16 cultivars including ‘Yves Piaget’ and ‘Papa Meilland’), rose-like scent with citrus nuance group whose characteristic compounds are geranial and neral (4 cultivars), sweet fruity scent group whose major compounds are acetate esters, such as geranyl acetate and 2-phenylethyl acetate (8 cultivars), tea-like scent group whose major compound is 3,5-dimethoxytoluene (21 cultivars), anise-like scent group whose major compound is 4-methoxystyrene (10 cultivars), and green-like scent group whose major compounds are cis-3-hexenyl acetate and germacrene D (3 cultivars). I selected 19 cultivars emitting particularly strong scent and analyzed daily changes of the emitted scent compounds from flowering to dropping in each cultivar. Some cultivars showed the largest amounts of emission of total scent compounds on the first day after flowering and then showed a gradual decline in emission. Other cultivars showed the largest amounts on the second or third day after flowering. Composition ratio of the scent compounds also changed after flowering. Evaluation of these characteristics provides important information about floral scents as they add commercial value to rose cultivars.

This work was supported by a grant for a commissioned project study on “Development of postharvest technology in cut flowers”, from the Ministry of Agriculture, Forestry and Fisheries,
Effects of sugars and methyl jasmonate treatment on vase life and scent emission in cut rose flowers

Hiromi Ikeura\(^a\), Daisuke Shimadzu\(^b\), Masaya Fukutani\(^b\) and Takashi Handa\(^{b*}\)

\(^a\) Organization for the Strategic Coordination of Research and Intellectual Properties, Meiji University, Kawasaki, Kanagawa, 214-8571, Japan
\(^b\) School of Agriculture, Meiji University, Kawasaki, Kanagawa, 214-8571, Japan
\(^{b*}\) thanda@meiji.ac.jp

Session: Secondary Metabolites

Roses (Rosa\(^*\)hybrida\(^*\) L.) are used for garden plants and cut flowers as well as a source of natural fragrance. Many modern rose cultivars have been mainly selected by novel flower color and shape, and longer flower longevity. For fragrant rose cultivars, flower scent is a crucial trait. Rosa ‘Yves Piaget’, which is a popular fragrant cultivar in Japan, has a strong damask-floral scent. However, cut flowers of ‘Yves Piaget’ have short vase life, and so addition of preservatives is useful after cutting. It was reported that treatment with methyl jasmonate (MeJA) delayed flower opening, and improved vase life. In this study, we investigated the effects of MeJA in combination with sugar treatment on the vase life, scent emission, endogenous volatile compounds of petals, and sugar contents of petals and leaves in cut flowers of ‘Yves Piaget’.

‘Yves Piaget’ flowers were cut when the flowers started to open, and subjected to eight treatments, 1; sucrose, 2; glucose, 3; fructose, 4; MeJA, 5; MeJA+sucrose, 6; MeJA+glucose, 7; MeJA+fructose, and 8; distilled water (control). Sugars and MeJA concentration were adjusted to 58.43 mM and 100 µM, respectively. Scent emission and endogenous volatile compounds extracted by solid-phase micro extraction (SPME) and by diethyl ether solvent extraction, respectively. These extracted compounds were identified and quantified by gas chromatography-mass spectrometry (GC-MS). Sugar contents of petals and leaves were quantified by high pressure liquid chromatography (HPLC).

Treatments of sucrose, glucose or fructose alone extended the vase life than control. Treatment of MeJA+glucose significantly extended the vase life than that of glucose alone. Control and treatment of MeJA alone decreased the relative concentration of scent emission compounds from 1\(^{st}\) day of the treatment. Treatment of MeJA+glucose raised the relative concentration of scent emission compounds until 3\(^{rd}\) day and then decreased, whereas treatment of MeJA+sucrose kept it until 5\(^{th}\) days. Treatment of MeJA+sucrose showed higher relative concentration of endogenous volatile compounds than other treatments from 1\(^{st}\) day until 5\(^{th}\) day. Treatment of MeJA+glucose showed highest concentration at 3\(^{rd}\) day.

These results suggest that MeJA+glucose extended vase life and MeJA+sucrose kept long emission of flower scent in ‘Yves Piaget’.
Session 3
Rose physiology
Role of ethylene in petal growth and senescence of roses

Nan Ma, Chao Ma, Changqing Zhang and Junping Gao*

China Agricultural University, Beijing 100193 China
* Gaojp@cau.edu.cn

Session: Rose physiology

Rose is one of the most important ornamental crops worldwide. In China, cut rose accounts for 30% of cut flower trade, while this number is 30% in Europe. In China, production of cut rose kept a steady rising trend over the past 20 years. Sale volume of cut rose was 5.64 billion stems in 2014, increased 111% compared to 2005. In China, ~60% cut rose flowers produce in Yunnan province in southwest China with lower latitude of 25 north and altitude of 1900-4500 m. Therefore, long distance transportation is necessary for supply of cut rose flowers, and postharvest loss of cut roses is usually over 30%, even 50% in some cases.

Ethylene is mainly produced by rose flowers and accumulates to a high concentration in a package during transportation. Accumulated ethylene usually influences flower quality, mostly resulted in repression of growth and acceleration of flower senescence of petals.

To understand the role of ethylene in petal growth, we conducted a high-throughout sequencing of mRNA and sRNA of rose petals and performed combined analysis of expression of miRNAs and their targets. miR164 and its target RnNAC100 exhibited high ethylene sensitivity. Based on comprehensive function analysis, we established a miR164-RnNAC100 module-centered regulatory network in cell expansion-driven petal growth. Transcript accumulation of RnNAC100 was rapidly and dramatically induced by ethylene via miR164-dependent post-transcriptional regulation. RnNAC100 was proved to be a transcription repressor and directly suppressed expression of several genes related to cell expansion, such as RhCesA2, RhPIP1;1 and RhPIP2;1.

In the aspect of effect of ethylene on petal senescence, we found that homeodomain-leucine zipper transcription factors contribute to hormone crosstalk between ethylene and other hormones in petal senescence. Among them, RhHB1 mediates the antagonistic effect of GAs on ethylene induced rose petal senescence. RhHB1 decreased the expression of a GA biosynthetic pathway gene, RhGA20ox1, which reduced the GA content in the senescing petals. RhHB6 functions as a brake of ethylene promoted senescence through increasing the CTK content. Ethylene induced RhHB6-RhPR10.1 regulatory module increased cytokinin content in the senescing petal to prevent premature organ senescence.

Taken together, our results demonstrate that ethylene has broad functions in petal growth and senescence. Future investigates will focus on the regulatory network and hormone crosstalk between ethylene and other phytohormones.
Digital image analysis to assess flower productivity and foliage retention in garden roses throughout the season

Wenji Xu\textsuperscript{a}, Yeyin Shi\textsuperscript{b}, and David Byrne\textsuperscript{c}

dbyrne@tamu.edu

\textsuperscript{a} Shenyang Agricultural University, Shenyang, China
\textsuperscript{b} Department of Biological Systems Engineering, Institute of Agriculture and Natural Resources, College of Engineering, University of Nebraska–Lincoln, Lincoln, NE USA
\textsuperscript{c} Department of Horticultural Sciences, Texas A&M University, College Station, TX USA

A good ornamental garden rose needs to maintain good foliage coverage and abundant flowers throughout the growing season. Unfortunately an evaluator or breeder generally only has the time to assess these characteristics 2 or 3 times during the 6 to 9 month growing season. Consequently much is missed and the best plants may not be identified. Thus a rapid phenotyping procedure which can be done on a weekly basis is needed. Overhead pictures of a series of rose plants were taken on a weekly or monthly basis during the growing season using a Samsung Galaxy Tab4 which was mounted on a selfie stick. At the same time, these plants were assessed for their percent defoliation and flower intensity. We developed algorithms to automatically estimate the rose canopy cover, density and the percentage of flower cover based on image segmentation and clustering in RGB and HSV bands. These algorithms were able to distinguish the flowers irrespective of their color from the leaves. The analysis was capable of calculating the percent of the canopy covered with green foliage and the percent of the canopy covered with flowers. This approach, incorporating a unmanned aircraft system (UAS) equipped with cameras and an analytical pipeline, has potential of rapidly acquiring plant development information essential for the proper evaluation of garden roses as well as for field physiology research.
Light Use Efficiency of a rose crop as influenced by the spectrum of the artificial light

Nieves Garcia Victoria\textsuperscript{a}, Sander Pot\textsuperscript{b}, Stiina Kotiranta\textsuperscript{c}

\textsuperscript{a} Wageningen University and Research, Business Unit Greenhouse Horticulture, Violierenweg 1, 2665 MV Bleiswijk, The Netherlands
\textsuperscript{b} Plant Dynamics BV, Koningin Julianastraat 23 6668 AG Randwijk, The Netherlands
\textsuperscript{c} Valoya Oy, Melkonkatu 26, 2nd floor, 00210 Helsinki, Finland
\textsuperscript{*}nieves.garcia@wur.nl

The cultivation of cut flowers such as roses at higher latitudes is a highly energy demanding enterprise, due to the need for artificial light to supplement the scarce sun radiation. In The Netherlands energy and labour are the two main cost components in commercial rose cultivation. For these reasons, saving energy while maintaining or even improving the high production and quality standard is an important drive for innovation. Efforts are done by government, growers and industry to decrease the environmental impact and increase the sustainability of rose cultivation. By replacing the commonly used High Pressure Sodium (HPS) lamps by the more energy-efficient Light Emitting Diodes (LED) lamps, it is possible to reduce the electricity demand for artificial light and save energy. An added advantage from LED’s is that they allow to manipulate the light spectrum in the greenhouse. Studies with different light wavebands in growth chambers have shown that growth and morphology of plants, as well as stomatal conductance can be strongly manipulated with the light spectrum. With the replacement of HPS lamps by LED in greenhouse increases the heat demand in winter to compensate for the loss of radiative heat. This is why “hybrid” lighting systems consisting of a mixture of both types of lamps are an interesting alternative. This paper describes an experiment that was conducted in a commercial rose nursery with the rose Avalanche+, where a “hybrid” light system was installed. The light installation consisted of 103 $\mu$mol /m$^2$s PAR from HPS lamps combined with Valoya LED lamp G1 with a light spectrum specially engineered for this purpose. Two different LED light intensities: 57 or 103 $\mu$mol /m$^2$s PAR were combined with the HPS light. Compared to the conventional installation of the company (191 $\mu$mol /m$^2$s HPS), the spectrum of the hybrid installation in both intensities increased the light use efficiency (LUE) by the crop, expressed as grams of good quality roses per mol light (natural + artificial) received. This offers possibilities for energy saving, when the energy efficiency of the lamps used is at least 1.7 $\mu$mol PAR per watt electric. The supportive morphology and photosynthesis measurements performed to explain this positive effect will be discussed. More research is needed about the effects of light colour on rose production. Remaining questions are if other rose varieties react the same to the hybrid light spectrum, and if manipulating the light spectrum can keep the crop compact in winter or give heavier flowers with a larger flower bud. The research was funded by the program “Greenhouse as Energy Source” (Dutch Ministry of Economy and the Horticultural Product Board), Valoya and Arend Roses.
Effects of Some Preservative Solutions on the Vase Life of Cut Rose Flowers

Soner KAZAZ*  Nurdan Tuna GÜNÈŞ Özge HORZUM

*Department of Horticulture, Faculty of Agriculture, Ankara University, Ankara, Turkey
Corresponding author: skazaz@ankara.edu.tr

Session: Rose physiology

Abstract

The effects of different concentrations of glycolic acid, succinic acid, citric acid, and salicylic acid on the vase life of Rosa hybrida cv. Samourai were investigated in the study. Distilled water was used as the control. The cut rose flowers were harvested from a grower greenhouse at the commercial harvest stage. The experiment was conducted in 3 replications, and 5 flowers were used in each replication. The effects of the treatments on vase life, relative fresh weight and water uptake were investigated.

The results showed that glycolic acid, succinic acid, citric acid and salicylic acid significantly increased the vase life as compared with the control.

Key Words: Cut rose, vase life, glycolic acid, succinic acid, citric acid, salicylic acid
Rhizogenesis and contents of polyphenolic acids in cuttings harvested in different phenological phases from the once-blooming shrub roses and treated with the rooting stimulants

Marta Joanna Monder\textsuperscript{a}, Andrzej Pacholczak\textsuperscript{b}

\textsuperscript{a}Polish Academy of Sciences Botanical Garden - Center for Biological Diversity Conservation in Powsin, Prawdziwa 2, 02-973 Warsaw, Poland

\textsuperscript{b}Warsaw University of Life Science, Department of Ornamental Plants, Nowoursynowska 159, 02-776 Warsaw, Poland

Session: Rose physiology

The once blooming shrub roses of older origin have a wide range of applications and are worth using in order to sustain biodiversity and historical heritage. The polyphenolic acids can affect some enzymes which take a part in the process of rooting. The aim of the studies was to evaluate the effect of phenological phases of rose stock plants and rooting stimulators on rhizogenesis of cuttings and changes in content of polyphenolic acids. The following once blooming cultivars were chosen: ‘Duchesse d’Angoulême’, ‘Hurdals’, ‘Maiden’s Blush’, ‘Mousseuse Rouge’. The cuttings were harvested from shoots in four phenological phases: flower buds open (P1), all flowers open (P2), immediately after petal shedding (P3), 7-14 days after petal fall (P4). Single node stem cuttings were treated with either (a) the standard rooting preparations containing 0.4% IBA (Ukorzeniacz A\textsubscript{aqua}) or 0.2% NAA (Ukorzeniacz B\textsubscript{aqua}); or (b) the biostimulants/plant origin preparations: Bio Rhizotonic, Root Juice\textsuperscript{TM}, Bio Roots. The rooting percentage and rooting degree as well as contents of polyphenolic acids in plant material and their correlations were evaluated. The content of polyphenolic acids was changing dynamically during blooming, within 15-34 days, according to the flowering period of a cultivar. In two cultivars which showed differences in the rooting percentage of control cuttings harvested in consecutive developmental phases (‘Hurdals’, ‘Maiden’s Blush’), the relationship between the content in polyphenolic acids before rooting and rooting percentage was proved. The cuttings from P4 stage rooted in a lower percentage (‘Maiden’s Blush’) or didn’t root at all (‘Hurdals’). The content of polyphenolic acids was not related to rhizogenesis in ‘Mousseusse Rouge’ and ‘Duchesse Angoulême’. The control untreated cuttings of these cultivars rooted similarly when harvested in each of four phenological phases. Generally, the content of polyphenolic acids decreased during rooting in control cuttings (‘Duchesse d’Angoulême’, ‘Maiden’s Blush’, ‘Mousseuse Rouge’) and after the use of the auxin-containing preparations. The use of plant origin preparations resulted in increasing or maintaining the levels of polyphenolic acids. The increase in content of polyphenolic acids correlated with the increase in rooting percentage. The quality of root system was the highest in cuttings from P1 stage. The use of rooting stimulants and the contents of polyphenolic acids in cuttings did not correlate with the rooting degree. The plant origin preparations positively affected rhizogenesis, however, their effect depended on a phenological phase and a cultivar. Bio Rhizotonic, Root Juice\textsuperscript{TM} and Bio Roots can replace the preparations containing IBA/NAA in stimulating rooting of the once blooming roses. This research was financially supported by National Science Centre (Poland), project no. NN 310008240, and multi-year programme IHAR-PiB/IO 2015-2020.
Optimum pH value for extended vase life of cut Rosa Cv. Tereasa

Nermeen T. Shanan

Department of Ornamental Horticulture, Faculty of Agriculture, Cairo University, Giza, Egypt.
Email: nermeenshanan77@gmail.com

Abstract

This experiment was conducted on cut Rosa L. (cv. Tereasa) during two summer seasons (2015 and 2016). Stems of cut Rosa L. flowers were dipped in solution to test five different an initial pH values, i.e. 3.0, 4.0, 4.5, 5.0 and 6.5 in the presence of 2 % sucrose. The pH values were adjusted through using 0.2 M Na₂HPO₄ and 0.1 M citric acid. The maximum vase-life over the two seasons was recorded with pH 3 followed by pH 4. Also, the lowest significant reduction in flower fresh weight was recorded with pH 3. In addition, the maximum water uptake (4.54 ml/g) was obtained with pH 3 followed by pH 4, which was highly correlated with vase life duration. The highest mean count of total spores forming bacteria in vase solution was recorded at pH 6.5, whereas the lowest count was obtained with pH 3. Increasing pH level negatively influenced Rose flowers longevity through increasing free total amino acid as well as reducing total sugar, chlorophyll and anthocyanin concentrations. Moreover, the pH 3 was able to maintain a higher osmotic potential of cells through enhancing total sugar chlorophyll and anthocyanin concentrations which were in conformity with enhancing antioxidant enzymes, i.e. superoxide dismutase (SOD) and catalase (CAT) activities in leaves. In conclusion, decreasing of solution pH enabled the cut Rose flowers to maintain higher osmotic potential, delaying senescence and enhancing flowers longevity.
Indolebutyric acid on cut rose seedling production by bench grafting on different rootstocks

Kathia Fernandes Lopes Pivetta*\(^a\), Marina Romano Nogueira\(^a\), Patricia Unger Cesar Pizetta\(^a\), Renata Bachin Mazzini-Guedes\(^b\), Claudia Fabrino Machado Mattiuz\(^c\)

\(^a\) Department of Crop Production, College of Agricultural and Veterinary Sciences, State University of São Paulo (FCAV/UNESP), Via de Acesso Professor Paulo Donato Castellane, s/n, CEP 14884-900, Jaboticabal/SP, Brazil.

\(^b\) Federal University of Paraná (UFPR), Rua Doutor João Maximiano, 426, Vila Operária, CEP 86900-000, Jandaia do Sul/PR, Brazil.

\(^c\) Department of Crop Science, Luiz de Queiroz College of Agriculture, University of São Paulo (ESALQ/USP), Avenida Pádua Dias, 11, CEP 13418-900, Piracicaba/SP, Brazil.

* kathiaflpivetta@hotmail.com

In Brazil, the commercial seedling production of cut roses was, for many years, performed only by budding. Subsequently, seedlings started to be produced by cuttings, when the method of bench grafting was also highlighted. However, many factors may interfere in these processes of seedling production. The objective of this work was to study the effect of indolebutyric acid (IBA) concentrations on seedling production (simultaneous rootstock rooting and graft survival) of Rosa sp. ‘Ambiance’ grafted on rootstocks of Rosa sp. ‘Natal Brier’ and Rosa manetti.

The experimental design was performed in randomized blocks, and treatments were arranged in a 2 x 4 factorial scheme (two rootstocks combined with four IBA concentrations: 0; 1,000; 2,000; and 3,000 mg L\(^{-1}\)). There were four replications and 10 grafts per plot. Variables evaluated were seedling formation (considering both rootstock rooting and graft survival), and number, length, and dry matter of roots.

