37th New Phytologist Symposium

Plant developmental evolution

Fragrant Hill Empark Hotel, Beijing, China
15 – 19 May 2016

Scientific Organizing Committee
Hongzhi Kong (Institute of Botany, the Chinese Academy of Sciences, Beijing, China)
Mark Rausher (Duke University, Durham, NC, USA)

New Phytologist Organization
Helen Pinfield-Wells (Deputy Managing Editor)
Sarah Lennon (Managing Editor)
Jill Brooke (Journal & Finance Administrator)

Acknowledgements
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New Phytologist Trust
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Programme, abstracts and participant list compiled by Jill Brooke
‘Plant development evolution’ logo by A.P.P.S., Lancaster, United Kingdom

Contact email: np-symposia@lancaster.ac.uk
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Information for Delegates

Symposium location
The 37th New Phytologist Symposium will be held at the Fragrant Hill Empark Hotel, No. 59 North Zhenghuangqi, Shijingshan, China.
http://fragrant-hill-empark-hotel.beijinghotelchina.net/#mobile-accordion

A map showing the location of the hotel can be found online at http://fragrant-hill-empark-hotel.beijinghotelchina.net/map/#mobile-accordion

All presentations will be given in the Kingcity Banquet Hall. Posters will also be displayed in this hall.

Catering
Please note that each day of the meeting there will be a morning tea and coffee break, there will also be two poster sessions please note these are included in your registration fee.

The following meals are also included in your registration fee.

Sunday 15th May – Welcome Dinner, Chinese Dining Room, Fragrant Hill Empark Hotel
Monday 16th May – Lunch and Dinner, Western Dining Room, Fragrant Hill Empark Hotel
Tuesday 17th May – Lunch and Dinner, Western Dining Room, Fragrant Hill Empark Hotel
Wednesday 18th May – Lunch, Western Dining Room, Fragrant Hill Empark Hotel; Symposium Dinner, Four Seasons Royal Garden International Hotel.
Thursday 19th May – Lunch, Western Dining Room

Excursion and Symposium Dinner
On Wednesday afternoon there will be a group excursion to the Summer Palace. Please note that the cost of this trip is included in your registration fee. Buses will depart from the Fragrant Hill Empark Hotel at 14:00. After the excursion we will stop for the Symposium dinner at the Four Seasons Royal Garden International Hotel and buses will then return to the Fragrant Hill Empark Hotel around 20:00.

Accommodation
If you are staying at the Fragrant Hill Empark Hotel, please note that check-in is from 14:00 and you should check-out before 12:00. If you have chosen to include accommodation in your registration this covers 4 nights (15th, 16th, 17th and 18th May). There is also an option to book additional nights by contacting New Phytologist. All accommodation includes breakfast.

Posters
Posters should be prepared so that they are no larger than A0 size, portrait orientation (118 cm high x 84 cm wide). Posters should be put up during registration (16:00–19:30 on 15th May) and will be displayed for the duration of the meeting. Delegates are welcome to view posters during coffee and lunch breaks, but there will be a dedicated poster sessions at 20:30–22:00 on Monday 16 May and Tuesday 17 May. Please stand by your poster for part of this session (we appreciate as poster presenters you will also want to view and discuss the other posters). Please note there will be prizes for the best poster presentations.

Internet access
Free wifi will be provided throughout the venue. If you are staying at the hotel wifi access information will be provided when you check in. Please ask a member of the New Phytologist team for access if you are not staying at the Fragrant Hill Empark Hotel and they will be happy to help.
Contact
For further information, and in case of any emergencies, please contact Helen Pinfield-Wells. Email: h.pinfield-wells@lancaster.ac.uk, np-symposia@lancaster.ac.uk; tel: +44 7966 450 389.
## Meeting Programme

### Sunday 15 May

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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</thead>
<tbody>
<tr>
<td>16:00–19:30</td>
<td>Arrival, check-in and registration</td>
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</table>

### 18:00

**Welcome Dinner, Chinese Dining Room**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>19:30–20:00</td>
<td>Welcome from the symposium organisers and <em>New Phytologist</em></td>
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<tr>
<td></td>
<td>Hongzhi Kong, Mark Rausher and Sarah Lennon</td>
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<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>20:00–21:00</td>
<td><strong>Keynote lecture with discussion - Mark Rausher</strong></td>
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<td></td>
<td>Evolutionary genetics of floral patterning</td>
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</tbody>
</table>

### Monday 16 May

**Session 1: Floral Development**

**Chair:**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09:00–12:30</td>
<td><strong>Introduction from Chair of the session</strong></td>
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<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09:00–09:05</td>
<td><strong>S1.1 Madeleine Bartlett</strong></td>
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<tr>
<td></td>
<td>The evolution of MADS-box protein-protein interactions and gene regulatory evolution</td>
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<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09:05–09:40</td>
<td><strong>S1.2 Hongzhi Kong</strong></td>
</tr>
<tr>
<td></td>
<td><em>Nigella</em> as a new model system for the study of plant developmental evolution</td>
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<th>Time</th>
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<tbody>
<tr>
<td>09:40–10:15</td>
<td><strong>S1.3 Chaoying He</strong></td>
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<tr>
<td></td>
<td>Evolutionary developmental genetics of fruit morphological variation in <em>Physalis</em></td>
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<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>10:15–10:50</td>
<td><strong>S1.4 Da Luo</strong></td>
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<td></td>
<td>TBC</td>
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<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>11:20–11:55</td>
<td><strong>S1.5 Lena Hileman</strong></td>
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<tr>
<td></td>
<td>Convergence in flower form: from evolutionary patterns to developmental processes</td>
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<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>10:50–11:20</td>
<td><strong>Break</strong></td>
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<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>11:20–11:55</td>
<td><strong>Lunch, Western Dining Room</strong></td>
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### 13:30–16:00

**Free Time**

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<th>Time</th>
<th>Activity</th>
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<tr>
<td>16:00–17:00</td>
<td>TBC</td>
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<tr>
<td>Time</td>
<td>Activity</td>
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<tr>
<td>17:30–19:30</td>
<td>Dinner, Western Dining Room</td>
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<tr>
<td>19:30–20:30</td>
<td><strong>Keynote lecture with discussion – Beverley Glover</strong></td>
</tr>
<tr>
<td></td>
<td>Integrated evo-devo of the petal epidermis: development, function and</td>
</tr>
<tr>
<td></td>
<td>evolution of structures that influence pollinator behaviour</td>
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<tr>
<td>20:30–22:00</td>
<td>Poster Session</td>
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**Tuesday 17 May**

**Session 2: Vegetative meristems, leaves, and inflorescences**  
**Chair:**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09:00–12:30</td>
<td>Introduction from Chair of the session</td>
</tr>
<tr>
<td>09:05–09:40</td>
<td><strong>S2.1 Neelima Sinha</strong></td>
</tr>
<tr>
<td></td>
<td>Heteroblasty and Heterophylly – when two programs collide</td>
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<tr>
<td>09:40–10:15</td>
<td><strong>S2.2 Mitsuyasu Hasebe</strong></td>
</tr>
<tr>
<td></td>
<td>Life cycle of <em>Physcomitrella patens</em> as transitions of eight types of</td>
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<td></td>
<td>stem cells</td>
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<tr>
<td>10:15–10:50</td>
<td><strong>S2.3 Paula Elomaa</strong></td>
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<tr>
<td></td>
<td>Recruitment of floral meristem identity genes for patterning of the</td>
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<tr>
<td></td>
<td>flower-like Asteraceae inflorescence</td>
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<tr>
<td>10:50–11:20</td>
<td>Break</td>
</tr>
<tr>
<td>11:20–11:55</td>
<td><strong>S2.4 Elizabeth Kellogg</strong></td>
</tr>
<tr>
<td></td>
<td>Evolution and function of CLE genes and the control of meristem size in</td>
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<tr>
<td></td>
<td>grasses</td>
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<tr>
<td>11:55–12:30</td>
<td><strong>S2.5 Angela Hay</strong></td>
</tr>
<tr>
<td></td>
<td>Morphomechanical innovation drives explosive seed dispersal</td>
</tr>
<tr>
<td>12:50–13:30</td>
<td>Lunch, Western Dining Room</td>
</tr>
<tr>
<td>13:30–16:00</td>
<td>Free Time</td>
</tr>
<tr>
<td>16:00–17:00</td>
<td>TBC</td>
</tr>
<tr>
<td>17:30–19:30</td>
<td>Dinner, Western Dining Room</td>
</tr>
<tr>
<td>19:30–20:30</td>
<td><strong>Keynote lecture with discussion – Miltos Tsiantis</strong></td>
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<tr>
<td></td>
<td>Development and diversitity of leaf shape: from understanding to</td>
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<tr>
<td></td>
<td>reconstructing</td>
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<tr>
<td>20:30–22:00</td>
<td>Poster Session</td>
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</tbody>
</table>

**Wednesday 18 May**
### Session 3: Selected talks from the poster abstracts

**Chair:**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session Details</th>
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</thead>
<tbody>
<tr>
<td>09:00–09:05</td>
<td>Introduction from Chair of the session</td>
</tr>
</tbody>
</table>
| 09:05–09:25 | **Jinshun Zhong**  
Functional changes in NAC-domain transcription factors are implicated in the evolution of petal fusion |
| 09:25–09:45 | **Lidan Sun**  
The genetic architecture of heterochrony in *Prunus mume* |
| 09:45–10:05 | **Nicola Illing**  
Evolution of vegetative desiccation tolerance in the resurrection plant, *Xerophyta humilis* |
| 10:05–10:25 | **Shihao Su**  
Unveiling the molecular basis of floral zygomorphy in Lamiales: *Torenia fournieri* as a model species |
| **10:25–11:00** | **Break** |
| 11:00–11:20 | **Teng Zhang**  
Dissecting the functions of *SEPALLATA*-like genes in patterning of the pseudanthium-type inflorescence of *Gerbera hybrida* (Asteraceae) |
| 11:20–11:40 | **Aaron Leichty**  
Heterochrony and patterns of leaf morphology in the Acacieae |
| 11:40–12:00 | **Yichun Qiu**  
Concerted neofunctionalization of duplicated gene products in the Brassicaceae PRC2 complexes rewiring the regulatory pathways in seed development |
| 12:00–12:20 | **Leandro Lucero**  
A mechanistic model of stamen filament development that may contribute to mating system evolution in Brassicaceae |
| 12:20–13:00 | Discussion |
| **13:00** | **Lunch, Western Dining Room** |
| **14:00** | **Buses leave for Excursion to the Summer Palace.** |
| **18:00** | **Symposium Dinner, Four Seasons Royal Garden International Hotel** |
| **20:00** | **Buses return the Fragrant Hill Empark Hotel** |

*Thursday 19 May*
**Session 4: Plasticity and life history evo-devo**  
**Chair:**  
09:00–13:15