The combination of Rosa sp. ‘Ambiance’ grafted on R. manetti resulted in higher percentage of seedling formation. Such combination also presented higher number of roots per seedling. Grafting of Rosa sp. ‘Ambiance’ on Rosa sp. ‘Natal Brier’ resulted in seedlings with less roots, which, in turn, had greater dry matter. The IBA application positively influenced seedling production, promoting superior general results from 1,000 mg L\(^{-1}\) IBA. For both rootstocks, best results for seedling rooting was obtained from 1,000 mg L\(^{-1}\) IBA; for root number, from 1,000 to 2,000 mg L\(^{-1}\) IBA; and the higher the concentration, the greater root dry matter, up to 3,000 mg L\(^{-1}\) IBA. Results of root length were slightly different for each rootstock: for ‘Natal Brier’, ideal concentration ranged from 1,000 to 2,000 mg L\(^{-1}\); for R. manetti, the higher the concentration, the greater root length, up to 3,000 mg L\(^{-1}\) IBA.
Performance of ‘Tineke’ rose cultivar grafted on nine rootstocks

Kathia Fernandes Lopes Pivetta*a, Marina Romano Nogueiraa, Patricia Unger Cesar Pizettaa, Renata Bachin Mazzini-Guedesb, Claudia Fabrino Machado Mattiuzc

a Department of Crop Production, College of Agricultural and Veterinary Sciences, State University of São Paulo (FCAV/UNESP), Via de Acesso Professor Paulo Donato Castellane, s/n, CEP 14884-900, Jaboticabal/SP, Brazil.

b Federal University of Paraná (UFPR), Rua Doutor João Maximiano, 426, Vila Operária, CEP 86900-000, Jandaia do Sul/PR, Brazil.

c Department of Crop Science, Luiz de Queiroz College of Agriculture, University of São Paulo (ESALQ/USP), Avenida Pádua Dias, 11, CEP 13418-900, Piracicaba/SP, Brazil.

*bkathiaflpivetta@hotmail.com

Session: Rose physiology

The rose cultivar ‘Tineke’ is one of the most cultivated in Brazil. The majority of its commercial propagation is performed by either grafting, budding, or bench grafting. The objective of this work was to evaluate the performance of ‘Tineke’ rose cultivar grafted on nine rootstocks commonly planted in Brazil.

The experimental design was set in randomized blocks with nine treatments, that comprised nine rootstocks (Rosa multiflora ‘Paulista’, R. multiflora ‘Japônês’, R. multiflora ‘Iowa’, R. multiflora ‘Kopman’s’, Rosa indica x R. multiflora, R. indica ‘Mayor’, Rosa sp. ‘Natal Brier’, Rosa manetti, and Rosa canina ‘Inermis’), and four replications with 10 plants per plot. Grafting was performed by bench grafting with rootstock cuttings harvested from semi-herbaceous stems and prepared with two buds and around 8 cm length. Graft cuttings were also collected from semi-herbaceous stems and had one bud and around 4 cm length. Basal parts of graft cuttings were treated with indolebutyric acid (2,000 mg L⁻¹) applied via powder, which were then placed on beds filled with carbonized rice husk maintained at 100% of its water retention capacity. The beds, which were located inside a greenhouse coated with translucid polyethylene, were also covered with the same material. After 30 days of rooting, seedlings were transplanted to the final location at a commercial production area in Andradas municipality, Minas Gerais State, Brazil (22°05’ S, 46°35’ W, at 1,251 m above sea level). Common practices of soil preparation for commercial rose production were performed inside a greenhouse entirely coated with translucid polyethylene and also side-coated with a 50% shading black net, where plants were disposed on beds of 1 m width and 50 m length following the double spacing with 0.30 m among plants and lines. Usual cultural, phytosanitary, and fertilization treatments were also applied. Evaluations started 24 months after transplanting, when flower production was entirely stabilized, and were conducted monthly along one year. Assessed variables were number of commercial flower stems plant⁻¹ month⁻¹, length and diameter of flower stems, neck length (from flower bud to first leaf), length and diameter of flower buds, and dry matter of flower stems and buds.

All rootstocks promoted similar yield of ‘Tineke’ cultivar. However, there were significant differences for some characteristics of flower stems and buds, but temporal patterns were not identified. In general, R. multiflora ‘Iowa’, R. multiflora ‘Japônês’, and R. multiflora ‘Kopman’s’ generated longer neck, while R. canina ‘Inermis’ showed shorter ones. R. manetti promoted longer and thicker flower stems with, consequently, greater dry matter. Length and diameter of flower buds were similar for all rootstocks. Thus, considering all evaluated variables, R. manetti was the rootstock that promoted best results from the combination with ‘Tineke’ cultivar, while R. canina ‘Inermis’ presented the worst ones.
Changes in Flower Quality and Plant Growth Substances of Rose cv. ‘Dolce Vita’ in Response to Different Nitrogen Sources in Soilless Culture

Mehdi Hosseini Farahi and Bahman Kholdebarin

1Young Researchers and Elite Club, Yasooj Branch, Islamic Azad University, Yasooj, Iran
2Department of Biological Science, Marvdasht Branch, Islamic Azad University, Marvdasht, Iran
*corresponding author: m.h.farahi@iauyasooj.ac.ir

Session: Rose Physiology

Abstract
In order to study the effect of different nitrogen sources in nutrient solution and their ratios on endogenous growth regulators and some postharvest parameters in cut flowers of Rose cv. Dolce Vita, a study was conducted in completely randomized block design with 3 replications. Rooted cuttings were planted in plastic pots filled with perlite and cocopeat with 1:1 ratio (v/v) and fertigated with nutrient solutions containing seven different ratios of urea: ammonium: nitrate (0:100:0, 0:50:50, 100:0:0, 50:0:50, 50:25:25, 70:15:15 and 100:0:0) for three months under greenhouse conditions. At the end of experimental period, vase life, flower length and some endogenous growth regulators were measured. Results indicated that along with the increase in urea and ammonium concentrations, the amounts of plants IAA, GA3, Zeatin, ABA and polyamines contents decreased significantly, although plants fertigated with nutrient solution containing urea: ammonium: nitrate (25:25:50) had the highest concentrations of growth regulators and also the highest stem length and flower vase life. As the ammonium ratios in the nutrient solution increased, the flower vase life decreased significantly. The lowest concentrations of plants putrescine and spermine were found in plants fertigated by solution containing ammonium as the sole nitrogen source. Thus, according to data presented, using urea: ammonium: nitrate at the ratios of 25:25:50, had the highest effects on improving the cut rose flowers quality by affecting plant growth regulators, and can be recommended for cut rose production in soilless culture systems.

Key words: Endognous growth regulators; Rosa hybrida, vaselife, urea
Changes in vase life and postharvest quality of cut rose (*Rosa hybrida* cv. Angelina) flowers by application of cumin (*Cuminum cyminum* L.) essential oil and 8-hydroxyquinoline sulfate

Yousef Payro¹ and Hosseini Payro¹

¹Department of Horticultural Science, Science and Research Branch, Islamic Azad University, Tehran, Iran

Session: Rose physiology

Abstract

To investigate the application effect of cumin (*Cuminum cyminum* L.) essential oil and 8-hydroxyquinoline sulfate on vase life and postharvest quality of cut rose (*Rosa hybrid cv. Angelina*) flowers, a factorial experiment was conducted on the basis of randomized complete blocks design agricultural faculty of Islamic Azad University of Yasooj in 2014. The treatments were cumin (*Cuminum cyminum* L.) essential oil (in three concentrations of 0 (distilled water), 100 and 150 mg.L⁻¹), 8-hydroxyquinoline sulfate (in four concentrations of 0 (distilled water), 200, 400 and 600 mg.L⁻¹) and measuring time (in three levels of 1st day, 8th day and 16th day) in three replications. The results showed that the interaction effect of cumin essential oil and hydroxyquinoline sulfate in measuring time was significant (P<0.05) on all of parameters except for Anthocyanin content in rose petals in a way that the highest amount for measured traits was obtained with treatment of in150 mg.L⁻¹ cumin essential oil and 400 mg.L⁻¹ 8-hydroxyquinoline sulfate.

**Keywords:** cut rose (*Rosa hybrid cv. Angelina*) flowers, cumin (*Cuminum cyminum* L.) essential oil, hydroxyquinoline sulfate.
Effect of polyamines on vegetative characteristics, mineral absorption and endogenous hormones in hydroponic grown rose cv. ‘Dulce Vita’

Mehdi HosseiniFarahi$^1$ and Mohammad Mahdi Jowkar$^2$

$^1$Department of Horticultural Science, Yasooj Branch, Islamic Azad University, Yasooj, Iran
$^2$Department of Agronomy and Plant Breeding, College of Agriculture, Kermanshah Branch, Islamic Azad University, Kermanshah, Iran.

Abstract:
Polyamines (PA) are one of the most important plant growth substances which have a major role in different physiological responses specially flower induction, development and senescence. In order to study the effect of polyamine foliar application on physiological and biochemical properties of 'Dulce Vita' rose plants, an experiment was conducted in a completely randomized block design on hydroponic grown rose. During growth, plants were sprayed with Putrescine (Put)(1, 2, 3 mM), Spermidine (Spd)(0.5, 1, 1.5 mM) and Spermine (Spm)(1, 2, 4 mM) and control (distilled water). Consequently vegetative characteristics, mineral absorption and endogenous hormones were studied. Results indicate that 1.5 mM Spd application resulted in the highest cut flower stem length and flower bud size. Between the different applied PAs, Spd had the most beneficial effect on vase life. Application of PA did increase vase life, but the increment was not significant. PAs foliar application significantly improved absorption and accumulation of various elements such as N, P, K, Ca, Fe, Zn and Cu compared to control. Endogenous level of plant hormone were also affected by PA treatment. 4mM Spm significantly increased endogenous levels of Aux, Cyt and GA. This was while ABA significantly increased by low levels of Spm.

Keywords: PGR, Putrescine, Soilless culture, Spermidine, Spermine.
Influence of Polyamines and CaSO₄ on mineral nutrient absorption of cut rose flower (Rosa hybrid) cv. ‘Dolce Vita’ in hydroponic culture

Mehdi Hosseini Farahi¹ and Hossein Payro²

¹Young Researchers and Elite Club, Yasooj Branch, Islamic Azad University, Yasooj, Iran.
²Department of Horticultural Science, Science and Research Branch, Islamic Azad University, Tehran, Iran

Abstract

Rose is one of the most important and most popular of cut flowers in the world. Due to high demand in the market, increasing the quantity and quality of roses is important. In this way, the use of minerals and polyamines can be effective in improving the quantity and quality of rose. For this propose this experiment was conducted in the randomize complete block design with ten treatments and three replications in a hydroponic greenhouse around of Yasooj city. Treatments were included control, Spm (0.5, 1 and 1.5 mM) CaSO₄ (2.5 and 5 mM) Spm 0.5 mM+ CaSO₄- 2.5mM, Spm 0.5 mM+ CaSO₄- 5mM, Spm1 mM+ CaSO₄- 2.5mM, Spm1 mM+ CaSO₄- 5mM. Traits such as length of flower stalk, stem diameter, flower buds diameter, flower stalks, fresh weight of stem, Chlorophyll content and vase life were measured. Results showed that effect of Spm and CaSO₄ has significant at 0.05% on all of traits except Chlorophyll content. The highest and lowest length of flower stalks (100 cm), stem diameter and fresh weight of stem was obtained in Spm1.5 mM and control respectively. The highest rate of flower buds diameter was observed in Spm 0.5 and Caso4 2.5 mM treatments. The most vase life obtained in Spm 0.5 + CaSO₄ – 5mM as compare to other treatments.

Key words: Spermidine, Spermin, Putricine, Vase life
The Effect of different media cultures and salicylic acid on qualitative and quantitative characteristics of cut rose flower in soilless culture

Mehdi Hosseini Farahi¹, Mehdi Hosseini² and Abdolhossein Aboutalebi²

¹Department of Horticultural Science, Yasooj Branch, Islamic Azad University, Yasooj, Iran
²Department of Horticultural Science, Jahroom Branch, Islamic Azad University, Jahroom, Iran

Abstract

The aim of this study was to investigation the effect of different media cultures and Salicylic acid (SA) on qualitative and quantitative of Rose cut flower (Rosa hybrida cv. Angelina) in soilless culture. A factorial experiment was carried out in a completely randomized block design in a hydroponic greenhouse with three replications. The first factor was including SA at 0, 1000, 2000 and 3000 mg l⁻¹ and second factor were eight different combinations of media culture including 1- Animal manure+ Perlite, 2- Poultry manure+ Perlite, 3- Poultry manure+animal manure, 4- Perlite+Cocopeat, 5- Poultry manure+Leaf Compost, 6- animal manure+leaf compost, 7- Leaf compost+Perlite, 8- Leaf compost+cocopeat as 50-50% ratio. Traits such as length of flower stalk, stem diameter, flower bud diameter, fresh and dry weight of stem, chlorophyll content, potassium and phosphorus content were measured. Results showed that effect of SA on all of traits was significant (P<0.01). Effect of media culture and interaction of different levels of SA and media culture on all of traits were significant (P<0.01). The highest flower stalk (43.74 cm), diameter of flower bud (20.68 mm), length of flower petiole (5.7mm), chlorophyll content (39.91), fresh weight (24.48 gr) dry weight (8.11gr), number of flower per plant (1.64), P and K content were obtained in spared plants with 3000 mg l⁻¹ SA. The highest flower stalk, diameter of stem and flower bud, length of flower petiole, chlorophyll content and K content were obtained in plants with Poultry manure+Leaf Compost. The highest diametre of stem, chlorophyll content, K content( 1.12 %dm) and P content (0.21 % dm) was obtained in interaction of 3000 mg l-1 SA and Poultry manure+Leaf Compost. Therefore, application of 3000 mg l⁻¹ SA and use of poultry manure+Leaf Compost, Leaf and use of vermicompost+ cocopeat as media culture in order to improvement of quality and quantity of rose cut flower in soilless culture is recommended.

Key words: compost, cocopeat, hydroponic greenhouse, vermicompost.
Changes in carbohydrate metabolism in incurved malformed flowers of fragrant cut rose variety ‘Yves Piaget’

Kaneeda, R*a, H. Ikeurab, T. Aiharac and T. Handad

*a Graduate School of Agriculture, Meiji University, Kawasaki, 214-8571, Japan
b Organization for the Strategic Coordination of Research and Intellectual Properties, Meiji University, Kawasaki, 214-8571, Japan
c Kanagawa Agricultural Technology Center, Hiratsuka, 259-1204, Japan
d School of Agriculture, Meiji University, Kawasaki, 214-8571, Japan

E-mail: *ef1012867@gmail.com

Session: Rose physiology

*Rosa ×hybrida* ‘Yves Piaget’ is a fragrant cut rose variety that sometimes bears malformed flowers known as ‘incurved flowering’. This ‘incurved flowering’ is characterized by adaxial curving of the petals, which decreases emissions of volatile compounds. In this study, we compared fresh/dry weight, levels of soluble carbohydrates and invertase activity, in both normal and malformed flowers. The flowers were harvested at five different flowering stages: stage 1: tight bud, stage 1A: mature bud, stage 1B: two opened petals, stage 2: five opened petals, and stage 3: ten opened petals. All the petals were removed from the flowers and their fresh weight was measured. The five outer petals and two upper leaves were used to analyse carbohydrate content and invertase activity.

The fresh weights and carbohydrate contents of malformed flower petals were higher than those of normal flowers by stage 2, but there were no significant difference by stage 3. Also, at stage 1A, the malformed flower petals showed had greater vacuolar invertase activity than normal flower petals. However, the malformed flower petals had weaker petal cell-wall invertase activity than normal flower petals at stage 2. In addition, the malformed flowers had lower leaf carbohydrate contents at this stage.

It is thought that rising carbohydrate levels in petal cells cause increases in osmotic pressure that would have enabled rapid water flow into the petal cells. However, water could not flow into the immature cells at the edges of the petals and this would have caused the adaxial curving of the petals. In addition, the malformed flowers had low leaf sugar contents, low petal cell-wall invertase activity, and little sugar supply to the flowers. As a result, it is thought that the petals of the malformed flowers could not complete their development due to insufficient carbohydrate at stage 3.
Evaluation of the ethylene effect on display quality and expression of some senescence related enzymes in potted Miniature rose

Azam Ranjbar, Nima Ahmadi*

Department of Horticultural Sciences, Tarbiat Modares University, Tehran, Iran

(*Corresponding Author Email: ahmadin@modares.ac.ir)

To investigate the effects of exogenously application of ethylene postharvest quality and expression of enzyme involved in leaf abscission, this research was conducted in a completely randomized experimental designs with three replications and three levels of ethylene treatment. Whole plants of potted Miniature rose cv. "Sanaz-e-Zard" were exposed to 0, 5 and 10 µLL-1 of concentration of ethylene for 12 hours in sealed glass aquarium container. Results showed that treatment of ethylene had significant effects on the physiological and biochemical characteristics of "Sanaz-e-Zard", including percentage of Leaf abscission, the activity of antioxidant enzymes, activity of laccase and MDA content. The higher abscission and activity of laccase was observed in 10 µLL-1 ethylene which was significantly (P <0.01) higher than control, while the lowest activity of peroxidase was found in plants which received 10 µL L-1 ethylene. In other side, increasing peroxidation rate of membrane lipids and the highest amount of MDA was appeared under 10 µL L-1 ethylene treatment. It seems that when the plant is exposed to oxidative stress, antioxidant enzymes have the potential ability to induce the immune system, encountering adversity condition. But when the response of the plant cells to stressful situation is insufficient, commitment to death happens.

Key words: Abscission, Antioxidant enzymes, Chlorophyll, Laccase, Peroxidase
Scientific collaboration to solve some ‘thorny’ problems?

Richard K.A. Boyle*\(^a\), Colum Donnelly\(^a\)

\(^a\)MM Flowers Limited, Ronald House, Fenton Way, Chatteris, PE16 6UP

*richard.boyle@mmflowers.co.uk

Session: Rose Physiology

MM Flowers (part of the AMC Group) has grown into the UK’s leading, integrated cut-flower business. MM is co-owned by two of the world’s leading cut rose growing operations; Elite and VP. Elite is the largest cut rose grower in South America with over 400ha of rose production across Colombia and Ecuador. Elite also represent Rosen Tantau, one of the oldest and largest breeders of roses worldwide. VP are the leading producer of cut roses in East Africa, with geographically diverse farms in Kenya and Ethiopia (highlands and lowland), producing intermediate, spray and T-hybrids across 250 ha’s. VP has made significant investments in rose breeding and are beginning to commercialise their first crossings from 2012. Both companies are dedicated rose specialists, controlling all aspects from breeding, through propagation to post-harvest treatments (PHT), processing and freight. Each discipline is developed to ensure that a robust, consistent product is delivered to consumers globally. With the collaboration of these stakeholders, MM is able to deliver truly innovative solutions to many of challenges facing the international rose industry.

One area of interest for the industry is the use of PHT, traditionally used to extend cut rose vase life. An example of research undertaken by MM is an investigation into the role of different transit/store treatments (TT) and vase water treatments (VT) on the vase life of *Rosa hybrida* ‘Topsun’. Flowers were transported from Kenya to the UK and simulated through a normal supply chain (depot, store and consumer phase). Roses were tested in bunches of 15 stems according to commercial specifications. Two TT and three VT including water as a control were tested in the UK in a full factorial design. All flowers were assessed daily, with the day and reasons for failure recorded until 50% of the stems had failed. Vase life of the cultivar ‘Topsun’ was significantly different between the TT regardless of the VT, with an average increase of one day. In contrast, differences in vase life between VT within a TT group were minimal. These results suggest that depending upon the cultivar, origin and supply chain, PHTs may have to be utilised in novel ways to maximise performance. Additional work is required to better understand this across multiple cultivars, along with further investigations into the response of the cultivar ‘Topsun’ from a physiological and molecular perspective.