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00–09:05</td>
<td>Introduction from Chair of the session</td>
<td></td>
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</tr>
<tr>
<td>09:05–09:40</td>
<td><strong>S4.1 Rowan Sage</strong></td>
<td>Reconfiguring leaf development during C₄ evolution</td>
<td></td>
</tr>
<tr>
<td>09:40–10:15</td>
<td><strong>S4.2 Dan Runcie</strong></td>
<td>Genetic signals accumulate throughout development to regulate flowering time in <em>Arabidopsis thaliana</em></td>
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<tr>
<td>10:15–10:50</td>
<td><strong>S4.3 Kathleen Donohue</strong></td>
<td>Pleiotropy in the environmental regulation of germination and flowering</td>
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<tr>
<td><strong>10:50–11:20</strong></td>
<td><strong>Break</strong></td>
<td></td>
<td></td>
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<tr>
<td>11:20–11:55</td>
<td><strong>S4.4 Martin Lercher</strong></td>
<td>Modeling the evolution of C₄ photosynthesis</td>
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<tr>
<td>11:55–12:30</td>
<td><strong>S4.5 Ana Caicedo</strong></td>
<td>All roads lead to weediness? Dissecting the extent of parallel evolution in weedy rice</td>
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<tr>
<td>12:30–13:00</td>
<td>Formal Discussion</td>
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<tr>
<td>13:00–13:15</td>
<td>Closing comments from organisers</td>
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<tr>
<td><strong>13:15</strong></td>
<td><strong>Lunch, Western Dining Room</strong></td>
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</tbody>
</table>
Speaker Abstracts

S=speaker abstract; P=poster abstract

Bartlett, Madeleine  S1.1
Caicedo, Ana  S4.5
Donohue, Kathleen  S4.3
Elomaa, Paula  S2.3
Glover, Beverley  Keynote
Hasebe, Mitsuyasu  S2.2
Hay, Angela  S2.5
He, Chaoying  S1.3
Hileman, Lena  S1.5
Kellogg, Elizabeth  S2.4
Kong, Hongzhi  S1.2
Lercher, Martin  S4.4
Luo, Da  S1.4
Rausher, Mark  Keynote
Runcie, Daniel  S4.2
Sage, Rowan  S4.1
Sinha, Neelima  S2.1
Tsiantis, Miltos  Keynote
Petal spots and other markings are generally believed to be adaptations for attracting pollinators. Little information, however, is available on the genetic and developmental changes that underlie the evolution of floral color patterns. In the genus *Clarkia*, many species have a single large spot on each petal. Our lab is investigating the genetic changes responsible for three facets of petal spot evolution: (1) the origin of spots; (2) the evolution of spot position; and (3) the evolution of spot color. In this talk, I will present evidence that spots originated from a duplication of an *R2R3Myb* anthocyanin transcription factor and that a shift in spot position from basal to central involved a change in the expression domain of that gene.
The abrupt origin and rapid diversification of the flowering plants presents what Darwin called ‘an abominable mystery’. Floral diversification was a key factor in the rise of the flowering plants, but the molecular underpinnings of floral diversity remain mysterious. One factor that has likely been instrumental in the evolution of floral diversity is the evolution of gene regulation downstream of the MADS-box transcription factors. The evolution of gene regulation has long been considered predominantly in terms of the evolution of regulatory DNA. However, theory shows that changing interactions between transcription factor proteins could be just as important as changing regulatory DNA. When considering the MADS-box proteins in particular, protein–protein interactions are likely to have been of fundamental importance in the evolution of downstream gene regulation. All MADS-box proteins bind DNA as dimers, and the floral MADS-box proteins probably function as part of large complexes in planta. In single species, altered MADS-box protein–protein interactions disrupt or change MADS-box protein function. Across evolutionary time, changing MADS-box protein–protein interactions have been repeatedly invoked for the origin of the flower, and in the evolution of floral diversity. In the grasses, I have shown that there have been frequent shifts in B-class dimerization, under positive selection. What has been missing is an experimental system to test evolutionary hypotheses about changing MADS-box protein–protein interactions and the evolution of gene regulation. My lab has been working to establish a system in the grasses where we can manipulate MADS-box protein-protein interactions, and directly test their impact on downstream gene regulation. I will discuss the evolutionary history of B-class MADS-box protein–protein interactions in the grasses and their relatives, and our work testing the impact of protein–protein interactions on the evolution of downstream gene regulation.
Nigella as a new model system for the study of plant developmental evolution

HONGZHI KONG

hzkong@ibcas.ac.cn

State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany; Chinese Academy of Sciences, Nanxincun 20, Xianshan, Beijing 100093, China
Evolutionary developmental genetics of fruit morphological variation in *Physalis*

**CHAODING HE**$^{1,2}$, **JING ZHAO**$^{1,2}$, **YING TIAN**$^1$, **LI WANG**$^1$, **ZHICHAO LI**$^{1,2}$, **JING LI**$^{1,2}$

chaoying@ibcas.ac.cn

$^1$State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing, China; $^2$Graduate University of Chinese Academy of Sciences, Beijing, China

Morphological variations of fruits such as shape and size are a result of adaptive evolution, and facilitate seed dispersal. The evolution of morphological novelties is particularly intriguing. An understanding of these evolutionary processes calls for the elucidation of the developmental and genetic mechanisms that underlie particular fruit morphological characteristics. Unlike *Solanum* and *Capsicum* species, *Physalis* has a distinguished fruit morphology with a papery husk as the accessory trait of fruits. The balloon-like structure encapsulates the berry inside. The distinct trait of *Physalis* species is termed Chinese lantern or inflated calyx syndrome (ICS) since it is a derivative of the calyx. Compared with most Solanaceous species, it is a post-floral morphological novelty. Here, I will report our main progress on the evolutionary developmental genetics of berry size variation and Chinese lantern in *Physalis*. We revealed that the origin of Chinese lantern is associated with heterotopic expression of the MADS-box gene *MPF2* in floral organs, while its identity is determined by another MADS-box protein *MPF3* that interacts with *MPF2*/*MPF2*. For natural variation of berry size, we found that the *Physalis Organ Size1* (*POS1*), an AP2-like gene, positively controls fruit size in *P. philadelphica* (tomatillo), and copy variation of a 37-bp repeats in the first intron of *POS1* alleles determines their differential expression levels in ovaries. While the heterochronic expression levels of another gene *POS2*, a putative ortholog of tomato *FW2.2*, in ovaries are negatively correlated with berry size variation among *Physalis* species. Our studies suggest that the recruitment of a pre-existing gene and subsequent modification of its interaction and regulatory networks are frequently involved in the evolution of morphological diversity. Our work also provides insights into plant developmental processes and will help to improve the productivity of crops. Moreover, *Physalis* has been established as an emerging model plant for development, evolution and ecology.
TBC