In order to successfully undertake and solve challenges such as those highlighted above, MM requires participation from all interested and able parties, from agronomists to academics. Industry-academic linked research is becoming essential, not only to allow knowledge and skill transfer, but to ensure that the work is driven towards commercial application.
Effects of Some Antimicrobial Compounds on the Vase Life of Cut Rose Flower

Soner KAZAZ\textsuperscript{a}\textsuperscript{*} Selma TUNA\textsuperscript{b} Yasin TUNCER\textsuperscript{c}

\textsuperscript{a}Department of Horticulture, Faculty of Agriculture, Ankara University, Ankara, Turkey
\textsuperscript{b}Mudurnu Süreyya Astarcı Vocational School, Abant İzzet Baysal University, Bolu, Turkey
\textsuperscript{c}Department of Food Engineering, Faculty of Engineering, Süleyman Demirel University, Isparta, Turkey

\textsuperscript{*}Corresponding author: skazaz@ankara.edu.tr

Session: Rose physiology

Abstract

The vase life of cut rose flowers is usually short due to vascular occlusion. The effects of some antimicrobial compounds on the vase life of \textit{Rosa hybrida} cv. Cherry Brandy were investigated in the study. The solutions of thyme oil, thymol and carvacrol at the concentrations of 50, 100, 150 mg L\textsuperscript{-1} and 8-hydroxyquinoline [8-HQ] at 200 mg L\textsuperscript{-1} with and without 4\% sucrose were used as the vase life solutions. Distilled water was used as the control. Vase life, relative fresh weight, vase solution uptake and the number of bacteria in the vase life solution were determined. The longest vase life was obtained from 100 mg L\textsuperscript{-1} of thymol plus 4\% sucrose (16.50 days), while the shortest vase life was obtained from the control treatment (11.0 days).

In the study, quite successful results were obtained from sucrose-containing thymol (100 and 150 mg L\textsuperscript{-1}), carvacrol (150 mg L\textsuperscript{-1}) and 8-HQ compounds to increase the vase life of the flowers.

\textbf{Key Words:} Cut rose, vase life, bacterium, sucrose, thymol, carvacrol, 8-HQ
Effects of Different Rootstocks on the Yield and Quality of Some Cut Rose Varieties propagated by Stenting

Soner KAZAZ\textsuperscript{a*} 
Serhan IŞIKAN\textsuperscript{b}

\textsuperscript{a}Department of Horticulture, Faculty of Agriculture, Ankara University, Ankara, Turkey 
\textsuperscript{b}Atılım Yapı Taahhüt ve Havacılık A.Ş., Şanlıurfa, Turkey
\textsuperscript{*C}orresponding author: skazaz@ankara.edu.tr

Session: Rose physiology

Abstract

Stenting is an efficient technique of propagation which is commonly used worldwide by cut rose growers and which has many advantages. The study was conducted to investigate the effects of 3 different rootstocks (Natal Briar, \textit{Rosa indica} ‘Major’, and \textit{Rosa multiflora}) on the yield and quality of hybrid cut rose cultivars (\textit{Rosa hybrida} L. cv. Samourai, Dolomite, and Kalinka) propagated by the stenting grafting technique. The highest number of stems produced per plant was determined as 19.75 and 22.22 in the plants grafted onto Natal Briar rootstock in ‘Samourai’ and ‘Dolomite’, respectively but as 20 in the plants grafted onto \textit{Rosa indica} ‘Major’ rootstock in ‘Kalinka’. In all of the varieties, both the longest stems [Samourai (71.25 cm), Dolomite (63.20 cm), and Kalinka (60.78 cm)] and the longest buds [Samourai (5.31 cm), Dolomite (5.65 cm), and Kalinka (5.88 cm)] were obtained from the plants grafted onto Natal Briar rootstock.

The results revealed that the most effective rootstock in terms of many parameters in varieties ‘Samourai’, ‘Dolomite’, and ‘Kalinka’ was Natal Briar.

**Key words:** Cut rose, stenting, rootstock, yield, quality
Asparagine and sugars are both required to trigger bud outgrowth and secondary axis elongation in *Rosa hybrida*

Marie-Anne Le Moigne, Vincent Guérin, Alain Vian, Jérémy Lothier.

IRHS, Agrocampus-Ouest, INRA, Université d’Angers, SFR 4207 QuaSaV, 49071, Beaucouzé, France

marie-anne.lemoigne@etud.univ-angers.fr

Nitrogen is required for optimal plant growth, especially in young organs such as secondary axes after axillary bud outgrowth. Several studies have shown an increase of nitrogen concentration in xylem sap concomitantly with bud outgrowth, but the relation between nitrogen, sugars and growth regulators in secondary axes still remains unclear.

We investigated in *Rosa hybrida* the involvement of nitrogen in bud outgrowth in relation with sugars and growth regulators by quantifying nitrogen fluxes (using $^{15}$N-labeled nitrate), sugars, amino acids and growth regulators. Besides, we measured the effect of the exogenous supply of these compounds on bud outgrowth using *in vitro* excised bud culture. We also measured growth regulator-related gene expression (using Real Time quantitative PCR).

We demonstrated that nitrogen in the secondary axis comes mainly from current uptake after beheading. Asparagine, which concentration increases in sap exudates and tissues during axis elongation, was the sole amino acid able to initiate an efficient elongation *in vitro* when supplied in combination with sucrose, through the stimulation of cytokinin biosynthesis and the inhibition of strigolactone signalling.

Taken together, these results show that the simultaneous presence of asparagin and sucrose is required to initiate axis elongation. Asparagine may also be considered as a signalling molecule in addition to its nutrition function.

**Keys words:** amino acids, asparagine, axis elongation, bud outgrowth, nitrogen, rose, sucrose.
Session 4
Rose genomics
The rose genome sequencing initiative.


The Rose Genome Sequencing Initiative

¹ INRA, IRHS, Angers, France ² Agrocampus Ouest, IRHS, Angers, France ³ University of St Etienne, BvPAM, St Etienne, France ⁴ Plant Breeding, Wageningen University & Research, The Netherlands ⁵ Leibniz University Hannover, Germany ⁶ ILVO-Plant, Belgium ⁷ Bioscience, Wageningen University & Research, The Netherlands ⁸ IFAPA, Málaga, Spain ⁹ T. Millán, University of Córdoba, Spain ¹⁰ Hebrew University of Jerusalem, Israël ¹¹ SLU Alnarp, Sweden ¹² AgroBioInstitute and Joint Genomic Centre, Bulgaria ¹³ University of Minnesota, USA ¹⁴ Texas A&M University, USA ¹⁵ Montreal Botanical Garden, Canada ¹⁶ Nagoya University, Japan ¹⁷ Chubu University, Japan ¹⁸ Yunnan Academy of Agricultural Sciences, Kunming, China ¹⁹ Chinese Academy of Agricultural Science, Beijing, China ²⁰ Huazhong Agricultural University, Wuhan, China ²¹ Université Aix Marseille, Marseille, France ²² CEA, Genoscope-CNS, Evry, France ²³ INRA, URGI, Versailles, France ²⁴ INRA, LIPM, Toulouse, France ²⁵ IPS2-Université Paris-Sud Orsay France, ²⁶ GDEC-INRA Clermont-Ferrand France, ²⁷ INRA-ENS, RDP, Lyon, France

For correspondence: mohammed.bendahmane@ens-lyon.fr, Jerome.Gouzy@toulouse.inra.fr, fabrice.foucher@inra.fr

Session: Rose genomics

Rose, genus Rosa, is the largest ornamental plant cultivated worldwide (accounting for around 30% of the market), in the form of garden roses, cut roses and potted plants. Rose is a suitable to become a plant model plant for woody ornamental plants in order to study important ornamental traits, such as seasonal blooming, flower or thorn development, plant shape and scent emission. To decipher these developmental and biochemical processes and also to understand rose domestication and selection, genomic approaches have to be developed, including a genome reference sequence. For this, the high level of heterozygosity is a complicating issue.

In the framework of an international initiative (Rose Genome Sequencing Initiative), coordinated by INRA, we aim to produce a high quality genome sequence of rose, based on the old diploid Chinese variety, *R. chinensis* ‘Old Blush’. This genotype is highly heterozygous. A first version of the genome of this variety has been obtained and consists of 16,000 scaffolds, with a N50 of 226kb. In order to tackle the heterozygosity challenge and to increase the quality of the sequence, we have implemented two additional strategies: development of a high-density genetic map to anchor the genome and development and sequencing of a haploid of ‘Old Blush’. Using an F1 progeny (151 individuals) from a cross between ‘Old Blush’ and *R. x wichurana*, a genetic map based on SNP markers has been developed (using the 68k rose Axiom Array). The female and male maps contain 5635 and 2331 SNP markers on 7 linkage groups with a size of 482 and 474 cM respectively (1.15 and 0.9 SNP markers/cM). In the mean time, a haploid of ‘Old Blush’ has been obtained and sequenced. The sequence of the haploid is being anchored to the genetic map to obtain the pseudo-molecules. The recent advances and the perspectives of this project will be presented.
Genome structure of *Rosa multiflora*, an ancestral wild rose of cultivated roses

Noriko Nakamura\(^a\), Hideki Hirakawa\(^b\), Shusei Sato\(^c\), Shungo Otagaki\(^d\), Shogo Matsumoto\(^d\), Satoshi Tabata\(^b\), Yoshikazu Tanaka*\(^a\)

\(^a\)Suntory Global Innovation Center Ltd., Soraku-gun, Kyoto 619-0284, Japan
\(^b\)Kazusa DNA Research Institute, Kisarazu, Chiba 292-0818, Japan
\(^c\)Graduate School of Life Sciences, Tohoku University, Aoba-ku, Sendai 980-8577, Japan
\(^d\)Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya 464-8601, Japan
* Yoshikazu_Tanaka@suntory.co.jp

Session: Rose genomics

The draft genome sequence of a wild rose (*Rosa multiflora* Thnub.) was determined by using Illumina MiSeq and HiSeq sequencers. Total length of the scaffolds was 739,637,845 bp, consisting of 83,189 scaffolds, which was close to 711 Mbp length estimated by k-mer analysis. N50 length of the scaffolds was 90,830 bp, and length of the longest scaffold was 1,133,259 bp. The average GC content of the scaffolds was 38.9%. After gene prediction, 67,380 genes having similarity against known genes and domains were extracted, which included complete and partial gene structures. According to the CEGMA analysis, 98% of the core eukaryotic genes were conserved in the scaffolds.

Genes involved in ornamentally important traits including flower color, scent, floral morphology, flowering, senescence and disease resistance were assigned. Clusters of glucosyltransferase, cytochrome P450 and disease resistance genes probably caused by gene duplication were observed in the genome. The results of this study will serve as a valuable resource for fundamental and applied research of rose, especially for rose breeding and genomic analysis of evolution of cultivated roses and related species.
The draft genome of *Rosa gigantea*

Shubin Li\(^{a,b,c}\), Siqin Wang\(^{a,*}\), Ningning Zhou\(^{b,c}\), Huang He\(^{a}\), Kaixue Tang\(^{b,c}\) and Silan Dai\(^{a,*}\)

\(^a\) College of Landscape Architecture, Beijing Forestry University, Beijing 100083, China
\(^b\) Flower Research Institute, Yunnan Academy of Agricultural Sciences, Kunming 650205, China
\(^c\) National Engineering Research Center for Ornamental Horticulture, Kunming 650205, China

**Key words**  Roses, Genome sequencing, *Rosa gigantea*, Floral genes

*Rosa gigantea* Coll. ex Crep is an important resource in *Rosa* genus, which had contributed the tea scent to modern rose breeding, as well as famous due to large flower size and early blooming in late winter. However, the genetic architecture of this diploid species is poorly investigated. In this study we employed a combination sequence strategy (Illumina shotgun sequence and PacBio single-molecule sequence) based on different DNA fragment size libraries to clarify the genome structure of *Rosa gigantea*. As a preliminary result, this batch of sequencing produced 336.46M raw reads. After low quality reads filtering, 315.46M reads (94.64 Gb) were used for further analysis. Total 173909 scaffold were assembled include 437872976 base pairs of the genome. The max length of scaffolds is 91995 base pairs and the N50 length of scaffolds is 4764 base pairs. GC content of contigs and scaffolds were analyzed, the peak of curves is GC content of the genome and the value is 38.93%. Genome size of *Rosa gigantea* is 548.26 Mbp, and the heterozygous ratio is 0.93%.

In addition, the result of single-molecule sequence assembly of *Rosa gigantea* and annotated floral genes will be presented in the Symposium.

* E-mail: silandai@sina.com
+ These authors contributed equally to this work.
Transcriptome of the floral transition in
*Rosa chinensis* ‘Old Blush’

Xuelian Guo¹, Le Luo¹, Chao Yu, Huitang Pan, Qixiang Zhang*

*Beijing Key Laboratory of Ornamental Plants Germplasm Innovation & Molecular Breeding, National Engineering Research Center for Floriculture, Beijing Laboratory of Urban and Rural Ecological Environment, Key Laboratory of Genetics and Breeding in Forest Trees and Ornamental Plants of Ministry of Education, School of Landscape Architecture, Beijing Forestry University, Beijing, 100083, China.*

Corresponding author: zqxbjfu@126.com

Session: Rose Genomics

The floral transition plays a vital role in the life of ornamental plants. Despite progress in model plants, the molecular mechanisms of flowering regulation remain unknown in perennial plants. *Rosa chinensis* ‘Old Blush’ is a unique plant that can flower continuously year-round. In this study, gene expression profiles associated with the flowering transition were comprehensively analyzed during floral transition in the rose, with cooperation of phenotypic characterization and physiological changes. 1,637 differentially expressed genes (DEGs) were identified, among which 32 unigenes were involved in the circadian clock, sugar metabolism, hormone, and autonomous pathways. Hormone contents and the expression of biosynthesis and metabolism genes fluctuated during the rose floral transition process. Gibberellins (GAs) inhibited the rose floral transition, the content of GAs gradually decreased and GA2ox and SCL13 were upregulated from vegetative (VM) meristem to floral meristem (FM). Auxin plays an affirmative part in mediating floral transition, auxin content and auxin-related gene expression levels were gradually upregulated during the floral transition of the rose. However, ABA content and the expression of ABA pathway genes were gradually downregulated, suggesting that ABA passively regulates the rose floral transition. Furthermore, sugar content and the expression of sugar metabolism genes increased during floral transition in the rose, which may be a further florigenic signal that activates floral transition. Additionally, FRI, FY, DRM1, ELIP, COP1, CO, and COL16 are involved in the circadian clock and autonomous pathway, respectively, and they play a positively promoting role in regulating floral transition. Overall, physiological changes associated with genes involved in the circadian clock or autonomous pathway collectively regulated the rose floral transition. Our results summarize a valuable collective of gene expression profiles characterizing the rose floral transition. The DEGs are candidates for functional analyses of genes affecting the floral transition in the rose, which is a precious resource that reveals the molecular mechanism of mediating floral transition in other perennial plants.

Keywords: Floral transition, Circadian clock, Sugar signaling, Hormone signaling, Recurrent flowering, Differentially expressed genes
A genotype-driven comparative informatics approach to discover useful disease resistance genes for rose improvement

Leon Van Eck\textsuperscript{a}, Peng Zhou\textsuperscript{b}, Kevin Silverstein\textsuperscript{c}, James Bradeen\textsuperscript{*a}

\textsuperscript{a} Department of Plant Pathology and Stakman—Borlaug Center for Sustainable Plant Health, University of Minnesota, St. Paul, MN 55108 USA
\textsuperscript{b} Department of Plant & Microbial Biology, University of Minnesota, St. Paul, MN 55108 USA
\textsuperscript{c} Minnesota Supercomputing Institute, University of Minnesota, St. Paul, MN 55108 USA
\textsuperscript{*} jbradeen@umn.edu

Session: Rose genomics

Roses are hosts to several diseases including black spot (caused by \textit{Diplocarpon rosae} Wolf) and creation of disease resistant cultivars is an important breeding goal. Identifying effective genes for disease resistance is a challenge in many crops, requiring resource intensive phenotyping followed by molecular mapping, tagging, and (in some cases) cloning. Across plant species and pathogen types, the NB-LRR superfamily of genes has been repeatedly implicated in detection and response to pathogens, yielding a resistance phenotype. While NB-LRR genes can be identified from DNA sequence it is impossible to associate a specific NB-LRR gene with a cognate pathogen species or race based on sequence alone. Working in the Rosaceae, we have developed a robust, semi-automated informatics pipeline to identify NB-LRR gene sequences from whole genome sequences and interpret evolutionary patterns across multiple species within the family. We’ve applied our comparative approach to 12 Rosaceous genomes including those of apple, pear, peach, strawberry, and several related species. Our analyses reveal 9 dominant NB-LRR gene lineages. With few exceptions, each lineage is present in each species, suggesting an ancient origin. While most NB-LRR lineages are found in each Rosaceous species, species differ profoundly in terms of allelic diversity within each lineage. The patterns of allelic diversification across species can be leveraged to develop hypotheses of gene function. Using apple scab resistance as a model, we demonstrate that agriculturally important disease resistance alleles are overrepresented in expanded, species-specific, and highly diversified allelic clades. This observation provides an informatics approach to mine genebank collections for useful disease resistance alleles. We propose that genotypic survey of genebank collections and comparative interpretation of patterns of allelic diversification followed by phenotypic survey of genotypes with novel alleles at target loci will accelerate discovery of useful alleles in a resource-efficient manner. Applied to rose, our approach could be leveraged to discover new black spot resistance alleles for breeding purposes. The potentials and challenges of this approach will be discussed.
The development of a dense SNP-based consensus map and QTL detection for black spot resistance in three diploid rose populations

Muqing Yan\textsuperscript{a}, Qianni Dong\textsuperscript{a}, David Byrne\textsuperscript{a}, Patricia Klein\textsuperscript{a}

\textsuperscript{a}Department of Horticultural Sciences, Texas A&M University, College Station, TX 77843

*pklein@tamu.edu

Black spot (BS) disease (\textit{Diplocarpon rosae} (Lib.) Wolf) of rose is the most important leaf disease of garden roses in warm humid areas. Although partial (horizontal) resistance to black spot has been shown to be moderately heritable, the responsible quantitative trait loci (QTL) remain unidentified. Because of the interspecific nature and high heterozygosity in commercial roses the genetic and genomic resources available for rose is limited. We utilized genotyping by sequencing (GBS) technology to discover SNP markers for construction of a high density genetic map for use in QTL discovery. GBS was performed using the methylation sensitive restriction enzyme \textit{NgoMIV} (G\textsubscript{v}C CGGC) to construct DNA template from three diploid rose populations segregating for resistance (derived from \textit{Rosa wichuriana}) to the black spot fungus. DNA template was pooled and sequenced on an Illumina Hiseq2500 platform using a single-end sequencing strategy. The 113 bp trimmed sequenced reads were mapped to the strawberry genome sequence and SNPs identified using the CLC Genomics Workbench. After filtering for informative polymorphisms, \textasciitilde 3500 SNPs were used for the development of a consensus linkage map. Initially maps were created for each individual population with \textasciitilde 1500 markers/map. A total of 677 SNPs were polymorphic across all three populations which were used to link the individual maps into the consensus map. Fourteen SSRs were put on the map to identify each of the seven rose linkage groups. The final consensus map contained a total of 3,527 markers across the 7 rose linkage groups with a total map length of 892.2\text{cM}. The average distance between markers was 0.25\text{cM}. This is the first report of a high-density integrated consensus map for diploid roses (ICD). Analysis of partial (horizontal) resistance to black spot as measured in a detached leaf assay among the diploid populations identified important QTLs for black spot resistance on several rose chromosomes.
Association studies in roses reveal robust markers for flower traits

Dietmar Schulz¹, Marcus Linde¹, Thomas Debener¹
Leibniz Universität Hannover, Institute for Plant Genetics, Hannover, Germany
debener@genetik.uni-hannover.de

Floral traits are the most important characteristics that determine the ornamental value of cultivated roses. A number of studies have been conducted on qualitative and quantitative factors influencing floral traits but almost all of these studies were based on biparental populations. Therefore, a general application of some of these markers linked to single genes or QTLs to broader germplasm collections still need verification. Here we present data on markers generated through an association study in a set of 96 diverse rose genotypes for flower colour, petal number, petal size and scent and the verification of some of these markers in sets of independent populations. Our data indicate that some marker trait associations are useful beyond our initial population and that these loci can provide information on putative candidate genes underlying these traits.
Preliminary Study on Molecular Mechanism of Phyllody Phenotype in *Rosa chinensis* cv. Viridiflora

Huijun Yan¹, Hao Zhang¹, Min Chen¹, Hongying Jian¹, Xianqin Qiu¹, Qigang Wang¹, Mohammed Bendahmane²* and Kaixue Tang¹*

¹Flower Research Institute of Yunnan Academy of Agricultural Sciences, Kunming, China,
²Laboratoire de Reproduction et Développement des Plantes, Université de Lyon, ENS de Lyon, UCB Lyon 1, CNRS, INRA, Lyon, France,

*mohammed.bendahmane@ens-lyon.fr; kxtang@hotmail.com

Session: Rose physiology

Chinese old roses have high ornamental, cultural, economic values, and represent an important rose germplasms resource. Among Chinese old rose species, the recurrent blooming *Rosa chinensis* was used in many breeding programs to select for the most advantageous traits such as recurrent blooming, scent. *R. chinensis* cv. Viridiflora is a rose cultivar, commonly known as the ‘green rose’, in which petals, stamens and pistils are converted into leaf-like organs. This phenomenon is known as phyllody.

In this study, we addressed the cause of phyllody phenotype in the rose Viridiflora. We show that phyllody phenotype in Viridiflora is not caused by Mycoplasma like organism (MLO) infection that is different from phyllody-like phenotype of other plants. To identify the molecular basis of the malformed flowers in Viridiflora, we used a transcriptomic approach to compare gene expression in flowers of *R. chinensis* cv. Old Blush and Viridiflora. A part from the phyllody phenotype, no other phenotypic differences were observed between Old Blush and Viridiflora. Our study identified that the phyllody in Viridiflora is associated with misexpression of the putative homologues of the flowering integrator *RcSOC1* and of ABCE flower organ identity genes *RcAP1, RcAP2, RcPI, RcAG*, and *RcSEP3*. Furthermore, we found some miRNAs were involved in phyllody of Viridiflora by qPCR, especially, mi172, miRNA159 and miR167. We will further research the role of miRNAs regulating the target genes.
**Bent-neck in roses - understanding the underlying causes**

B.G.A. Lear *, A.M. Marchbank b, N.A. Kent b, R. Crompton c, T.J. Wheeler c, H.J. Rogers b, A.D. Stead a

* School of Biological Sciences, Royal Holloway, University of London, Egham, UK, TW20 0EX  
b School of Biosciences, Cardiff University, Cardiff, UK, CF10 3AT  
c Flamingo Flowers Ltd., Sandy, UK, SG19 2AJ  
*Bianca.Lear.2015@live.rhul.ac.uk

Roses are a highly valuable product for the cut flower industry, with 80% of all bouquets sold in the UK containing one or more rose stems. However, ‘bent-neck’ or ‘necking’ remains a primary cause of reduced vase life for roses; a phenomenon in which the flower head droops due to a bending of the pedicle, resulting in premature death. Bent-neck is widely thought to be a symptom of water stress; either caused by an air embolism or bacterial blockage of the xylem, preventing water uptake. However, it is not known what is happening in rose tissues at the time of necking at a biochemical and molecular level.

The present project has taken pedicle samples of *Rosa x hybrida* cultivar ‘H30’ at three stages of necking (straight, <90 degrees and >90 degrees) and extracted RNA to produce RNAseq data. Due to the high amounts of polyphenols and polysaccharides present in the plant material, a modified CTAB method adapted for woody plants was found to be the best method for the isolation of pure, high quality RNA. To date >200M reads have been obtained and the analysis of these data will be presented. As there is considerable variation in the occurrence of necking amongst rose cultivars, an understanding of the molecular dissimilarities between the cultivars could lead to the breeding of plants resistant or with a low frequency of bent-neck.
Sequence and copy number variation of Ty1/copia retrotransposon RoRE1 in the rose genome

Shungo Otagaki*, Takeshi Nakaoa, Hibrand-Saint Oyantb, Fabrice Foucherb,
Shogo Matsumotoa, Koji Kawamurac

a Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya, 464-8601, Japan
b INRA, UMR1345 Institut de Recherche en Horticulture et Semences, Beaucouzé, France
c Department of Environmental Engineering, Osaka Institute of Technology (OIT), Asahi-ku, Osaka, 535-8585, Japan
* sotagaki@agr.nagoya-u.ac.jp

Session: Rose genomics

Research objective: Modern rose cultivars exhibit a continuous-flowering behavior due to the repression of the expression of flowering repressor gene RoKSN. In most modern roses, this repression is caused by the insertion of the Ty1/copia retrotransposon RoRE1 into the second intron of RoKSN. This result suggests that RoRE1 has a potential to retrotranspose into genic regions and could be used as an insertional mutagen for producing transposon-tagged lines in rose. In the present study, we conducted following three analyses to examine this hypothesis: (i) characterization of the RoRE1 copies present in rose genome; (ii) Estimation of the RoRE1 insertion sites in rose genome; (iii) RoRE1 copy number analysis in rose by southern blotting.

Materials and methods: Full length sequence of RoRE1 was isolated from the progeny of the F1 mapping population FW (Kawamura et al., 2011). BLAST search against the R. multiflora genome (Nakamura et al., unpublished data) was carried out using an open reading frame (ORF) of RoRE1 as a query. Flanking sequences of RoRE1 were obtained from FW by Sequence-Specific Amplification Polymorphism (S-SAP) marker and blasted against the R. multiflora genome. For southern blotting, genome DNA was extracted from the leaf of 14 rose species/cultivars and hybridized with labeled long terminal repeat (LTR) sequence.

Results and conclusions: Sequence analysis revealed that RoRE1 was comprised of two ORFs and all domains essential for the retrotransposition was encoded in ORF1. BLAST search identified 4 regions highly homologous to ORF1 of RoRE1 and two out of them contained 5’ and 3’ LTRs. However, these four RoRE1 copies do not retain the retrotransposition activity due to the presence of premature stop codon in ORF1, suggesting the absence of recent retrotransposition of RoRE1 in R. multiflora. Meanwhile, sequencing analysis of fragments obtained from S-SAP markers revealed that 6 out of 19 of the RoRE1 insertion sites were located at the genic region. Finally, we investigated the copy number variations of RoRE1 in 14 samples belonging to several lineages by southern blotting but failed to detect a burst of retrotransposition and estimated copy number per haplotype was between 2 and 5.5. These results suggest that RoRE1 has a potential to act as a mutagen but further screening of roses containing actively retrotransposing RoRE1 is necessary for establishing tagging lines in rose.
Development of a complete process of in vitro culture and *Agrobacterium tumefaciens*-mediated genetic transformation of Rose cultivars

Hamama L., Foucier S., Voisine L., Pierre S., Cesbron D., Jeuffre J., Bosselut J., Foucher F., Hibrand-Saint Oyant L.*

*Genetic and Diversity of Ornamentals team, Institut de Recherche en Horticulture et Semences (INRA, Agrocampus-Ouest, Université d'Angers), SFR 4207 QUASAV, BP 60057, 49071 Beaucouzé Cedex, France

laurence.hibrand-saint-oyant@angers.inra.fr, 33 (0) 241 225 755

Session: Rose genomics

Rose is one of the most important plants in the ornamental sector worldwide and is increasingly gaining importance as a major driver for research in ornamental plants. In order to study candidate genes in a functional validation process it is essential to use biotechnology methods such as regeneration tissues combined with transgenic approaches.

In Rose, we developed a complete process of clonal cycle including plant elongation, multiplication and rooting on 7 genotypes (a hybrid of *Rosa wichurana* RW, *Rosa chinensis* ‘Old Blush’ OB, ‘Félicité et Perpétue’ FP, ‘Little white Pet’ LWP, two *Rosa hybrida*: Guy Savoy® GS, Pimprenelle® P, a rootstock genotype Natal Briar NB).

Hormonal variation and carbohydrate composition (concentration and type) were investigated during clonal cycle and regeneration induction steps and we defined the best physiological state of donor-plants allowing to obtain the maximum level of regeneration. Two ways of regeneration were attempted via *de novo* shoot organogenesis (DNSO) and via indirect somatic embryogenesis from all genotypes. As well as the percentage of DNSO varied from 35% (for OB) to 87% (for NB) and we obtained between 1 embryogenic line (for NB genotype) to 15 embryogenic lines (for RW). These target tissues were used to improve an *Agrobacterium tumefaciens*-mediated genetic transformation protocol. While the DNSO were unable to regenerate after the inoculation step with *Agrobacterium tumefaciens*, several assays using embryogenic callus as target tissue have given regenerated plants. The efficiency rate varied from 0 to 12.5% of transformation events. These low transformation rates show real problems for mastering the key factors controlling regeneration and transformation in rose.

The key steps of our protocol, the strategy for practical application and the main results obtained will be presented.
Search for polymorphism in *Rosa* chloroplast genomes

Jordan Marie-Magdelaine\(^a\), Aurélie Bérard\(^b\), Annie Chastellier\(^a\), Fabrice Foucher\(^a\), Marie-Christine Le Paslier\(^b\), Alix Pernet\(^a\), Tatiana Thouroude\(^a\), Jérémy Clotault\(^a\)*

\(^a\) IRHS, Agrocampus Ouest, INRA, Université d’Angers, SFR 4207 QuaSaV, 49071, Beaucouzé, France  
\(^b\) EPGV, INRA, CEA-Institut de Génomique/CNG, 91057, Evry, France  
*jeremy.clotault@univ-angers.fr*

Session: Rose genomics

The *Rosa* genus is composed of approximately 100 to 200 shrub species, and its evolutionary history is quite complex. Despite numerous studies, relationships between species or hybrids are still badly identified. This may be explained by a fair tendency to hybridization. Moreover, polyploidy species are frequent in this genus, making genotyping difficult, and for hybrids, the direction of the cross is unknown in most cases. A solution to by-pass this last hurdle is to rely on chloroplast genome sequences, the chloroplast being a haploid organelle known for having made significant contributions to phylogenetic and genealogic studies of several plant families.

Based on these observations, we tried to question the development and the use of plastid markers for genotyping studies, through a characterization of the observed polymorphism of complete chloroplast genomes. The main idea was to be able to use these new plastid polymorphic markers in association with nuclear ones, thus taking advantage of the oriented heredity (which is often maternal in plants) to establish with more reliability relationships between *Rosa* species or pedigrees.

To do so, we made use of approximately 200 Go of *Rosa* sequencing data obtained over the last years, as well as new bioinformatics tools and methods. We assembled 9 complete chloroplast genomes and compared them with 2 other ones collected from the NCBI, thus maximizing the phylogenetic variability in this genus. We also identified highly polymorphic markers from both these 11 complete genomes and some other sequences collected from the NCBI.

Chloroplasts polymorphisms inside the *Rosa* genus will be described in terms of nature and quantity, and the inheritance pattern of the chloroplast genome in the rosebush will be determined. Looking forward, the markers we identified will be used to reconstruct rosebush pedigrees and to compare these deduced pedigrees to the kinship relations known through historic sources. Other studies could also rely on these markers to focus on the evolution of the family or on the identification of specific examples of plastid gene transfer to plant nuclear or mitochondrial genomes. Our results could then help to shed new light on the relationship between these three genomes in plants.
Genome assembly in *Rosa wichurana* using cytogenetic and sequencing tools

Kirov I.\(^a,b\), Van Laere K.\(^a\), De Keyser E.\(^a\), De Riek J.\(^a\), Leus L.\(^a*\), Van Huylenbroeck J.\(^a\), Haegeman A.\(^a\), Liu C.\(^c\) and Ruttink T.\(^a\)

\(^a\) ILVO, Plant Sciences Unit, Caritasstraat 39, 9090 Melle, Belgium

\(^b\) Russian State Agrarian University - MTAA, Listavennichnaya 5, 127550 Moscow, Russia

\(^c\) ZMBP, Universität Tübingen, Auf der Morgenstelle 32, D-72076 Tübingen, Germany

Although roses are the most important ornamentals, the genomic toolbox is currently still limited. Genome sequencing is still ongoing and no publicly available genome sequence is published yet. We initiated the reconstruction of a rose genome in the species *Rosa wichurana* (2n=2x=14; 1,13 pg/2C; 1106,23 Mbp/2C). This rose was involved in the breeding history of modern rose cultivars.

125 million 2x250 paired-end Illumina reads were assembled using Discovar. We used in situ Hi-C sequencing and Lachesis to build a genome contact-probability map in which 16771 scaffolds larger than 10 kb were ordered into 7 pseudochromosomes (~0.7 genome equivalent).

Complementary to this genomic resource, fluorescent in situ hybridization (FISH) is a valuable tool to map repetitive sequences and to integrate genome assembly with chromosomal landmarks, such as heterochromatin and (peri)centromeric regions. We located the centromeres on the pseudochromosomes using centromeric repeat signatures in the Hi-C data in combination with highly sensitive Tyramide-FISH. In addition, 18 single-copy Tyramide-FISH probes were used on pachytene chromosomes to examine the physical order of genes on chromosome 7 and to validate the Hi-C based scaffold order. The collinearity between the global gene order in *Fragaria vesca* and *Rosa wichurana* was determined to investigate the degree of synteny and to identify chromosomal rearrangements.

Furthermore, ongoing work will be discussed involving a GBS-based genetic map, RNA-seq data and additional long-read PacBio sequencing to obtain a high-quality genome assembly and to have more molecular tools available for rose breeding purposes.
Molecular dissection of important traits in roses

Micai Zhong1#, Shubin Li2#, Xue Dong1#, Xiaodong Jiang1, Dongmin Jin1, Kaixue Tang2, Jin-Yong Hu1*

1. Group of Plant Molecular Genetics and Adaptation, Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences. Lanhei Road 132, Heilongtan, Kunming 650201, Yunnan Province, P.R.China. 2. Flower Research Institute, Yunnan Academic of Agriculture Sciences, Kunming 650201, Yunnan Province, P.R.China.

* For correspondence: hujinyyong@mail.kib.ac.cn;
# These authors contributed equally to this work.

Session: Rose genomics

Roses, as one of the most popular ornamental plants, have great economical and biological values. The domestication of cultivated roses mainly involves hybridization among different species of the plants in Rosa, while the Chinese rose like *R. chinensis* contributes many key traits including perpetual flowering, scent, color, and so on. However, molecular mechanisms underlying the genetic control of key traits for roses remain illusive. Here, we will report our efforts in dissecting the transcriptome diversity in roses to clarify the fluctuation of gene expression following developmental stages. Combining the published and newly sequenced dataset, we assembled a high quality reference transcriptome for *R. chinensis* and *R. wichuriana* and applied this reference to distinguish the expression divergence between species which featuring contrasting morphological characters. We detected a strong bias with plant hormone signaling, photoperiodic, splicing machinery and several other pathways in gene expression between these two species. We expect our trials to shed light on the understanding and improving the biodiversity of roses.
Session 5
Abiotic stress
Salt tolerance in garden roses

Genhua Niu and Youping Sun

Texas A&M AgriLife Research Center at El Paso, Texas A&M University System, 1380 A&M Circle, El Paso, TX 79927, USA
gniui@ag.tamu.edu

Session: Abiotic stress

Soil salinity is one of the major abiotic stresses negatively affecting plant growth and development. Global constraints on fresh water supplies and urban population growth have intensified the interest of using alternative waters such as treated municipal wastewater for irrigating landscapes. In addition, there are agricultural and industrial waste waters that can be potentially used for irrigation. All these alternative waters contain relatively high levels of salts, which could cause salt damage on sensitive plant species. Although quantitative information on crop salt tolerance exist for many agronomic crops, limited information is available for horticultural crops. Garden rose (Rosa spp.) is one of the most economically important and popular ornamental crops planted in many private and public landscapes in the world. Rose has been traditionally categorized as a salt-sensitive species. However, our research on salt tolerance of various cultivars of garden roses has showed promising results in finding moderately salt tolerant rose cultivars. In this review, some general information is presented on how salinity affects plant growth and development and how to quantify the salinity stress during the study and plant responses to salinity, including visual quality, growth, and physiological responses of garden roses.
Light targets cytokinins as early signaling vectors to control bud outgrowth in Rose

Hanaé ROMAN\textsuperscript{a}, Tiffanie GIRAULT\textsuperscript{a}, François BARBIER\textsuperscript{a}, Thomas PERON\textsuperscript{a}, Nathalie BROUARD\textsuperscript{a}, Ales PENCÍK\textsuperscript{b}, Ondřej NOVACK\textsuperscript{b}, Alain VIAN\textsuperscript{a}, Soulaïmane SAKR\textsuperscript{a}, Jérémy LOTHIER\textsuperscript{a}, José LE GOURRIEREC\textsuperscript{a} and Nathalie LEDUC\textsuperscript{a}

\textsuperscript{a} IRHS, Université d’Angers, Agrocampus-Ouest, INRA, SFR 4207 QuaSaV, 49071, Beaucouzé, France

\textsuperscript{b} Laboratory of Growth Regulators and Department of Chemical Biology and Genetics, Palacký University and Institute of Experimental Botany, Academy of Sciences of the Czech Republic, CZ-78371 Olomouc, Czech Republic

* Nathalie.Leduc@univ-angers.fr

Session: Abiotic stress

Branching determines the final shape of plants, which influences adaptation, survival and for crop plants such as Rose, important characters such as flower yield, visual quality and disease resistance. Branching results from several successive processes: axillary bud formation, dormancy induction and release then bud outgrowth. This last phase itself involves extension of bud preformed leaves and of their internode outside bud scales and initiation of new leaf primordia by the shoot apical meristem. Environmental factors finely control the activity-dormancy cycle of buds and shoot growth. Among these factors, light environment significantly impacts branching in numerous species (Huché-Thélier et al., 2016, Demotes-Mainard et al., 2016). Yet, the molecular basis of the perception and transduction of the light signal within buds is poorly understood (Leduc et al., 2014). Rose (Rosa hybrida) exhibits a strong inhibition of bud outgrowth in the absence of light and reveals therefore an excellent plant model for the study of light control over branching (Girault et al., 2008). Our research in this species has allowed identifying the site of perception of the light signal involved in the triggering of bud outgrowth as well as major molecular targets of light, among them hormones and sugars (Girault et al., 2008, 2010; Henry et al., 2011, Rabot et al., 2012, 2014; Choubane et al., 2012, Djennane et al., 2014.). In particular, recent results (Roman et al., 2016; 2017) reveal that cytokinins are initial targets of the light signal perceived by buds and that photo-regulation of these hormones plays a pivotal role in the control of major molecular mechanisms of bud outgrowth (sugar sink strength, xylem sap flux, auxin synthesis and transport, strigolactone signalling, cell division and expansion). A model showing interactions between light, cytokinins and other molecular actors during bud outgrowth will be presented.