DA LUO

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School of Life Sciences, Sun Yat-Sen University, Guangzhou 510275, China
Convergence in flower form: from evolutionary patterns to developmental processes

LENA HILEMAN¹, CAROLYN WESSINGER¹, JILL PRESTON², MARK RAUSHER³

lhileman@ku.edu

¹Ecology and Evolutionary Biology, University of Kansas, Lawrence KS, USA; ²Plant Biology, University of Vermont, Burlington VT, USA; ³Biology, Duke University, Durham NC, USA

Convergent flower phenotypes have been largely shaped by repeated evolution of plant-pollinator interactions. Parallel genetic mechanisms determining convergent floral traits suggest that certain transitions are not only repeatedly favored, but can be readily generated through recurrent mutation. During angiosperm diversification, bilaterally symmetrical flowers have evolved multiple times from radial symmetry, and reversals from bilateral to radial symmetry are not uncommon. Our data contribute to a growing literature suggesting that independent origins of bilateral flower symmetry involve repeated recruitment of a CYCLOIDEA-dependent developmental program, and that reversals to radial symmetry largely involve regulatory changes to this program. Breaking radial symmetry can be considered a largely qualitative change in floral morphology. However, many differences in floral form, especially among closely related species that differ in mating system or pollination biology, are quantitative, for example the size and shape of floral organs. To test whether convergent evolution of quantitative floral differences utilizes parallel genetic mechanisms, we have developed the genus Penstemon as a model study system. Penstemon exhibits a dynamic history of flower evolution. Our phylogenomic results demonstrate that hummingbird adapted flowers have evolved multiple times within bee adapted lineages. Importantly, many floral trait differences associated with the two pollination strategies are quantitative. Although we have yet to determine the genetic basis for multiple transitions to hummingbird pollination, our characterization of the genetic architecture of hummingbird adaptation in one species pair suggests that few mutations of large effect may spur the initial shift in floral traits. We also find that individual loci may pleiotropically influence multiple floral traits, which may accelerate evolutionary shifts to hummingbird pollination.
Flowers and the animals that pollinate them interact at a single key point – the petal epidermis. It is this single layer of tissue that provides the visual surface that advertises nectar and pollen rewards. It is on this layer of tissue that pollinators land, finding grip or slipping, and using tactile cues to locate rewards. And it is often from this layer of tissue that the scents that attract pollinators over longer ranges are released. Our recent research has focused on the optical and tactile effects of the petal surface. The majority of petal surface morphologies will act to support certain plant/pollinator interactions but not others, providing opportunities for reproductive isolation and speciation within the angiosperms. I will present recent work on the nanoscale and microscale properties of the petal surface, describing an integrated approach that combines developmental genetic, evolutionary and pollinator behavioural perspectives.
How morphological diversity has arisen is a key question in biology. Angiosperms exhibit a great diversity in leaf shape and leaf development has been characterized in several species, making leaves ideal targets to understand the mechanism behind morphological natural variation. Leaves are also functionally significant for generating biomass and leading to agricultural yield. We have deduced a gene co-expression network underlying leaf development in tomato and its relatives. Molecular experiments and hypothesis testing validated the bioinformatically predicted GRN and identified key components, such as BLADE-ON-PETIOLE (BOP), within the gene network module regulating leaf shape. Alteration in BOP expression by transgenic experiments in tomato, S. pennellii and S. habrochaites, can recreate naturally occurring leaf phenotypes in the tomato species complex. In addition to evolutionary and developmental variability, leaves also exhibit phenotypic plasticity. We are analyzing gene expression alterations when leaf complexity changes in response to either developmental time or environmental perturbations to determine what common features are shared between these two diverse programs.
Stem cells self-renew and produce cells that differentiate to become the source of the plant body. The moss *Physcomitrella patens* forms eight types of stem cells during its life cycle and serves as a useful model in which to explore the evolution of such cells. The common ancestor of land plants is inferred to have been haplontic and to have formed stem cells only in the gametophyte generation. A single stem cell would have been maintained in the ancestral gametophyte meristem, as occurs in extant basal land plants. During land plant evolution, stem cells diverged in the gametophyte generation to form different types of body parts, including the protonema and rhizoid filaments, leafy-shoot and thalloid gametophores, and gametangia formed in moss. A simplex meristem with a single stem cell was acquired in the sporophyte generation early in land plant evolution. Subsequently, sporophyte stem cells became multiple in the meristem and were elaborated further in seed plant lineages, although the evolutionary origin of niche cells, which maintain stem cells is unknown. Comparisons of gene regulatory networks are expected to give insights into the general mechanisms of stem cell formation and maintenance in land plants and provide information about their evolution. *Physcomitrella patens* develops at least seven types of simplex meristem in the gametophyte and at least one type in the sporophyte generation and is a good material for regulatory network comparisons. In this talk, I will summarize recently revealed molecular mechanisms of stem cell initiation and maintenance in the moss and their evolution in land plants.
Recruitment of floral meristem identity genes for patterning of the flower-like Asteraceae inflorescence