Evaluating landscape rose performance on reduced irrigation

Karrie Reid*, Lorence Okib, and Jared Sisnerozc

aUniv. of California Cooperative Extension, 2101 E. Earhart Ave., Stockton, CA 95206 USA
bUniversity of California Cooperative Extension, 1 Shields Ave. Davis, CA 95616 USA
cUniversity of California Davis, Dept. of Plant Sciences, 1 Shields Ave., Davis, CA 95616 USA
*skreid@ucanr.edu

Session: Abiotic stress

Water conservation has become an increasingly important issue in urban landscapes, particularly in summer-dry climate regions where irrigation must be applied to keep plants healthy. Part of the strategy for reducing landscape water use is incorporating plants with low water needs into the design. Because of this, both growers and landscapers need information on an expanding number of attractive and available plants that can perform acceptably in the landscape on low water, but research-based plant water-use information is often unavailable, especially on new introductions. Since 2005, University of California researchers have performed trials to evaluate in-ground landscape plant performance on various levels of irrigation. Included in these trials have been plants already in the trade and new introductions from growers and breeders. Between 2009 and 2016, ten Rosa hybrida L. cultivars were evaluated with other genera on four different irrigation treatments. Cultivars evaluated during that time were ‘Aushouse’, ‘Gruss an Aachen’, ‘KORbin’, ‘KORelamba’, ‘KORfloci01’, ‘KORSixkono’, ‘KORsteimm’, ‘Meidrifora’, ‘Meigalpio’, and ‘Meijocos. The irrigation treatments were based on levels of reference evapotranspiration (ET0) at 20%, 40%, 60%, and 80% of ET0 in a water budget model using data from a nearby weather station in the California Irrigation Management Information System. After one year of establishment irrigation at 100% ET0, irrigation treatments were applied during the second year to six reps of each cultivar on each treatment. Data was taken monthly: growth measurements and quality ratings of foliage, flowering, pest tolerance, disease resistance, and overall appearance. Statistical analyses using ANOVA and Tukey’s HSD showed few significant differences in growth between treatments at p≤0.05, while for some cultivars, some or all quality parameters were higher on one or more levels of irrigation than others. While some cultivars performed best on the 60% ET0 treatment, most performed acceptably at 40% and 20% of ET0 as well. These data have been used to make recommendations for landscape hydrozoning (grouping by water needs) and irrigation scheduling for optimal landscape water use efficiency.
Seasonal changes in cold hardiness of garden roses

Lin Ouyang*a, Leen Leusb, Marie-Christine Van Labekea

a Department of Plant Production, Ghent University, Coupure links 653, 9000 Gent, Belgium
b ILVO, Plant Sciences Unit, Caritasstraat 39, 9090 Melle, Belgium

*Lin.ouyang@UGent.be

Session: Abiotic stress

Garden roses are grown worldwide, however, in northern regions, cold stress is an important environmental factor that can seriously affect growth and development of garden roses.

Seventeen genotypes of garden roses belonging to different USDA plant hardiness zones, ranging from 2b (-42.8°C) to 6b (-17.8°C), were selected for a field screening in Melle, Belgium (51°0'N, 3°48'E). During three consecutive winters (2014-2015-2016) stem segments were sampled on a day in January or February each winter after negative temperature were appeared for minimal 6 consecutive days. On these stem segments, injury index was determined by a controlled freezing test at -20°C. Based on the results, the genotypes were separated into three different groups: most cold hardy, medium hardy and most susceptible to cold.

Six genotypes were chosen based on the result of the first winter: most hardy: ‘Dagmar Hastrup’ and ‘John Cabot’, medium hardy: ‘Abraham Darby’ and ‘Yesterday’ and most susceptible: ‘Chandos Beauty’ and R. wichurana. For these genotypes, the seasonal changes in cold hardiness and carbohydrate metabolism were studied in the winter 2015.

The cold hardiness level was determined by the temperature resulting in 50% electrolyte leakage of stem segment (LT50). LT50 value showed a seasonal trend and again separated the three groups. The most hardy genotypes had a LT50 value of both -30°C. For the most susceptible genotypes the LT50 value were -18.5°C and -20.1°C.

Sugars contribute to cold acclimation in plants. Soluble carbohydrates: sucrose, hexoses (fructose and glucose), raffinose and stachyose were analysed in the six rose genotypes of the three groups. Sucrose levels were highest in November-December for the most hardy genotypes, but decreased towards February. In April sucrose levels were lowest in all cultivars except in R. wichurana which did not show a seasonal tendency. Hexoses (glucose, fructose) levels increased towards the end of the winter for the most hardy genotypes and for ‘Yesterday’ (medium hardy), while no seasonal trend was observed for the other three genotypes. In all genotypes, raffinose was found in higher concentrations than stachyose during November-January. Our results indicated that raffinose contributes to cold hardiness in ‘Dagmar Hastrup’ and ‘John Cabot’ (cold hardy), ‘Yesterday’ (medium hardy) and ‘Chandos Beauty’ (most susceptible).

Cell dehydration is also reported as an adaptive strategy to cold. At the beginning of the cold season, the lowest water content was found in the most hardy genotypes. In two genotypes, ‘Chandos Beauty’ and ‘Abraham Darby’, the water content dropped dramatically from January to March, while no fluctuation was found in other four genotypes.

Cold hardiness showed seasonal changes in the six chosen rose genotypes. During cold acclimation, water content and different soluble carbohydrates played a different role according to the rose genotype.
Heat tolerance in garden roses

Ockert Greyvenstein\textsuperscript{a}, Terri Starman\textsuperscript{b}, Brent Pemberton\textsuperscript{c}, Genhua Niu\textsuperscript{d} and David H. Byrne\textsuperscript{b}

\textsuperscript{a}Ball Horticultural Company, Guadaloupe, CA USA
\textsuperscript{b}Department of Horticultural Sciences, TAMU, College Station, Texas USA
\textsuperscript{c}Texas A&M AgriLife Research and Extension Center, Overton, Texas USA
\textsuperscript{d}Texas AgriLife Research Center at El Paso, 1380 A&M Circle, El Paso, Texas USA
*dbyrne@tamu.edu

Session: Abiotic stress

Roses generally experience a decrease in flower productivity and size in response to summer temperatures greater than 30 C which is common throughout the southern states of the USA. In 2011, the August mean and mean maximum temperatures in College Station were about 32C and 40C respectively. Under these extreme heat stress conditions, large rose germplasm collections in two field trials in Texas were evaluated for flowering intensity which takes into account both flower number and flower size. Of the 600 accessions evaluated, 20 (3\%) showed excellent flower intensity and 86 (14\%) showed good to very good flower intensity during August. Experiments done in the growth chamber with potted roses containing young flower buds indicated that a 3-hour heat shock (44C) treatment resulted in decreased flower size and increased flower abscission. Consequently, this approach was used to assess the heat tolerance of 18 rose cultivars. The results indicated that field ratings of heat tolerance based on flower productivity were negatively correlated to flower abscission and leaf necrosis (\( r = -0.55\)\textsuperscript{*} and \( r = -0.64\)\textsuperscript{**}) and not correlated with leaf CMT (cell membrane thermostability) of the potted rose plants subjected to the heat shock treatment.
Irrigation of Oil-Bearing Rose (*Rosa damascena* Mill.) In Turkey

Yusuf UÇAR\(^a\)*, Soner KAZAZ\(^b\), Sabri ERBAŞ\(^c\)

\(^a\) Department of Agricultural Structure and Irrigation, Faculty of Agriculture, Süleyman Demirel University, Isparta, Turkey

\(^b\) Department of Horticulture, Faculty of Agriculture, Ankara University, Ankara, Turkey

\(^c\) Department of Field Crops, Faculty of Agriculture, Süleyman Demirel University, Isparta, Turkey

*Corresponding author: yusufucar@sdu.edu.tr

Session: Abiotic stress

Abstract

Oil-bearing rose (*Rosa damascena* Mill.) is a scented rose species of the highest economic value for the perfumery, cosmetics, pharmaceutical, and food industries. With its production area of 2,800 ha, Turkey is one of the most important oil-bearing rose production centers of the world together with Bulgaria. Isparta in particular and Afyonkarahisar, Burdur and Denizli provinces, also known as the District of Lakes today, are important production centers for oil-bearing rose in Turkey, where the first oil-bearing rose production started in 1888. The most important products obtained from oil-bearing rose are rose oil, rose concrete, rose absolute, and rose water.

Although oil-bearing rose is generally grown on sloping areas far from water resources in Turkey, in the recent years, the oil bearing rose plantations have been established in the places which are flat and close to water resources. It is observed that irrigation with the drip irrigation method has become widespread in the new plantations in order to increase the rose flower yield. In oil-bearing rose, as in other plants, the attainment of the increase in yield that is expected from irrigation depends on the determination of water-yield relationships and the use of the obtained results by the growers. Otherwise, a deficit water application leads to a decrease in yield and poor quality, whereas an excess water may cause such environmental problems as drainage and salinity. Even though some studies on the irrigation of oil-bearing rose have been carried out in Turkey, it is not possible to say that they are at an adequate level. With this study, the studies on the irrigation of oil-bearing rose have been compiled; the results have been discussed; and recommendations have been made.

**Key words:** Oil bearing rose, *Rosa damascena* Mill., irrigation, rose oil yield.
Does ploidy level affects the response to drought stress in roses?

Marie-Christine Van Labeke\textsuperscript{a}, Hannes De Deurwaerder\textsuperscript{a}, Johan Van Huylenbroeck\textsuperscript{b}, Leen Leus\textsuperscript{b}

\textsuperscript{a} Ghent University, Faculty of Bioscience Engineering, Coupure links 653, 9000 Gent, Belgium
\textsuperscript{b} ILVO, Plant Sciences Unit, Caritasstraat 39, 9090 Melle, Belgium

\textsuperscript{*}mariechristine.vanlabeke@UGent.be

Session : Abiotic stress

In nature higher ploidy levels in plants are more frequently found in more severe growing conditions, indicating that ploidy level affects stress tolerance. Here we investigated if in rose genotypes chromosome doubling might assess plant reaction towards drought stress. Twelve diploid rose genotypes were used: ten F1-hybrids of ‘Yesterday’ x \textit{R. wichurana}, the species \textit{Rosa laevigata} and the \textit{R. multiflora} hybrid D 95/13 39. In preceding experiments these diploid genotypes have shown a differential response to drought stress. For all the genotypes tetraploids were obtained by mitotic polyploidisation. All plant material was multiplied by cuttings.

Both the diploids and the tetraploids were subjected to either a normal irrigation treatment (= control non stressed conditions) or a drought treatment (= complete irrigation stop). After 30 days post stress (DPS) the experiment was stopped and the above ground biomass of the plants was harvested. Fresh and dry weights were measured and several yield-selection criteria were calculated and used in a principal component analysis (PCA). The tetraploids showed in both treatments a decrease in biomass compared to the diploids. The effect of polyploidisation on drought tolerance was genotype dependant. After polyploidisation some genotypes were more resistant to drought stress, while other genotypes were more susceptible. In a third group no changes in behavior to drought stress were observed.

In a subsequent experiment three selected genotypes with differential response to drought stress (two F1 genotypes and \textit{R. laevigata}) were used. Next to the control treatment a drought treatment for 23 days was applied. The stomatal conductance [mmol m\textsuperscript{-2} s\textsuperscript{-1}] (\(g_s\)) was measured to assess stress levels and leaf samples were taken to determine the abscisic acid (ABA) content by UHPLC-MS/MS. Differences between the 3 genotypes were observed. For the F1 genotypes the low \(g_s\) indicated that severe drought stress (\(g_s < 50\) mmol m\textsuperscript{-2} s\textsuperscript{-1}) was imposed between 5 and 15 DPS, while in \textit{R. laevigata} no drought stress was observed during the whole experimental period. The two F1 genotypes showed a differential reaction: in one genotype severe stress was first observed in the diploid, while in the other it was the reverse. An increase in the ABA levels was observed for the F1 genotypes in both ploidy levels. In \textit{R. laevigata} no higher levels of ABA were found, confirming that this genotype was not stressed at all.

It can be concluded that drought stress resistance was more influenced by the rose genotype than by the ploidy level. Above ground biomass and yield-selection criteria have potential as proxies for identifying drought tolerant rose genotypes. ABA, known for its inducing effect on stomatal closure, and the stomatal conductance are good parameters to assess drought resistance and are able to identify genotype differences towards drought stress.
What are the contributions of cytokinins, abscisic acid and sugars in bud outgrowth regulation by light intensity in rose?

Adrien Corot, Hanaé Roman, Jessica Bertheloot, Nathalie Leduc, Soulaiman Sakr, Sabine Demotes-Mainard*

IRHS, Agrocampus-Ouest, INRA, Université d’Angers, SFR 4207 QuaSaV, 49071, Beaucouzé, France

*sabine.demotes-mainard@inra.fr

Session Abiotic stress

In ornamentals, particularly in rose bush, the visual quality of a plant is an important element of its quality. Bud outgrowth, which is at the origin of branching, strongly impacts plant shape and compactness, that are two traits involved in rosebush visual quality (Boumaza et al. 2009).

Changes in the environmental conditions, in particular in light intensity, can impact the number of buds that grow out and change bud outgrowth gradient along a stem in various species, including rose (Leduc et al. 2014; Furet et al. 2014). Bud outgrowth is controlled by a network of interacting hormones, the principal ones are auxin, cytokinins and strigolactones, but the role of abscisic acid is also emerging. Sugars are involved in bud outgrowth regulation too and they interact with the hormonal network. A natural hypothesis is that decreasing light intensity may limit bud outgrowth via a shortage in sugars and changes in plant hormonal content. However, the mechanisms by which light intensity affects bud outgrowth, especially the respective role of the different hormones and sugars in this regulation, is still poorly understood.

The objective of this work was to test if the control of bud outgrowth gradient along the stem by light intensity is mediated by sugars, cytokinins and/or abscisic acid and to assess which of these actors is the main limiting actor. The study was conducted on whole plants and attention was paid to the location of bud outgrowth along the shoot.


Acknowledgments. This research was conducted in the framework of the regional program "Objectif Végétal, Research, Education and Innovation in Pays de la Loire", supported by the French Region Pays de la Loire, Angers Loire Métropole and the European Regional Development Fund.
Session 6
Social sciences and humanities
Session 6 Keynote Lecture

Roses in the Horticultural Context of 19th Century in France. Questioning the Diversity in Historical Sources

Cristiana Oghina-Pavie\(^a\), Annie Antoine\(^a\), Aurélie Béard\(^b\), Céline Briée\(^a\), Annie Chastellung\(^c\), Jérémy Clotault\(^c\), Sylvain Gaillard\(^c\), Agnès Grapin\(^b\), Marie-Christine Le Paslier\(^b\), Shubin Li\(^d\), Mathilde Liorzou\(^c\), Valéry Malécot\(^c\), Gilles Michel\(^c\), Alix Pernet\(^e\), Vanessa Soufflet-Freslon\(^c\), Tatiana Thouroude\(^c\), Stéphane Tirard\(^b\), Fabrice Foucher\(^f\)

\(^a\) Université d’Angers, FRE CNRS 6258 CERHIO, Centre de recherches historiques de l’Ouest, 5 bis Bd Lavoisier 49045 Angers, France
\(^b\) EPGV, INRA, CEA-Institut de Génomique/CNG, 91057, Evry, France
\(^c\) IRHS, Agrocampus Ouest, INRA, Université d’Angers, SFR 4207 QuaSaV, 49071, Beaucouzé, France
\(^d\) Flower Research Institute, Yunnan Academy of Agricultural Sciences, Kunming, China
\(^e\) Centre François Viète, Université de Nantes, 44322, Nantes, France

* cristiana.pavie@univ-angers.fr

Session: Social sciences and humanities

The rose became the leading ornamental plant in France, in the first decades of the 19th century, simultaneously with the emergence of modern horticulture. From an ordinary garden plant, cultivated since ancient times, and invested with a rich symbolic and artistic heritage, modern horticulture has transformed roses into objects of collection, trade and study. These changes are well documented in historical sources: monographs, horticultural societies’ transactions, almanacs, gardening magazines, nurseries’ trade catalogue, scientific publications, etc.

The FloRHiGe project, funded by “Pays de la Loire” region, studied the impact of horticulture on the genetic diversity of roses cultivated in the 18\(^{th}\) and 19\(^{th}\) centuries. This interdisciplinary approach corroborated genetic data with historical information.

This study describes the main characteristics of the horticultural pattern in France in the 19\(^{th}\) century. It highlights significant changes induced by horticulture in cultivation practices and in the manner of thinking about rose diversity.

French horticulture developed in a bourgeois society. Cultural conditions promoted a new taste for roses at the beginning of the 19\(^{th}\) century. Moreover, roses had some qualities that made them suitable for urban middle-classes customers: easy growing, variability and reproducibility.

Neither nurserymen nor connoisseurs were contented any longer to discover and describe diversity, as natural sciences did before them, but to actively act in order to improve it. They formed international networks which enriched collections with new plants originating from Asia and America. They became involved in an intense breeding activity to attempt new, fashionable and valuable rose varieties. Diversity enrichment was a goal of the horticulturists of the time, their emulation being encouraged by both commercial and prestige competition.

Horticulturists considered diversity at the level of the varieties. They defined a rose variety in a horticultural sense, which differs from the botanical one, as an individual replicated by grafting or cutting. Each variety was identified by a commercial name and, since 1820-1830, by the name of the breeder and the year of the first flowering. Varieties were distinguished by discrete traits: color, shape and size of the flower, fragrance, habit of the plant, flowering season.

The status of novelty in horticulture oriented rose breeding. Breeders focused on roses which satisfied ancient ornamental criteria (double flower, pleasant fragrance, easy cultivation) and made a difference. The difference might be a rare color, a dwarf or vigorous habit, a mossy growth, or a large and full flower. Continuous blooming, introduced from China, appeared as a novelty in 1820-1830 and became a discriminant criterion in selection after 1850.

In conclusion, this study shows how historical sources can contribute to a more accurate understanding of the diversity of roses.
The Great Leap Forward towards Chinese genetic background: Impact of practices of French breeders from the nineteenth century on the evolution of the diversity of garden roses

Jérémy Clotault, Annie Antoine, Aurélie Bérard, Céline Briée, Sylvain Gaillard, Agnès Grapin, Marie-Christine Le Paslier, Shubin Li, Mathilde Liorzou, Valéry Malécot, Gilles Michel, Cristiana Oghina-Pavie, Alix Pernet, Vanessa Soufflet-Freslon, Tatiana Thouroude, Stéphane Tirard, Fabrice Foucher

a IRHS, Agrocampus Ouest, INRA, Université d’Angers, SFR 4207 QuaSaV, 49071, Beaucouzé, France
b Université d’Angers, UMR CNRS 6258 CERHIO, Centre de recherches historiques de l’Ouest, 5 bis Bd Lavoisier 49045 Angers, France
c EPGV, INRA, CEA-Institut de Génomique/CNG, 91057, Evry, France
d Flower Research Institute, Yunnan Academy of Agricultural Sciences, Kunming 650205, China
e Centre François Viète, Université de Nantes, 44322, Nantes, France
* jeremy.clotault@univ-angers.fr

Session: Rose genetics and Breeding

The nineteenth century was marked by transformations in French society that had large consequences on horticulture. Growing interest for novelty led both professional breeders but also amateurs to carry out work to create varieties with new characters, while collections of plants appeared. Heredity and hybrid concepts took shape at the same time. By its strong symbolic power, its wide phenotypic diversity and its capacity to be multiplied vegetatively, the rose was the plant that received the most attention.

The testimony of these practices is still available today through the many genetic resources preserved in several rose gardens in France, and the rich historical sources (catalogs, archives, horticultural journals, monographs, etc.) left by horticulturists and botanists. The aim of the project FloRHiGe, funded by the French region ‘Pays de la Loire’, was to understand the historical construction of the diversity of roses from the 18-19th centuries by a mixed genetic and historical interdisciplinary approach.

The study highlights the importance of some varieties from China introduced in Europe at the end of the 18th century. Thus, the analysis of a wide biological sample of rosebushes identified changes of phenotypic and genetic diversity of hybrids obtained in the nineteenth century, both in the genetic background but also at some key genes involved in the selected traits.

The genotyping of 1228 genotypes with microsatellite markers highlighted a progressive shift of the genetic background of European rose hybrids. Their old European genetic background was replaced during the nineteenth century by a genetic background indistinguishable from that of Asian roses. Recurrent crossings of European roses with Chinese roses, in order to introduce new traits in Europe (recurrent blooming, perfume, colours, etc.) may have resulted in this pattern.

On a sample of around 300 rosebushes phenotyped weekly during three years for flowering patterns, we confirmed that since 1850, a significant number of European hybrids were recurrent flowering, while this trait was originally almost absent in Europe but present in China. Along the nineteenth century, rosebushes tend also to be more and more early flowering. While a high diversity of flowering dates was probably sought in once-flowering rosebushes, we hypothesized that the emergence of reblooming roses shifted breeders’ objectives towards early-flowering roses only.

Sequencing of several candidate genes, including RoKSN and RoFT, on this sample allowed to test these hypotheses. In particular, a signature of selection was detected for non functional alleles of the flowering repressor RoKSN.

In conclusion, this study shows how the enlargement of the genetic background through new introductions has allowed rose growers to answer to their quest for novelty.
Legacies of Robert Basye and Ralph Moore: Historical Perspective

David Byrne and Natalie Anderson

Department of Horticultural Sciences, Texas A&M University, College Station, TX
*dbyrne@tamu.edu

Session: Social Sciences and humanities

Contributions by Robert E. Basye and later by Ralph Moore are responsible for the Texas A&M University Rose Breeding and Genetics program. Dr. Basye was a mathematician who worked at Texas A&M University (College Station, Texas) and was an active rose breeder. His goal was to “develop the bush on which to hang those wonderful flowers”. To this end, he explored various species as sources of good adaptation and disease resistance. He actively intercrossed diploid species and then doubled their chromosomes with colchicine so he could cross them with the tetraploid commercial garden roses. In addition, he employed some native North American species (Rosa carolina and Rosa virginiana) in his breeding. Although he was not a commercial breeder, several of his releases such as Basye’s Purple, Belinda’s Dream, Basye’s Legacy, and Basye’s Blueberry are still commercially available. In the early 1990s, Dr. Basye endowed the Chair in Rose Genetics and the Texas A&M University Rose Breeding and Genetics Program was born.

Later, Ralph Moore enriched the program by contributing his rose germplasm to the program. Ralph Moore was a commercial rose breeder who was known as the Father of the Miniature Rose. Although more than half of his 500 rose releases were miniature roses, he also worked on a range of other rose types (climbers, floribundas, and shrub) and unique rose traits (striped flowers, mossy foliage and flowers, crested sepals, and halo flowers). As did Dr. Basye, he incorporated a range of species into the modern rose germplasm. Throughout his career, he was the recipient of many honors reflecting his excellent breeding work but also his enthusiasm in sharing his experiences and knowledge with others. His generosity and enthusiasm about sharing his germplasm and knowledge is best characterized by what he frequently said, “The only things that I saved are those that I gave away.” Both Dr. Basye and Ralph Moore built their success on those that came before them and subsequently shared with rose world. As a result, the world of rose breeding has been significantly influenced by their work. About 2010, Ralph Moore donated his germplasm to Texas A&M University which has been incorporating the exceptional horticultural traits from Moore’s breeding into the well adapted and disease resistant germplasm developed by Dr. Basye and the Texas A&M Rose Breeding and Genetics program.
The rise and decline of the ‘Scots Rose’ phenomenon c.1800-1860

Peter D. A. Boyd
Holder of UK National Collection of Scots Roses (Plant Heritage)
peterboyd@btinternet.com

Session: Social sciences and humanities

A few single and double ‘coloured’ cultivars of *Rosa spinosissima*, known as ‘Scots Roses’ or ‘Scotch Roses’, had been selected or bred by the late 1700s but it was not until the early years of the 19th century that the enthusiasm of a few individuals to breed new Scots Roses led to a rapid increase in the variety and number of cultivars. This paper seeks to examine the work of some of the individuals who bred, collected and distributed Scots Roses worldwide and explore the factors that caused the growth and decline of a little recognised horticultural phenomenon. By 1840, there were more named cultivars of *Rosa spinosissima* than all the Albas, Centifolias, Damasks, Gallicas etc. combined but they had virtually disappeared from nursery catalogues within a few years.

Initially, the leading breeders of Scots Roses were Robert Brown and Robert Austin in Scotland but other nurserymen in Scotland, England and mainland Europe soon joined the enterprise. Progress in raising new cultivars had been slow 1799-1815, during the Napoleonic Wars between France and Britain with its allies. The cessation of hostilities in 1815, after the Battle of Waterloo, allowed individuals to pursue more peaceful activities. Some French nurserymen such as Descemet had bred *Rosa spinosissima* cultivars but his nursery suffered severe damage from enemy troops and he suffered loss of income. In 1818 he was forced to take up a job in Odessa in ‘New Russia’ as Director of the Botanic Garden. In contrast, the end of conflict between Britain and France allowed an English nurseryman, Calvert, to establish a rose nursery in France at Rouen through which he could introduce British roses to France and French roses to Britain (including *R. spinosissima* cultivars).

Several French and other European nurserymen raised *R. spinosissima* cultivars in the 1820s but relatively few compared with the hundreds of cultivars raised in Scotland and England in the same period.

Scots Roses were to become very popular in Nordic countries but, in Sweden, Lundström was growing only 25 Scots Rose cultivars (imported from Britain) in Stockholm by 1834. Müller’s Swedish list c. 1858 included French-bred Pimpinellifolias.

Although the first Scots Roses reached Australia in the 1820s, and New Zealand by about 1840 (via Scottish and other immigrants), an indigenous nursery trade was slow to develop, so Scots Roses were not widely available until later.

The main champions of Scots Roses in the U.S.A. were Winships of Boston, Massachusetts who offered about 60 cultivars in their 1833 catalogue (more than William Prince in New York) and they won several prizes for displays of Scots Roses at horticultural shows. However, the Winship brothers had both died by 1850.

Robert Brown, who had pioneered double coloured Scots Roses, emigrated to the U.S.A. in 1837 and died in Philadelphia in 1845. Robert Austin had died in Scotland in 1830. Therefore several pioneers and champions of Scots Roses died within a few years of each other. Loss of champions and the introduction of repeat-flowering roses led to a decline in Scots Roses but they persist in old gardens and cemeteries around the World. Ironically, Scots Roses are now seen more frequently in New Zealand, Tasmania and Nordic gardens than in Britain!
Survey of the rose community: desired rose traits and research issues

David H. Byrne\textsuperscript{a}, H. Brent Pemberton\textsuperscript{b}, Don J. Holeman\textsuperscript{c}, Thomas Debener\textsuperscript{d}, Tina M. Waliczek\textsuperscript{e} and Marco Palma\textsuperscript{f}

\textsuperscript{a}Department of Horticultural Sciences, Texas A&M University, College Station, TX USA
\textsuperscript{b}Texas AgriLife Research and Extension Center, Texas A&M System, Overton, TX USA
\textsuperscript{c}Rose Hybridizer Association, Enfield, CT USA
\textsuperscript{d}Leibniz University of Hannover, Institute of Plant Genetics, Hannover, Germany
\textsuperscript{e}Department of Agriculture, Texas State University, San Marcos, TX USA
\textsuperscript{f}Department of Agricultural Economics, Texas A&M University, College Station, TX
*dbyrne@tamu.edu

Session: Social Sciences and Humanities

In 2012-2013, an online survey run by the Rose Hybridizer Association and Texas A&M University asked the rose community for input on the importance of rose traits in the selection of rose cultivars. When ranked on importance compared to other traits, the most important trait was disease resistance. When asked what would be the biggest improvement that roses breeders could make in developing new rose cultivars, 53% of those that responded (n=1260) indicated that disease resistance would be the most important improvement with the most frequently mentioned disease being black spot followed by mildew, rust and rose rosette disease. Pests mentioned were Japanese beetles and thrips. Among abiotic traits that were mentioned, cold hardiness was the most mentioned followed by heat, drought, and shade tolerance. Among the breeders who responded (n = 106), 79% listed disease resistance as very important with the most importance put on black spot, mildew, rose rosette, cold hardiness, heat and drought. For horticultural traits, the most desired trait was improved fragrance with 30% overall and 23% of the breeder comments mentioning its importance. A survey is currently being done to update our assessment of rose traits desired in new rose cultivars and to identify important research issues.
American Rose Trials for Sustainability® (A.R.T.S.): A New United States Rose Trialing Program for Identifying and Promoting Regionally Adapted Roses

Gaye Hammond*, David C. Zlesakb, Michael Schwartzc, Peter Kukielskid, Steve Georgee, Mark Chambleee, Randy Nelsonf, Kathy Zuzekg, Kerry Ann McLeanh, David Freedmani, and Ralph Finkc

© Houston Rose Society, 5020 Montrose Blvd., 9th Floor, Houston, TX 77006
bUniversity of Wisconsin-River Falls, 410 S. 3rd Street, River Falls, WI 54022
cNaugatuck Valley Community College, 750 Chase Pkwy, Waterbury, CT 06708
d20 Highland Street, Portland, Maine 04103
eTexas A&M AgriLife Extension Service, 17360 Coit Road, Dallas, TX 75252
fChamblees Roses, 10926 U.S. Highway 69 North, Tyler, TX 75706
gUniversity of Minnesota Extension-Clay County, 715 11th St. N., Suite 107B, Moorhead, MN 56560
h39920 Trulson Road, North Branch, MN 55056
iT Terrain, 914 Baltimore Pike, Glen Mills, PA 19342

*gayeh@lpm-triallaw.com

There are numerous rose trialing programs worldwide that evaluate new roses in the marketplace and they differ in: number of sites and climatic conditions represented, level of scientific rigor employed, the evaluation criteria used, maintenance of roses, determination of awards, and the transparency with which the programs are organized and supported. The American Rose Trials for Sustainability® (A.R.T.S.) program is a new rose trialing program initiated in 2012 in the United States by experts representing leading universities, rose nurseries, public gardens, and rose societies with the shared goal of identifying and promoting strong performing roses evaluated under low input conditions. A.R.T.S trials are managed by university scientists with years of experience in field research. The A.R.T.S. leadership team consulted a wide range of stakeholders to ascertain which cultivar characteristics they felt were most important and developed a new evaluation protocol in response. As with other ornamental plant evaluation programs, attractive floral attributes and flowering throughout the season are highly valued (42.5% of score). Also of great importance are foliar health and quality (45%) and growth habit (12.5%). Scientific credibility and transparency of A.R.T.S. are strengthened in multiple ways including using: the Köppen climate classification system for region delineation, a randomized complete block experimental design, a generated code for each genotype to blind evaluators from the identities of the cultivars and breeders, and reference cultivars. Awards are determined on a regional basis with those cultivars earning awards in four or more regions designated as Master Roses. There are seven roses earning awards for 2018, the debut of the program to the public, with three roses (Double 10™, ‘LIM10’; Icecap™, ‘MEIradena’; and Peachy Knock Out®, ‘RADgor’) earning Master Rose designations.
Neuromarketing, a Novel Approach to Determine the Consumer Preferences and Willingness-to-pay for Rose Attributes

Marco Palma\textsuperscript{a}, Luis Ribera\textsuperscript{a}, Charles Hall\textsuperscript{b} and David H. Byrne\textsuperscript{b}

\textsuperscript{a}Department of Agricultural Economics, Texas A&M University, College Station, TX
\textsuperscript{b}Department of Horticultural Sciences, Texas A&M University, College Station, TX

*dbyrne@tamu.edu

Session: Social sciences and humanities

Discrete Choice Experiments (DCE) are used to investigate consumer preferences and willingness-to-pay for roses. DCE is a technique for measuring buyers’ tradeoffs among multiple attributes of products and services. It has been widely used in the field of marketing research to determine consumer’s preferences for products. It is based on the simple premise that consumers evaluate the overall value of a product, service, or idea by combining the separate amounts of value provided by each product attribute. In this DCE of disease resistant roses, evaluated features include price, disease tolerance, pesticide dependency, number of blooms, range of flowering time, flower color, flower size and form, foliage damage, life expectancy of the plants, genetically modified roses versus conventional roses, and other key rose characteristics.

Data will be collected using a neuromarketing approach. This includes eye-tracking and facial expression analysis. The eye-tracking data will be recorded using a Tobii T/X 300 eye-tracking device to reveal visual attention to rose attributes. Information collected includes the time to first fixation or how long it took participants to look at an area of interest for the first time; fixation duration or how long they looked at each area; and fixation count or how many times they look at an area. The eye-tracking data is used to complement the choice data for attribute attendance in order to obtain more accurate measures of willingness to pay. However, participants may be interested in specific areas because of mixed emotions (i.e. they may like or dislike what they are seeing). The facial expression analysis of muscle activity will assess the overall emotional responses (positive, negative or neutral) of the consumer as well as potentially detect some basic emotions such as joy, anger, surprise, fear, sadness, disgust, and contempt.
The American Hand in Rose Hybridization

Ping Lim*

plim@altmanplants.com

Session: Social science and humanities

Abstract

Although rose experts and botanists agree that the modern rose has evolved out of combine exchanges from China and Europe, most overlook the hand that America has had in developing this internationally loved plant.

While the American Civil War dampened national enthusiasm and only handful rose breeders interested in rose hybridization, the U.S. was significantly involved in international exchanges of rose breeding materials both before and after the war. In 1803, for instance, Thomas Jefferson shared numerous bushes and seeds of species native to America with France. That same year, a South Carolina farmer, John Champney, used lines from France that had come from China to develop the first Hybrid Perpetual, Champney's Pink Cluster, which led to the creation of Noisette and later elaborated with the first modern Hybrid Tea rose (La France in 1867). Following the release of La France, rose hybridization took off.

By the early 1900s, the American rose industry was booming. With this increase in productivity came concerns about intellectual rights, and the U.S. took the lead on establishing plant patent laws in the 1930s. By reassuring breeders a level of legal protection, the U.S. not only boosted national plant research but also encouraged international plant trade. European nations soon followed suit.

The history of the rose reflects the global scale and impact of plant breeding science. Though as relatively late player in the game, the United States has nonetheless become a key influencer and, at times, a leader, in the evolution of the modern rose.

*Ping Lim

Director of Ornamental Plant Research for Altman Plants, USA

Tel: 670. 272. 5570
Email: plim@altmanplants.com

Breeding Rose since 1992, hybridization efforts focus on ‘Eco friendly’ with less energy used for stress resistance to combine fragrance, grand petals, lasting color, compact form and quick blooming cycle.

- Twenty Easy Elegance Roses were patented.
- Three times AARS Award: ‘Love and Peace’™, ‘DayDream’™, and ‘Rainbow Sorbet’™
- Four 911 Roses: Forty Heroes, The Finest, Patriot’s Dream and Survivors
- Two emblem Roses: “Macy’s Pride” and “Centennial” (St. Paul, Minnesota)
- Two Biltmore International Rose Trial Award: “FlyingKiss” and “Double 10”
- Nine Portland Best Roses Awards since 2005
- Rose Hill International Rose Trial Award: Goldmine 2016
- American Rose Trials for Sustainability™(A.R.T.S. ™) All-Star winner 2017
- Website: www.rosesbyping.com
- Youtube: http://www.youtube.com/user/u2ac
- FaceBook: https://www.facebook.com/RosesByPing
Session 7

Biotic stress
Combating Rose Rosette Disease US National Project

David Byrne\textsuperscript{a}, Mark Windham\textsuperscript{b}, Francisco Ochoa Corona\textsuperscript{c}, Jen Olson\textsuperscript{c}, Mathews Paret\textsuperscript{d}, Binoy Babu\textsuperscript{d}, Gary Knox\textsuperscript{d}, Ramon Jordan\textsuperscript{e}, John Hammond\textsuperscript{e}, Kevin Ong\textsuperscript{f}, Ronald Ochoa\textsuperscript{g}, Gary Bauchan\textsuperscript{h}, Tom Evans\textsuperscript{i}, Patricia Klein\textsuperscript{a}, Alan Windham\textsuperscript{l}, Frank Hale\textsuperscript{l}, Charlie Hall\textsuperscript{a}, Luis Ribera\textsuperscript{k}, Marco Palma\textsuperscript{k}, and H. Brent Pemberton\textsuperscript{l}

dbyrne@tamu.edu

\textsuperscript{a} Department of Horticultural Sciences, Texas A&M University, College Station, TX USA
\textsuperscript{b} The University of Tennessee, Entomology and Plant Pathology Dept, Knoxville, TN USA
\textsuperscript{c} Dept. of Entomology and Plant Pathology, Oklahoma state University, Stillwater, OK USA
\textsuperscript{d} North Florida Research & Education Center, 155 Research Rd., Quincy, FL USA
\textsuperscript{e} Floral and Nursery Plants Research Unit, USDA, ARS, Beltsville, MD USA
\textsuperscript{f} The Texas Plant Disease Diagnostic Lab., 1500 Research Parkway, College Station, TX USA
\textsuperscript{g} Systematic Entomology, ARS, USDA, Beltsville, MD USA
\textsuperscript{h} Electron & Confocal Microscopy Unit, USDA-ARS, BARC-West, Beltsville, MD USA
\textsuperscript{i} Department of Plant and Soil Sciences, University of Delaware, Newark, DE USA
\textsuperscript{j} The University of Tennessee, Soil, Plant and Pest Center, Marchant Drive, Nashville, TN USA
\textsuperscript{k} Department of Agricultural Economics, Texas A&M University, College Station, TX
\textsuperscript{l} Texas AgriLife Research and Extension Center, Texas A&M System, Overton, TX

*dbyrne@tamu.edu

Session: Biotic stress

In the past few decades, Rose Rosette Disease (RRD) has spread from its source in western North America through the Mid-West to the East coast. It now threatens to decimate the US rose industry. Garden roses, which form the cornerstone of the multi-billion dollar landscape industry, annually generate wholesale US domestic bare root and container production valued at ~ $400 million. RRD is caused by an emaravirus, \textit{Rose rosette virus} (RRV), which is transmitted by wind-blown eriophyid mites (\textit{Phyllocoptes fructiphilus}). Unlike other rose diseases, it can kill a rose within two to three years of infection. In collaboration with scientists from 6 states, private rose breeders, the American Rose Society, AmericanHort, and the rose industry, a project was initiated to develop a multidisciplinary approach to control the disease. In the short term, the project is working to develop Best Management Practices and educational materials based on host, virus, and vector biology to minimize the effects of RRD. Key to this effort is the development of efficient user-friendly diagnostic tools. In the long term, roses are being assessed for resistance to RRD using both replicated field trials and observational data from collaborators. Marker-trait associations for RRD resistance and consistent flower productivity are being identified to move RRD resistance efficiently into elite rose germplasm. Economic and marketing studies are being done to assess the economic effect of RRD on the rose industry, improve our understanding of consumer preferences, and identify barriers to rose sales.
Development of tools to study rose resistance to black spot

Soufflet-Freslon V. a, Marolleau B. b, Thouroude T. b, Chastellier A. b, Pierre S. b, Bellanger M.N. b, Le Cam B. b, Bonneau C. c, Porcher L. c, Leclere A. d, Robert F. e, Felix F. f, Foucher F. b, Hibrand-Saint Oyant L. b

a Institut de Recherche en Horticulture et Semences - UMR 1345, Agrocampus Ouest, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France
b Institut de Recherche en Horticulture et Semences - UMR 1345, INRA, SFR 4207 QuaSaV, 42 rue Georges Morel, 49071 Beaucouzé, France
c Vegepolys Innovation, 26 rue Dixmèras, 49066 Angers Cedex 01, France
d SIRPHE, 19 rue du Docteur Curie, 59700 Marcq-en-Barœul, France
e Astredhor, 44 rue d’Alésia, 75682 Paris Cedex 14, France
f FNPHP, 19 bd Magenta, 75010 Paris, France
* vanessa.soufflet-freslon@agrocampus-ouest.fr

Session: Biotic stress

Black spot (caused by the fungal pathogen *Diplocarpon rosae*) is the most severe disease of roses in the outdoor landscape. Most cultivars are susceptible to this disease and its control requires many fungicide treatments. New rules on pesticide use encourage breeders to develop roses with a high resistance level to black spot. Growing genetically resistant rose cultivars should provide an alternative to chemical control of the disease.