YAFEI ZHAO1, TENG ZHANG1, SUVI K. BROHOLM1, SARI TÄHTIHARJU1, KATRIINA MOUHU1, VICTOR A. ALBERT2, TEEMU. H. TEERI1, PAULA ELOMAA1

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A key question in biology is to understand how organismal form is generated. In plants, an important aspect of the form is the architecture of inflorescences that may vary from a single flower to large flower clusters, and is thus one of the major determinants of crop yield and reproductive success of plants. Still, the development and evolution of distinct inflorescence forms remain poorly understood. Most of our knowledge on the molecular underpinnings of inflorescence architecture is based on studies in the classical model plants; Arabidopsis with racemes and Solanaceous species such as petunia and tomato with cymes. In the large sunflower plant family, Asteraceae, the inflorescence (flower head, or capitulum) forms a pseudanthium, a “false flower” that superficially resembles a solitary flower but is a highly compressed structure consisting of different types of flowers. In the model plant Gerbera hybrida, capitulum development involves rapid expansion of the meristem, initiation of hundreds of individual flowers in a spiral manner, and differential development of distinct flower types. We have conducted functional analyses for the gerbera orthologs of LEAFY (GhLFY) and UNUSUAL FLORAL ORGANS (GhUFO) and show that these highly conserved genes that regulate flower meristem identity of single flowers in many conventionally used model plants, have been recruited for patterning of the entirety of this unique structure. Especially GhLFY has evolved novel functions in specifying the determinacy of the inflorescence meristem that can assume floral fate upon ectopic GhUFO expression. We also provide evidence that LFY regulates the early ontogeny of the marginal ray flowers and has a key role in differentiation of peripheral ray flowers. Altogether, our data clarifies the distinct botanical hypotheses that have been proposed for the evolutionary origin of this complex and evolutionary successful inflorescence architecture in Asteraceae.
Evolution and function of CLE genes and the control of meristem size in grasses

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Genes related to CLAVATA3 (CLV3) in Arabidopsis and the ESR genes in maize (CLE genes) produce proteins that are processed to release small signaling peptides of 14 amino acids. These peptides are involved in a wide variety of cell-cell signaling processes, with some of the best-characterized ones regulating meristem size. We have used model-based searches to retrieve over 1000 CLE genes from available plant genomes, and have identified sets of genes with similar sequences. We find that the CLE genes must have diversified early in the evolution of land plants; they underwent additional duplications in major clades of angiosperms. Genes with similar sequences in the CLE domain apparently share developmental roles, although this hypothesis has not been widely tested. One cluster of proteins includes CLV3, the rice protein FLORAL ORGAN NUMBER2 (FON2), and putative orthologs in various grasses. Surprisingly FON2 is in a very dynamic genomic region, such that apparently orthologous genes in maize, Setaria and Brachypodium are broadly syntenic but colinearity is disrupted. Multiple CLE genes (not just FON2-like genes) are up-regulated during inflorescence development of Setaria and maize, although the FON2 orthologs themselves are expressed at relatively low levels. If FON2-like genes are indeed involved in maintaining meristem size, as appears likely from their expression pattern and sequence similarity to CLV3, then they may play an important role in controlling inflorescence architecture and phyllotaxy. The size of branch meristems relative to the inflorescence meristem varies considerably among grasses and leads to marked differences in adult morphology. In particular, grasses related to maize and sorghum produce spikelets in pairs; the pair arises from a meristem that is notably larger than a single spikelet meristem. We suggest that CLE genes may be involved in the maintenance and possibly the evolutionary origin of the spikelet pair.
Morphomechanical innovation drives explosive seed dispersal

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How mechanical and biological processes are integrated across different scales to create complex traits is largely unknown. In this work, we combine biological, mathematical, and computational approaches to understand the mechanical basis for explosive seed dispersal – a key life history trait underpinning invasive behavior in the common weed Cardamine hirsuta. We have exploited the experimental tractability of C. hirsuta – a close relative of the model organism Arabidopsis thaliana – to understand the mechanism of explosive pod shatter and provide insights into the origin of this striking trait.
A key challenge in biology is to understand how diversity in organismal form is generated. Genetic analyses in model systems have identified key regulators that sculpt the body plans of metazoa and seed plants. However, less is known about how the action of such regulators produces particular organ shapes, or how the balance of conservation versus divergence of such form regulating pathways generated the tremendous morphological diversity of multicellular eukaryotes. One impediment to answering these questions is the relative paucity of experimental platforms where genetic tools can be utilized to unambiguously study morphogenesis and its evolution in a genome-wide, unbiased fashion. To circumvent this problem we developed the *Arabidopsis thaliana* relative *Cardamine hirsuta* into a versatile system for studying morphological evolution. We aim to understand the molecular mechanisms through which leaf morphology evolved in these species, resulting in simple, undivided leaves in *A. thaliana* and dissected leaves with distinct leaflets in *C. hirsuta*. This presentation will discuss our progress towards understanding the genetic pathways that specify dissected versus entire leaf shapes and that regulate the number, position and timing of leaflet production.
### Session 3: Selected talks from the poster abstracts

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Reconfiguring leaf development during C₄ evolution