Resistance durability depends on the kind of resistance, the plant genetic background, the spatial and temporal deployment of resistances, the integration of resistances in cultural systems, and also on the dynamic of pathogen adaptation.

To date, both dominant resistance genes and partial resistance loci have been revealed particularly in the genetic background of *Rosa multiflora*. In this study, a genotype closely related to a wide rose (*Rosa x wichurana*) was considered to detect new resistance genes. Two progenies, connected by the resistant male parent, were scored for black spot resistance after natural infections in field over three years in three and one French locations for HW and OW progenies, respectively. Genetic maps based on microsatellite and SNP markers were developed for HW and OW progenies, respectively. One common quantitative trait locus (QTL) was localized on linkage group 3 (LG3) of the male maps; it was revealed in the two progenies for several years and in different locations. Another QTL was identified but only in the HW progeny in one year in two locations; it was mapped on LG5. The effectiveness of these QTL should be confirmed against a widest range of pathogen isolates.

To provide tools to study the genetic diversity of *D. rosae*, we sequenced two strains using illumina paired end sequencing technology, which allowed to identify and develop polymorphic microsatellite markers. The genome size of the two strains was estimated to 31.1 and 35.2 Mb; a set of 32 polymorphic markers was obtained. 77 monoconidial strains of *D. rosae* isolated from leaves of *Rosa spp.* with black spot symptoms were obtained from various locations in Europe and Asia. The analysis of this Eurasian pathogen collection revealed a strong genetic differentiation between wild populations and populations from gardens.

In order to screen the resistance level of rose genotypes against pathogen diversity, we developed a pathological assay in greenhouse conditions. Cuttings were inoculated with monoconidial strains. Disease symptoms were scored 10 and 28 dpi. This pathological test showed contrasted resistance levels in rose against pathogen diversity on a French scale, and revealed genotypes interesting for breeding program.

The data presented here help to characterize genetic resistance to black spot disease in rose.
Resistance of Garden Roses to Cercospora Leaf Spot

Stella Kang*a, Muqing Yan*a, Ellen Roundey*a, Jeekin Lau*a, Brent Pemberton*b, Cody Bishop*b, Kevin Ong*c, David Byrne*a

*aDepartment of Horticultural Sciences, Texas A&M University, College Station, TX USA

*bTexas A&M AgriLife Research and Extension Center, Texas A&M System, Overton, TX,

*cTexas Plant Disease Diagnostic Laboratory, 1500 Research Parkway, College Station, TX,

*stellakang@email.tamu.edu

Session: Biotic stress

Cercospora leaf spot (Cercospora rosicola) is a fungal disease that is prevalent in the Southeast of the United States. It causes leaf spotting and plant weakening, which may lead to premature defoliation. The current cercospora management practice is repeated fungicide applications throughout the season. Replicated garden rose cultivar field trials in south central (College Station) and northeastern (Overton) Texas were rated monthly from May through November in 2016 on a 0 to 9 scale, which is based on the percent of leaves with cercospora lesions, to assess the relative resistance of rose cultivars to cercospora leaf spot. Although both sites had a wide range of cercospora lesion incidence on the roses, the Overton site had a greater average (2.54 vs 0.46) cercospora leaf spot rating than College Station due to higher precipitation. At the higher disease pressure location, of the 374 roses accessions evaluated, ~5% were highly susceptible with > 50% of the leaves infected with cercospora and ~36% of the cultivars appeared resistant with less than 10% of the leaves with cercospora lesions. Although there are differences among rose cultivars in their susceptibility to cercospora infection, little is known about the genetic control of the resistance. To assess the inheritance of the resistance to cercospora, 16 diploid rose families which had the resistant species, Rosa wichuriana, in their parentage were evaluated four times in field plantings in College Station for the percentage of leaves with lesions. The restricted estimated maximum likelihood (REML) analysis of the genetic variance indicated that the narrow sense and broad sense heritabilities were 0.51 and 0.72 respectively. This indicates that the selection for cercospora resistant cultivars should be possible. Further work to determine markers associated with the resistance is ongoing.
Testing EDNA-ROSE: a novel in silico approach for detection of rose viruses combining next generation sequencing and bioinformatics.

Lizbeth Peña-Zuñiga\textsuperscript{a}, Andrés Espíndola\textsuperscript{a}, Patricia Klein\textsuperscript{b}, Thomas Debener\textsuperscript{c}, Jasper Rees\textsuperscript{d}, David Byrne\textsuperscript{b}, and Francisco M. Ochoa-Corona\textsuperscript{a}.

\textsuperscript{a}Oklahoma State University, Stillwater, OK, USA.  
\textsuperscript{b}Texas A&M University, College Station, TX, USA.  
\textsuperscript{c}Leibniz Universität Hannover, Institute of Plant Genetics, Hannover, Germany  
\textsuperscript{d}Agricultural Research Council, LNR, Onderstepoort, South Africa  
*ochoaco@okstate.edu

Session: Rose genomics

The garden rose production is seriously affected by viral infections in USA. Twenty-four viruses have been reported to infect rose worldwide and numerous are reported in the USA and in Europe. Early viral infections in rose may not be diagnosed until symptoms develop. Currently single-virus assay methods are used in the diagnosis and detection for most of these pathogens.

Next-generation sequencing (NGS) can be used as a diagnostic tool because of its ability to amplify multiple unique DNA signatures of infecting viruses. Electronic probe Diagnostic Nucleic acid Analysis (EDNA) was used to detect rose viruses in simulated metagenomics runs (mock sequencing databases, MSDs) containing rose-virus reference sequences as positive controls and rose host genome sequences. MSDs were generated using MetaSim, and were configured simulating Illumina average read length and error rates.

Electronic probes (e-probes) with lengths of 20-40 nucleotides were designed by comparing the target viral genome versus all potential co-infecting viral genomes. To avoid false positives, e-probes were curated by BLAST alignments of sequences from published public databases (nt NCBI). Positive MSDs containing only the intended target viral genome were considered positive controls. MSDs mimicking single and multiple infections were also generated. Generated E-probes were tested \textit{in silico} and \textit{in vitro}.

If compared with other NGS procedures, EDNA is a relatively rapid response methodology that provides the framework for a new sequence-based diagnosis. EDNA-ROSE can also be combined with other diagnostics methods for virus monitoring in microbial forensics, biosecurity and epidemiological studies of rose plants.
Rdr1 provides broad spectrum black spot resistance in various genetic backgrounds

Ina Menz¹, Marcus Linde¹, Thomas Debener¹
¹Leibniz Universität Hannover, Institute of Plant Genetics, Hannover, Germany
debener@genetik.uni-hannover.de

Black spot of roses caused by the hemibiotrophic fungus *Diplocarpon rosae* is the most damaging disease of field grown roses in the temperate regions. Some time ago we genetically characterised the single dominant resistance-gene Rdr1 and isolated the responsible TNL sequence. Stable transgenic clones harbouring Rdr1 display the full resistance reaction as seen in the donor genotype. The progeny of crosses between transgenic and non-transgenic clones as well as conventional progeny shows that this single R-gene confers resistance to a broad collection of pathogenic races in a wide range of genetic backgrounds. This indicates that Rdr1 acts independent of specific factors present only in the original donor genotype. Although Rdr1 does not act against all known pathogenic races of *D. rosae* it is an interesting tool for resistance breeding if combined with other genes providing additional R-gene specificities.
Towards MLO mediated powdery mildew resistance in tetraploid roses

Juliane Geike¹, Helgard Kaufmann¹, Thomas Debener¹

¹Leibniz Universität Hannover, Institute of Plant Genetics, Hannover, Germany
debener@genetik.uni-hannover.de

Powdery mildew caused by Podosphaera pannosa (Wallr.: Fr.) de Bary is one of the most severe diseases of roses. The reproductive biology and race structure of P. pannosa limit the effectiveness of race-specific, monogenic resistances in breeding programs making the application of fungicides indispensable. An alternative to overcome this problem can be the mildew resistance locus o (mlo)-mediated resistance which has been characterized in barley, A. thaliana, tomato and pea. The loss-of-function of specific members of the MLO gene-family leads to a recessive and durable broad-spectrum resistance in these species. In rose four MLO homologs (RhMLO1, RhMLO2, RhMLO3 and RhMLO4) genetically closely related to the functional ones in A. thaliana, pea and tomato have been sequenced and mapped. Here we present data on the stable and transient knock down of individual rose MLO via RNAi as well as first results on the targeted mutagenesis of these genes by either TALENs or CRISPR strategies.
Quantitative factors influencing leaf spot diseases in roses

, Marcus Linde¹, Chieh Ming Liao¹,Dietmar Schulz¹, Thomas Debener¹

¹Leibniz Universität Hannover, Institute of Plant Genetics, Hannover, Germany
debener@genetik.uni-hannover.de

Leaf spotting diseases as black spot and spot anthracnose, caused by Diplocarpon rosae and Sphaceloma rosarum, lead to considerable damage in field grown roses across the temperate regions. Disease resistance conferred by single dominant genes is often rapidly overcome by the development of new pathogenic races. An alternative to pyramiding single R-genes, which needs several rounds of crossbreeding, is the use of resistance QTLs that are less prone to the so called “boom and bust” cycles. Using an association panel of 96 tetraploid rose genotypes we developed markers either from known pathogen related genes or from a large collection of SNPs that are linked to QTLs for reduced susceptibility to both black spot and spot anthracnose in roses.
Transcriptome analysis of the defense response of roses in the interaction with Diplocarpon rosae and Podosphaera pannosa using the MACE technique

Enzo Klein¹, Helgard Kaufmann¹, Helena Domes¹, Thomas Debener¹

¹Leibniz Universität Hannover, Institute of Plant Genetics, Hannover, Germany
debener@genetik.uni-hannover.de

Induced resistance to pest and pathogens is regulated at several levels in the plant one of which is a massive transcriptional reprogramming. Our work deals with the defense responses of roses against two major fungal pathogens Diplocarpon rosae and Podosphaera pannosa. These interaction systems are of particular interest because the two pathogens display very different lifestyles. D. rosae is a hemibiotrophic ascomycete, whereas P. pannosa is an obligate biotrophic ascomycete. We performed a transcriptome analysis with the new MACE (Massive Analysis of cDNA Ends)-technique and for some samples also with RNA-seq to obtain data for three interaction systems: A compatible interaction of the susceptible rose variety “Pariser Charme” inoculated with P. pannosa, a compatible interaction of “Pariser Charme” with D. rosae and an incompatible interaction of resistant genotype 91/100-5 with D. rosae. Non-infected leaves of “Pariser Charme” were used as controls. Samples for three different time points (0, 24, 72 hpi) were taken and all inoculation experiments has been performed three times independently. Here we present data on differential expression of key factors known to be important for transcriptional reprogramming during plant pathogen interactions as well as so far unknown factors.
Rose Rosette Disease: It all started with a tiny mite

G. Bauchan*a  R. Ochoa*b  G. Otero-Colina*c  J. Hammond*d  R. Jordan*d

*a USDA, ARS, Electron and Confocal Microscopy Unit, Beltsville, MD. USA
*b USDA, ARS, Systematic Entomology Laboratory, Beltsville, MD. USA
*c Colegio de Postgraduados, Texcoco, Mexico;
*d USDA, ARS, US National Arboretum, Beltsville, MD. U.S.A.

Session: Biotic Stress

A small eriophyid mite, *Phyllocopetes fructiphilus*, has been shown to be the vector for an eamaravirus, *Rose rosette virus*, the causal agent of rose rosette disease (RRD). We are studying mites on roses by microscopy techniques include bright field, differential interference contrast (DIC), variable pressure SEM, low temperature SEM and confocal microscopy. The eriophyid mite was first described by Keifer in 1940 but it was first suggested as the vector of RRD by the same author in 1966. The mites were originally collected from seeds and fruits and around the petiole bases of *Rosa californica* in Clarksburg, California. Today *P. fructiphilus* is widely distributed in the U.S. on wild (*Rosa multiflora*) and commercial roses with different levels of virus damage and its presence is directly affecting rose production and gardening areas. Current studies on roses from several states indicate the presence of multiple species of eriophyid mites during various seasons of the year on different parts of the rose plants. Mites are primarily found on enclosed petioles/scales of vegetative buds, inside the flower sepals appressed to the ovary/seeds, and on open leaves during the growing season. Mites appear to be hiding amongst dense simple and bulbous, glandular hairs (trichomes). The eriophyid mites also overwinter in these same locations. In addition, we found predatory mites in the families *Phytoseiidae*, *Tydeidae* and *Bdellidae* associated with these mites that may be useful as biological control agents of the eriophyid mites. Control of RRD should include the removal of mature fruits from all plants to reduce overwintering mite populations, and removal of all infected plant tissue including the root ball to remove virus sources.
A Simplified Technique for Counting Eriophyid Mites on Roses that are Endangered by Rose Rosette Disease

Sara Collins\textsuperscript{a}, Katherine Solo\textsuperscript{a}, Alan Windham\textsuperscript{b}, Frank Hale\textsuperscript{b}, and Qunkang Cheng\textsuperscript{a} and Mark Windham\textsuperscript{a*},

\textsuperscript{a}University of Tennessee, 370 Plant Biotech Bldg, 2505 E.J. Chapman Drive, Knoxville, Tennessee, USA 37996
\textsuperscript{b}Soil, Plant and Pest Center, 5201 Marchant Drive, Nashville, Tennessee, USA 37211
\textsuperscript{*}mwindham@utk.edu

Session: Biotic Stress

Rose rosette disease, caused by \textit{Rose Rosette Virus} which is vectored by the eriophyid mite, \textit{Phyllocoptes fructiphilus}, is difficult to control in wholesale and retail nurseries and public and private gardens. One reason for this difficulty is the inability by nursery and landscape professionals and homeowners to determine when eriophyid mite populations begin to increase in their plantings, so as to know when applications of miticides could be applied. Although methodology has been published for counting eriophyid mites, laboratory equipment is often costly (may be in excess of $9,000 (U.S. dollars)) and these costs prohibit many individuals from counting eriophyid mites in their roses. The objective of this study was to develop a method for counting eriophyid mites with materials that were readily available to horticultural professionals and private individuals, and where combined costs of materials would be less than $100. An eriophyid mite counting kit that achieves this economic goal (<$100) has been developed and includes a handbook that describes the kit and how to use items in the kit. The kit allows the user to use a cellphone to photograph the eriophyid mites they are counting. Twelve kits were distributed to nursery owners, professionals who maintain rose gardens, and private garden owners. Each kit recipient was asked to fill out a survey on kit ease-of-use and ability of the kit operator to obtain satisfactory results. The economical eriophyid mite counting kit will be described in our presentation/poster.
Black spot and Cercospora Leaf Spot Resistance in Cultivated Roses

Mark Windham\textsuperscript{a*}, Alan Windham\textsuperscript{b}, and Qunkang Cheng\textsuperscript{a}

\textsuperscript{a}University of Tennessee, 370 Plant Biotech Bldg, 2505 E.J. Chapman Drive, Knoxville, Tennessee, USA 37996
\textsuperscript{b}Soil, Plant and Pest Center, 5201 Marchant Drive, Nashville, Tennessee, USA 37211
\textsuperscript{*}mwindham@utk.edu

Session: Biotic Stress

Black spot (BS), \textit{Diplocarpon rosae}, caused extensive defoliation in the eastern United States and Cercospora leaf spot (CLS), \textit{Cercospora rosicola}, causes severe spotting and defoliation of foliage in southeastern states. Although considerable efforts have been placed recently on developing black spot resistance in rose cultivars, little attention has been given to CLS. In our study, 146 cultivars of roses with resistance claims in commercial catalogs were screened for resistance to BS and CLS in two locations in Tennessee. Test roses were arranged in a completely randomized design with every fourth rose in each trial being of the known susceptible cultivar ‘Peace’. ‘Peace’ was used to confirm that BS pressure was high and to serve as an inoculum source for \textit{D. rosae}. Inoculum of \textit{C. rosicola} was from spores that drifted into test plots. For each cultivar roses were rated for severity of BS, CLS and defoliation using the following scale: 0 = no disease or defoliation, 1 = $\leq$ 2\% disease or defoliation, 2 = $\leq$ 10\% disease or defoliation, 3 = $\leq$ 25\% disease or defoliation, 4 = $\leq$ 50\% disease or defoliation and 5 = $>50$\% disease or defoliation. Data were collected every two weeks from May through August each year. Disease progress curves were determined for each cultivar/disease combination. Area under the curves were calculated and used to separate means using PROC Mixed in SAS and means were separated using Bonferroni’s method ($\alpha=0.05$). The number of cultivars resistant to BS and CLS were 34 and 13, respectively. Only the cultivars ‘All the Rage’, ‘Baby Bloomer’, ‘Hansa’, ‘Knock Out Rose’ and ‘Pink Knockout’ were resistant to both diseases and suffered no defoliation.
Controlling Rose Rosette Disease with Cultural and Chemical Methods

Mark Windham\textsuperscript{a*}, Alan Windham\textsuperscript{b}, Frank Hale\textsuperscript{b}, and Qunkang Cheng\textsuperscript{a}

\textsuperscript{a}University of Tennessee, 370 Plant Biotech Bldg, 2505 E.J. Chapman Drive, Knoxville, Tennessee, USA 37996
\textsuperscript{b}Soil, Plant and Pest Center, 5201 Marchant Drive, Nashville, Tennessee, USA 37211
* mwindham@utk.edu

Session: Biotic Stress

Rose rosette disease has destroyed thousands of roses in commercial and private gardens in the United States. The disease agent is a negative strand RNA virus, Rose Rosette Virus, and the virus is vectored by the eriophyid mite, Phyllocopites fructiphilus. The only known remedy for this disease is to destroy symptomatic plants. We evaluated cultural and chemical control strategies to reduce the impact of this disease. Pruning to remove symptomatic canes at first detection of symptoms was ineffective for preventing other canes from becoming symptomatic on test plants. The use of Miscanthus sinensis as a green barrier, reduced incidence of rose rosette disease in test plots although once the disease became established in test plots, the rate of disease progression was similar to that observed in plots without barriers. Plants sprayed at 14 day intervals with Akari, Forbid, Kontos or Talstar did not develop symptoms whereas all control plants (sprayed with water) became symptomatic for the disease. Spray treatments of Avid+horticultural oil and Sevin were ineffective. The use of miticides for reducing the impact of rose rosette is promising. More research is need to determine when spraying should be triggered, how many sprays are needed, if spray intervals can be increased to reduce the amount of pesticide used and if spray intervals are the same for all miticides.
Eriophyid Mite Populations Found on Different Rosa Species

Sara Collins\textsuperscript{a}, Qunkang Cheng\textsuperscript{a}, Brent England\textsuperscript{b}, Katherine Solo\textsuperscript{a}, Frank Hale\textsuperscript{c}, Alan Windham\textsuperscript{c}, Dave Byrne\textsuperscript{d}, Natalie Anderson\textsuperscript{d} and Mark Windham\textsuperscript{a*}

\textsuperscript{a}University of Tennessee, 370 Plant Biotech Bldg., 2505 E.J. Chapman Dr., Knoxville, TN 37996
\textsuperscript{b}University of Tennessee, 320 Exper. Station Road, Crossville, Tennessee, USA 38571
\textsuperscript{c}Texas A&M University, Dept. of Horticulture, 2133 TAMU, College Station, TX 77843-2133
\textsuperscript{d}Soil, Plant and Pest Center, 5201 Marchant Drive, Nashville, TN USA 37211
\textsuperscript{a*}mwindham@utk.edu

Session: Biotic Stress

\textit{Rose Rosette Virus} has destroyed thousands of roses in the United States. The virus is vectored by the eriophyid mite, \textit{Phyllocoptes fructiphilus}. This mite is only found on \textit{Rosa} species. However, little is known about the host range of eriophyid mites within the genus \textit{Rosa}. To determine if resistance to eriophyid mites (defined in this study as lack of reproduction on the host), eighteen \textit{Rosa} species were planted in a completely randomized design at the Plateau Research and Education Center. Eriophyid mite populations were estimated every two weeks from May to September in 2016 by destructive sampling of shoots from which mites were extracted via sieving and then counted using a stereomicroscope. Mite counts were expressed as number of mites per gram of leaf tissue. Due to large variation in data (on a given date, mite counts could range from more than 900 mites/g plant tissue to 30 mites/g plant tissue for \textit{R.} species where mites could reproduce), the mite counts were converted into a binomial variable where 0 (mite not reproducing on the plant) was less than 20 mites/g plant tissue and 1 (mite reproduction on plant) indicated samples with more than 20 mites/g plant tissue. Low levels of mites were expected on all plants since this study was located in an area with high numbers of roses heavily infested with eriophyid mites which were constantly ballooning onto test plants. Entries of five species (\textit{R. arkansana, R. palustris} EB, \textit{R. clinophylla, R. nitida} and \textit{R. wichuriana} Basye ARE) maintained low mite populations that were not statistically different from zero (p= .05). There were differences in the eriophyid mites’ ability to reproduce on the different accessions of \textit{R. wichuriana} and \textit{R. palustris} tested, indicating intraspecific variability in the resistance to mite reproduction. This report uses data from the first year of a multiyear study.
Evaluation of Rose Cultivars for Resistance to Rose Rosette Disease

David Byrne\textsuperscript{a}, Natalie Anderson\textsuperscript{a}, Tom Evans\textsuperscript{b}, Sara Collins\textsuperscript{c}, Brent England\textsuperscript{d}, Katherine Solo\textsuperscript{c}, Alan Windham\textsuperscript{e}, Frank Hale\textsuperscript{e} and Mark Windham\textsuperscript{c*}

\textsuperscript{a}Texas A&M University, Dept. of Horticulture, 2133 TAMU, College Station, Texas, USA 77843
\textsuperscript{b}University of Delaware, 152 Townsend Hall, Newark, Delaware, USA 19716
\textsuperscript{c}University of Tennessee, 370 Plant Biotech Bldg., 2505 E.J. Chapman Dr., Knoxville, Tennessee, USA 37996
\textsuperscript{d}University of Tennessee, 320 Exper. Station Road, Crossville, Tennessee, USA 38571
\textsuperscript{e}Soil, Plant and Pest Center, 5201 Marchant Drive, Nashville, Tennessee, USA 37211
\textsuperscript{*}mwindham@utk.edu

Session: Biotic Stress

Rose rosette disease has devastated rose plantings in the eastern United States. In the last twenty years, numerous anecdotes of resistant rose cultivars have been reported. However, these reputedly resistant roses have not been evaluated for resistance to rose rosette disease in a replicated trial. One hundred and ninety one cultivars of roses were evaluated for resistance to rose rosette disease in Newark, Delaware and Crossville, Tennessee (2-5 replicates per location). Plants were exposed to natural inoculum via ballooning eriophyid mites and infested with mites collected from plants symptomatic for rose rosette disease. Ninety-seven cultivars have shown symptoms for rose rosette in at least one replicate at one or more test sites. Since infections of \textit{Rose Rosette Virus} can remain latent for at least twelve months, plants of the eighty-four remaining asymptomatic cultivars will be monitored in 2017. At the end of this study, all asymptomatic cultivars will be tested for \textit{Rose Rosette Virus} using PCR to insure the roses are not symptomless carriers of the virus. Cultivars with resistance for this disease will be used in breeding programs to incorporate resistance into roses with superior horticultural traits.
National Clean Plant Network for Roses

H. Brent Pemberton\textsuperscript{a}, David Byrne\textsuperscript{b}, Deborah Golino\textsuperscript{c}, Natalie Anderson\textsuperscript{b}, Sue Sim\textsuperscript{c}, and Kevin Ong\textsuperscript{d}

\textsuperscript{a}Texas A&M AgriLife Research and Extension Center, Texas A&M System, Overton, TX, USA
\textsuperscript{b}Department of Horticultural Sciences, Texas A&M University, College Station, TX, USA
\textsuperscript{c}Foundation Plant Services, University of California, Davis, California, USA
\textsuperscript{d}The Texas Plant Disease Diagnostic Laboratory, Texas A&M AgriLife Extension, College Station, TX, USA

\texttt{\textsuperscript{b}-pemberton@tamu.edu}

Session: Biotic Stress

At the urging of the grape and fruit tree industries, the National Clean Plant Network (NCPN) was established to provide high quality asexually propagated plant material free of targeted plant pathogens and pests for growers in the United States. In 2008, the NCPN was initiated with grapes and fruit tree crops. This was followed by the addition of citrus, berries and hops in 2010 and roses and sweet potatoes in 2015. Each specialty crop has its own commodity network composed of representatives from industry, academia, extension, state government and other interested experts. This program supports translational research, education and extension initiatives to maintain the network’s high quality collections and strengthen its services. Since being established in 2015, the National Clean Plant Network for Roses (NCPNR) has been working to augment, renovate and improve the current virus indexed rose collection at the Foundation Plant Services (Davis, CA), to assess the frequency of viruses in roses in the USA, to develop educational materials, and to establish the best protocols for determining the pathogen status of a rose.
Categorization of Garden Roses for Field Growth Response to Black Spot Disease

H.B. Pemberton\textsuperscript{a}, D.H. Byrne\textsuperscript{b}, W.R. Roberson\textsuperscript{a}, and Andy Black\textsuperscript{b}

\textsuperscript{a}Texas A&M AgriLife Research and Extension Center, Texas A&M System, Overton, TX, USA
\textsuperscript{b}Department of Horticultural Sciences, Texas A&M University, College Station, TX USA

\textsuperscript{b}-pemberton@tamu.edu

Session: Biotic Stress

Five garden rose cultivars and an accession of Rosa roxburghii were field planted at Overton in randomized complete blocks of 5 plants per plot to determine plant growth responses to black spot disease. Half of the plots were protected with fungicide applications and compared to the plots that were not sprayed. After two seasons of treatment, disease ratings confirmed that the fungicide applications fully controlled the disease. Disease ratings for unprotected plants corresponded to a reduction in growth in relation to the protected plots as measured by final height and dry weight. The cultivars Sun Flare and Peace were the most affected and had the only mortality in the study with a loss of 100\% and 55\% of the unsprayed plants, respectively. The cultivars Red Radiance, Carefree Wonder, and Old Blush exhibited moderate reductions in growth due to lack of fungicide protection. There was no difference in growth between sprayed and unsprayed plots of Rosa roxburghii corresponding to a lack of disease on unprotected plants. The plant responses in this study show the range of response of garden rose types to black spot infection in northeast Texas.
Virus Elimination of Rose Viruses Using Microshoot Tip Tissue Culture

S.T. Sim\textsuperscript{a}, J. Shoulders\textsuperscript{a}, N. Khuu\textsuperscript{a} N.H. Hoang\textsuperscript{a}, D.A. Golino\textsuperscript{ab\ast}

\textsuperscript{a} Foundation Plant Services, University of California, Davis, One Shields Avenue, Davis, CA 95616

\textsuperscript{b} Department of Plant Pathology, University of California, Davis, One Shields Avenue, Davis, CA 95616

\ast dagolino@ucdavis.edu

Session: Biotic stress

Foundation Plant Services at the University of California, Davis provides virus-tested rose propagation material to the rose nursery industry in the United States. Before 1999, heat treatment of potted plants was used to eliminate viruses. Success was varied and often the plant died during the treatment or was still virus-infected at the end of treatment period. In 2007 we reported on successful elimination of Apple mosaic virus (ApMV) and Prunus necrotic ringspot virus (PNRSV) using microshoot tip culture for six cultivars. Regenerated plantlets were tested by ELISA and bioassays on Rosa multiflora and Prunus serrulata ‘Shirofugen’ (cherry). However, survival was low and was cultivar dependent. In the period 2013 to 2016, 35 rose cultivars were subjected to microshoot tip tissue culture therapy; 21 cultivars were modern hybrid roses and 14 were heirloom or species roses. Microshoot tips measuring 0.5 to 0.7mm, consisting of the meristem dome plus several pairs of leaf primordia, were excised from actively growing vegetative shoots and cultured in aseptic conditions. Different media, light intensity and rooting protocols were trialed. To date the most promising two media are: MS salts and vitamins with 3% sucrose, 10 µmole benzyladeninepurine (BA) and 1.7µmole indole-3-acetic acid (IAA) or the same except with 2.5 µmole BA and 0.4 µmole IAA. A reduced light intensity to 65µmole was beneficial for initiation and maintenance of meristem shoot tips. Ex vitro rooting was more successful than in vitro rooting. 89% of plants developed roots ex vitro vs. 64% in vitro. Ex vitro rooting involved transplanting approximately 5 cm long shoots into a sealed container of moist perlite to keep humidity high. Modern rose cultivars were more amenable to tissue culture than heirloom or species roses. Plants were regenerated from 62% of the modern cultivars vs. 7% heirloom or species roses. Preliminary testing by ELISA shows that ApMV was eliminated; plants were still infected with PNRSV. Further testing and trials are ongoing.
Combating Rose Rosette Disease: Exploring development of accurate, rapid, efficient, easy-to-use and affordable virus diagnostic tools

Ramon Jordan\textsuperscript{a}, John Hammond\textsuperscript{a}, Francisco Ochoa-Corona\textsuperscript{b}, Jennifer Olson\textsuperscript{b}, Mathews Paret\textsuperscript{c}, Binoy Babu\textsuperscript{c}, Kevin Ong\textsuperscript{d} and David Byrne\textsuperscript{d}

\textsuperscript{a}Floral and Nursery Plants Research Unit, US National Arboretum, ARS, USDA, Beltsville, MD 20705 [ramon.jordan@ars.usda.gov and john.hammond@ars.usda.gov]
\textsuperscript{b}Department of Entomology & Plant Pathology, Oklahoma State University, Stillwater, OK 74078 [ochoaco@okstate.edu and jen.olson@okstate.edu]
\textsuperscript{c}North Florida Research and Education Center, University of Florida, Quincy, FL 32351 [paret@ufl.edu and binoybabu@ufl.edu]
\textsuperscript{d}Texas A&M University, College Station, TX 77843 [kevo@tamu.edu and dbyrne@tamu.edu]
*\textsuperscript{d}byrne@tamu.edu

Session: Biotic stress

Over the past several decades Rose Rosette Disease has become very serious and threatens to decimate the US rose industry. The causal agent, \textit{Rose rosette virus} (RRV, \textit{Emaravirus}), is transmitted by wind-blown eriophyid mites (\textit{Phyllocoptes fructiphilus}) and can kill a rose within 2-3 years of infection. A recently-funded USDA, NIFA, Specialty Crops Research Initiative grant involves 17 scientists in 6 states working on a range of approaches to study this disease and determine how best to manage it. The only strategy currently available for disease management is early identification and eradication of the infected plants, thereby limiting its potential spread. Key to this effort is the development of efficient and affordable diagnostic tools to enable accurate detection of the virus. Molecular- and serological-based assays with potential for technology transfer and/or on-site implementation should be easy to use, offering visual detection, reliability and sensitivity to the end user. RRV-specific primers and probes (for nucleic acid-based tests) and monoclonal and polyclonal antibodies (for serology-based tests) have been developed. The rabbit polyclonal and five mouse monoclonal RRV-specific antibodies can detect viral nucleoprotein in various ELISA and western-blot formats. Validation of detection of virus from field-collected samples is in progress. An additional goal is to produce a serological lateral flow device for in-field diagnosis. Loop-mediated isothermal amplification (LAMP) and thermophilic helicase dependent amplification (tHDA) assays have been developed and are isothermal DNA amplifications which combine several desirable criteria and do not require a thermocycler. A rapid 15 minute probe-based isothermal Reverse Transcription-recombinase polymerase amplification (RT-exoRPA) assay was also developed. Broad detection of \textit{Emaravirus} and species discrimination was targeted with Reverse Transcription polymerase chain reaction (RT-PCR) coupled to High Resolution Melting (HRM) analysis. A single primer-set suitable for use with three different chemistries [Endpoint RT-PCR, TaqMan-quantitative RT-PCR (RT-qPCR) and SYBR Green RT-qPCR with High Resolution Melting] was also developed. An immune-capture RT-PCR based protocol will be evaluated. The most consistent assay(s) will be tested and validated by several diagnostic labs and then moved via outreach to other plant diagnostic labs. The contribution of these methods within a holistic perspective of RRV diagnostics will be presented.
Thrips management program for ornamental plants

Vivek Kumar\textsuperscript{a*}, Garima Kakkar\textsuperscript{b}, Cristi Palmer\textsuperscript{c}, Wayne Myers\textsuperscript{d}, Cindy L. McKenzie\textsuperscript{e} and Lance S. Osborne\textsuperscript{a}

\textsuperscript{a}University of Florida, Mid-Florida Research & Education Center, 2725 S. Binion Road Apopka, FL 32703, USA
\textsuperscript{b}UF/IFAS St. Lucie County Extension, 8400 Picos Road, Suite 101, Ft. Pierce, FL 34945, USA
\textsuperscript{c}The State University of New Jersey, IR-4 Project Headquarters, 500 College Road East
Suite 201 W Princeton, NJ 08540, USA
\textsuperscript{d}Deep South District of the American Rose Society, St. Augustine, FL, USA
\textsuperscript{e}United States Horticulture Research laboratory, ARS-USDA, 2001 South Rock Road
Fort Pierce, FL 34945, USA

\*vivekiari@ufl.edu

Session: Biotic Stress

Among the 5,500 (or more) well-described species of thrips (Thysanoptera: Thripidae) worldwide, nearly 1% are known as economically important pests Owing to their polyphagous nature and damage potential to nursery and greenhouse production, thrips inflict millions of dollars loss annually. Thrips can reduce yield and/or the aesthetic or economic value of plants directly by causing feeding and egg laying injury, and indirectly by transmitting plant-damaging viruses to their hosts. Their small size (1–2 mm), tendency to hide in tiny spaces, high reproductive rate, and ability to survive in a wide range of climatic conditions help explain their significant representation on invasive pest lists of many countries. Thrips infestations can greatly impact regional and international trade of plant materials and products, due to the quarantine risks and damage associated with several species in the order.

There are multiple thrips species known to cause economic damage to rose production in the US, among which in recent years chilli thrips, \textit{Scirtothrips dorsalis} Hood has been a frequent invader. Based on the available record in Global Pest and Disease Database, \textit{S. dorsalis} is extremely polyphagous, feeding on more than 200 different plant taxa, and is one of the only 14 species in the order Thysanoptera known to transmit plant damaging tospoviruses. Their small size (>2 mm), high reproductive potential, multivoltine nature, ability to feed and reproduce on multiple hosts and adaptation to a wide range of climatic conditions makes \textit{S. dorsalis} a major concern for agriculture in many countries. After the United States invasion in 2005, established populations of \textit{S. dorsalis} have been reported on numerous hosts from 30 different counties in Florida, 8 counties in Texas, 2 counties in California with detections in Alabama, Louisiana, Georgia, New York and Massachusetts. In recent years, it has emerged as a major problem for local rose growers in FL, TX, and CA. In the wake of the economic importance of this pest on the United States rose industry, we developed a management program to control \textit{S. dorsalis} along with another thrips species, \textit{Frankliniella occidentalis} (Pergande) known to attack different cultivars of rose in the region. The Thrips Management Program does not recommend insecticide applications when thrips are first detected. Instead, the program outlines steps to manage and maintain thrips populations throughout initial plant propagation and growth stages at levels that allow the final plant material to be shipped. The program provides guidance on best management practices, including scouting, sanitation, exclusion, biological control, and chemical control.
VII International Symposium on Rose Research and Cultivation

July 2-7, 2017        Angers (France)
VII International Symposium on Rose Research and Cultivation

July 2-7, 2017
Angers (France)

Organized by

With the support of

Sponsors & Partners

information

https://symposium.inra.fr/ishs-rose2017