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C₄ photosynthesis is a complex evolutionary syndrome arising from rearrangements in leaf structure and metabolism that enable CO₂ concentration around Rubisco. Despite its complexity, it is one of the most convergent of traits, with over 60 independent origins. These many origins facilitate comparative studies that evaluate developmental transitions leading to C₄ photosynthesis. With our collection of closely related C₃, C₄ and C₃-C₄ intermediate species from a dozen lineages, we are conducting comparative studies addressing hypothesis regarding i) the earliest events in C₄ evolution; ii) altered patterns of chloroplast development in mesophyll (M) and bundle sheath (BS) cells; and iii) variation in the timing of developmental events affecting Kranz anatomy. Transcriptome profiles were coupled with phenotypic analysis to assess potential genetic controls altered during C₄ evolution. In both monocots and dicots, the earliest events in C₄ evolution are associated with increased organelle number and polarity in BS cells of C₃ ancestors. In these species, mitochondria and peroxisome localize along the inner edge of the sheath cells, indicating the BS physiology becomes more engaged with vascular function. In all twelve lineages, C₄ plants had half as many chloroplasts in M cells than their C₃ ancestors. Along a phylogenetic gradient from C₃ to C₄ species of Flaveria, M chloroplast numbers are correlated with C₄ cycle strength and reduced expression of the chloroplast division genes FtsZ-1 and FtsZ-2. Reduced transcript abundance of these genes indicate evolution targeted Z-ring formation as a means to implement the C₄ pattern. In numerous eudicot and grass species, vascular tissue development is accelerated in C₄ relative to the C₃ plants, and in Atriplex, this acceleration is correlated with increased transcript abundance of genes known to control vascular specification, such as the auxin exporter PINFORMED 1 and auxin response factor MONOPTEROS.
The timing of flowering time in annual plants is regulated by numerous environmental and endogenous cues. This plasticity is critical for fitness and is frequently under strong natural selection. Genetic and developmental mechanisms underlying flowering time plasticity have been well characterized in *Arabidopsis thaliana*. However, predicting how any particular combination of genetic variants will affect flowering time remains a challenge, particularly in natural environments where environmental conditions change continuously. An important question is how rapid reactions of genetic signaling pathways to fluctuating environmental cues can be integrated into robust seasonal responses. Recent work has shown that combining genetic information with ecophysiology-based models can accurately model the plasticity of certain genotypes in natural environments.

Here, we investigate the hypothesis that physiology (photosynthesis, growth) and morphology (plant size and conformation) are critical for seasonal integration of fluctuating cues. We use a combination of computational modeling and gene expression assays to test this hypothesis and propose an integrated physiological-genetic framework for understanding flowering time variation across genotypes and seasonal environments.
Pleiotropy occurs when one gene regulates more than one trait, and it can be a strong constraint on the adaptive evolution of trait combinations. In many organisms, several major developmental transitions between life stages are regulated by seasonal environmental factors, and the appropriate coordination of developmental transitions across the lifecycle is necessary to express adaptive life-history schedules. Many life stages may be sensitive to the same environmental factors, but they must respond to them differently. How do multiple life stages use the same environmental inputs to regulate their independent developmental transitions in a manner that results in adaptive life-history expression? We examined pleiotropy between the environmental regulation of two important life-stage transitions in plants: seed germination and the transition to reproduction. We tested whether genes known to regulate flowering responses to environmental cues also regulate seed germination in *Arabidopsis thaliana*. We found extensive pleiotropy between flowering and germination regulation. First, the major flowering gene *Flowering Locus C (FLC)* contributes to seed germination, such that increased FLC activity is associated with increased germination. Regarding the vernalization pathway, both promoters and repressors of FLC expression also contribute to germination, but in ways that are not predicted based on their function in the flowering pathway. Likewise, genes in the autonomous pathway and the photoperiod pathway contribute to germination, but in ways that are not always predictable from their function in the flowering pathway. In sum, genes in the vernalization flowering pathway, the autonomous flowering pathway, and the photoperiod flowering pathway all contribute to seed germination. The combined results suggest that, although the same environmental-sensing pathways are used to regulate these two developmental transitions, the function of genes in those pathways is not always concordant across germination and flowering. Despite pleiotropy, these two developmental transitions appear to be able to be regulated independently to a great degree.
Modeling the evolution of C₄ photosynthesis

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The prediction of long-term metabolic adaptation is generally hampered by incomplete information on environmental changes. One exception is the evolution of C₄ metabolism as an adaptation to rising oxygen levels, which independently occurred in over 60 plant lineages. C₄ photosynthesis is an adaptation to environments prompting high rates of photorespiration. Using a mechanistic model of carbon fixation under conditions favorable for C₄, we have shown that C₄ photosynthesis evolves on a very simple, ‘Mount Fuji’-like fitness landscape. Experimental data from C₃–C₄ intermediate plants fall along the clustered trajectories predicted by a simple evolutionary model. Surprisingly, individual adaptive steps towards C₄ metabolism provide fitness advantages of roughly uniform size, and the rate of adaptation does not slow down during the progression towards the peak of highest fitness. Linking the mechanistic model for carbon fixation with a whole-cell constraint-based model allows to explore different pathways to relieve the nitrogen imbalance caused between mesophyll and bundle sheath cells by the C₂ cycle, a frequent evolutionary predecessor to C₄ photosynthesis. The results suggest that balanced C₂ cycles may already implement important components of the C₄ cycle, thereby further accelerating the evolution of C₄ photosynthesis.

Compared to the ancestral C₃ pathway, C₄ metabolism is energetically more costly. To determine the dependence of C₄ evolution on the availability of light and nitrogen, on temperatures, and on atmospheric CO₂ and O₂ levels, we have recently extended the previous model that assumed highly favorable conditions for C₄. With this model, we show that the optimal distribution of resources – nitrogen and energy – across cell types and pathways explains photosynthetic characteristics of C₃, C₃-C₄ intermediate, and C₄ species from the genus Flaveria under various environmental conditions.
All roads lead to weediness? Dissecting the extent of parallel evolution in weedy rice

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Agricultural weeds are one of the largest constraints on crop productivity. This is due, in part, to weedy plants’ intrinsic capacity for adaptation. Various traits such as rapid growth, herbicide resistance, efficient seed dispersal, and seed dormancy are common in weed species and may help their adaptation to the agricultural environment. However, except for the well-studied phenomenon of herbicide resistance, little is known about how traits that enhance weediness evolve. Weedy or red rice (Oryza spp.) is a conspecific weed of cultivated rice that infests rice fields worldwide. Its close relationship with cultivated rice (O. sativa), for which numerous genetic and genomic resources exist, make weedy rice an ideal system in which to study the evolutionary genetics of weedy traits. We have been characterizing genomic patterns of polymorphism in populations of weedy rice around the world. Our results indicate that weedy rice has evolved independently multiple times, and has done so from a diversity of ancestral backgrounds, which include cultivated rice varieties as well as wild rice groups (O. rufipogon/nivara). To understand the mechanisms by which these weedy lineages are continuously arising, we are assessing the extent of convergence at the genetic and phenotypic level among independently evolved populations of weedy rice. Seed shattering, a mechanism that aids in seed dispersal, seems the most broadly convergent trait across weedy rice groups. However, QTL mapping in crop × weed crosses suggests that independent genetic mechanisms underlie the shattering trait in different weed populations. Comparative genome scans of selected weeds and their crop ancestors support very limited genetic convergence among weedy rice types. The multiple genetic paths through which weedy rice can evolve, and the apparently few phenotypic constraints, have important implications for management of this noxious weed.
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Improving rice photosynthesis by QTL screening: Developmental aspects

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Efforts to improve rice yield include enhancing photosynthetic capacity. In order to improve photosynthesis in rice, we have been using a QTL approach to identify genomic regions associated with greater photosynthesis rate per leaf area in indica and japonica cultivars of rice. Although we have identified numerous QTLs for greater photosynthesis rate, including GPS (Takai et al., 2013; Sic. Rep. 3: 2149), none of the regions include known photosynthetic genes, indicating the photosynthetic enhancement may have come through altered leaf development or altered biomass allocation and/or resource patterns that allowed the plant to maintain photosynthetic protein content at the flag leaf stage. Using a growth analysis, comparison of leaf and root allocation patterns between Oryza sativa cv. Takanari, an indica cultivar with high photosynthetic capacity at the flag leaf stage, and cv. Koshihikari, a japonica line with lower photosynthetic capacity, showed greater allocation of biomass to roots in cv. Takahari, which indicates greater ability to sustain nutrient acquisition and in turn, leaf photosynthetic capacity. Such results would be consistent with GPS function, which is linked to increased root weight in rice. These results demonstrate how improved photosynthesis could arise through altered development, rather than enhanced performance of existing photosynthetic machinery.
A phylogenetic framework for the carpel development regulation: mixing and matching old with new

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A major evolutionary innovation in the plant lineage is the angiosperm carpel, their unifying character and most complex plant organ, composed of many clearly distinct tissue types to ensure reproductive success. However, the origin of the carpel is unknown, but many components of the gene regulatory network (GRN) governing carpel development and their genetic interactions are described in Arabidopsis thaliana. To unravel the evolution of the carpel GRN and to discriminate between “early” and “late” steps in carpel evolution we calculated thorough phylogeny reconstructions based on sequenced genomes such that orthologs of the major A. thaliana carpel GRN are now placed in their phylogenetic context. We find that the carpel GRN components are of various ages, and identify especially high retention rates for carpel development genes in Brassicaceae leading to Brassicaceae-specific interactions of carpel GRN members. Further, our data indicate that developmental processes present already in the most recent common ancestor of seed plants, such as reproductive meristem termination or adaxial/abaxial polarity specification requires few interacting transcription factors, which are not retained in duplicates after whole genome duplications (WGD). In contrast, developmental processes associated with derived carpel characters, such as the transmitting tract require larger numbers of interacting transcription factors which were retained as duplicates after WGD.

Genome and karyotype evolution of duckweeds with striking retention of juvenile characteristics

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The monocotyledonous duckweeds are widely distributed in still or slightly moving freshwater ecosystem. Duckweeds represent the smallest and fastest growing plants, which makes them ideal for biomass production and bioremediation. The recently published genome sequence of Spirodela polyrhiza offers a suitable reference for investigations on genome architecture of the 37 species belonging to five genera with variable genome sizes (0.158 to 1.88 Gbp). By using consecutive multicolor fluorescence in situ hybridization (mcFISH) analyses, we aligned the 32 originally assembled pseudomolecules to the 20 small S. polyrhiza chromosome pairs. A Spirodela cytogenetic map containing 96 BAC markers with an average distance of 0.89 Mbp was constructed. Using a cocktail of 41 BACs in three colors, all chromosome pairs could be individualized simultaneously. Furthermore, seven ancestral blocks emerged from duplicated chromosome segments of 19 Spirodela chromosomes. Applications of this resource for studying chromosome homoeology and karyotype evolution of duckweed species will be discussed.
Evolution of plant breeding systems: Male form and function in the nightshade family

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‘How does stamen morphology evolves to improve pollinator efficiency and/or attraction in a buzz pollinated genus?’ is the key question this project addresses using a 3 strand approach to answer the ‘what’ ‘how’ and ‘why’ of anther morphology in the genus Solanum. Solanum is entirely buzz pollinated, in which the plant’s gametes are used as the reward to pollinators. This places special selective pressures on both plant and pollinator leading to adaptation in the morphology of the highly diverse Solanum anthers. This project investigates key evolutionary transitions in stamen morphology at both a macro- and micro-morphological level (including traits of epidermal morphology, heteranthery, filament length, stamen cone shape) across the Solanum phylogeny. Once identified, selected key evolutionary transitions will be further investigated from a developmental genetic point of view using the MYB transcription factor MIXTA in a candidate gene approach to investigate the genetic control and development of some of these transitions through gene over-expression and CRISPR gene knockout. The interactions of pollinators with different stamen morphologies in a controlled environment will then be examined using sister pairs of plants with contrasting morphologies. Overall this will give greater understanding of the driving forces behind evolution of an economically important genus.

The evolution of pitchers in Nepenthes khasiana: how many and which genes does it take to make a pitcher?

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A structural phenomenon seen in certain lineages of angiosperms that has captivated many scholars including Charles Darwin is the evolution of plant carnivory. We now understand why carnivory evolved but how carnivorous plants acquired these attributes remain a mystery. In an attempt to understand the evolution of Nepenthes pitchers, we de novo assembled for the first time the leaf transcriptome sequence of Nepenthes khasiana (Nepenthaceae). We generated more than 180 million Illumina reads from the highly specialized N. khasiana leaf comprising the leaf base, tendril, digestive zone, waxy zone and lid. We then mapped respective reads into the de novo assembled reference transcriptome to quantify transcript abundance. We detected highest number of uniquely expressed transcripts in the tendril followed by waxy zone, digestive zone, lid and leaf base. Hierarchical clustering of 5994 differentially expressed genes indicated functional relationship and similar cellular processes underlying the leaf base and pitcher tube, thereby implying that the Nepenthes pitcher is indeed a modified leaf. Taking cues from SEM and LM photomicrographs, we found altered expressions of key regulatory genes involved in leaf development. In light of these observations, this dataset will allow further research into this area and serve as the basis for understanding Nepenthes pitcher development.
Origin and evolution of peloric florist gloxinia (*Sinningia speciosa*)

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The origin and spread of novel adaptive traits consequent upon domestication are complex and unexplored in horticultural plants. The florist gloxinia (*Sinningia speciosa*) has been cultivated since the 19th century with attractive brilliant peloric flowers that influenced the thinking of Darwin. However, the origin and the genetic basis of peloria in gloxinia remain largely unknown. Here, we demonstrate that the modern peloric gloxinias are derived from the wild gloxinia *Sinningia speciosa* “Jurape” by a recessive mutation. We further characterized that a 10-bp deletion in the Sscyc1 coding sequence, which results in a nonfunctional truncate protein with 45 aa in length, is responsible for the development of peloric flowers in gloxinia. The nonfunctional Sscyc1 protein is associated with the loss of dorsal specific expression of Sscyc1 by disrupting the positive auto-regulatory loop. The contribution of Sscyc1 to peloric flower development was further evidenced by dominant repression of SsCYC1 in WT gloxinia, which results in perfect ventralized peloric flowers. Consistently, severe artificial selection has targeted the Sscyc1 locus by removing all the rare haplotypes in peloric gloxinia populations. This study defines the molecular basis of the peloric flower mutation and provides the first clear example for the evolutionary dynamics of horticultural ornamental plants.

Temporal control of plant organ development by RBE and TCP transcription factors

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Plant organ development is a highly ordered process. At the cellular level, early stage organs consist of cells undergoing active cell division. As the organ grows, cells will cease division and enter the phase of expansion and differentiation. This transition often occurs in a temporal and spatial specific fashion that largely determines the final form of the organ. The *Arabidopsis* petal is an excellent model for dissecting the temporal and spatial regulation of plant organ growth. In this report, we demonstrate that, early in petal development, C2H2 zinc finger transcriptional factor RABBIT EARS (RBE) represses a suite of CIN-TCP genes that function as inhibitors of cell division. The temporal alleviation of this repression results in the transition from cell division to post-mitotic cell expansion during petal development, thus acts as an important mechanism to control the temporal progression of petal growth and maturation. We will also discuss our ongoing investigation of the downstream genetic networks of RBE and TCP genes, and how they interact to control the temporal growth of the petal.
Evolution of vegetative desiccation tolerance in the resurrection plant, *Xerophyta humilis*

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Resurrection plants display vegetative desiccation tolerance (VDT) and can survive loss of up to 95% of cellular water, a feat only seen in the seeds and pollen of other angiosperms. We investigated the hypothesis that VDT in the monocot *Xerophyta humilis*, is derived from the networks that control desiccation tolerance in seeds and germinating seedlings. The *X. humilis* desiccation transcriptome was successfully assembled from sequencing samples at five relative water contents (100%, 80%, 60%, 40% and 5%) and 18,737 transcripts were significantly differentially expressed. These included many seed-specific genes, such as LEA and seed storage proteins. Desiccation was associated with successive waves of transcription factor induction, as well as widespread down-regulation of histone modification enzymes. Differentially expressed ABF transcription factors, which are activated downstream of the ABA-signalling pathway, were most similar to those induced by drought in *Arabidopsis* rather than seed maturation. Of the canonical seed master regulators (such as the LEC1/ABI3/FUS3/LEC2 network and ABI5) only three ABI3 transcripts were expressed, all of which encoded proteins lacking the seed motif-binding B3-domain. VDT in *X. humilis* is thus not associated with re-activation of seed master regulators in leaves, but may instead involve activation of seed genes by vegetative drought response regulators.

Evolution of nickel hyperaccumulation in *Senecio coronatus*

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Hyperaccumulators are a rare group of plants that can accumulate high concentrations of heavy metals in their shoots. Although nickel hyperaccumulators are by far the most common group, and the first such plant species was described in 1948, we know relatively little about the genetic basis of this extreme trait. While histidine and nicotianamine are known to chelate Ni, the genes responsible for other key processes such as Ni uptake, xylem loading and vacuolar sequestration are unknown, as are the genomic changes underpinning the evolution of this trait. We are using *Senecio coronatus* (Asteraceae) as a model system to investigate the evolution of Ni hyperaccumulation in plants. This species is apparently unique in that both Ni hyperaccumulating and non-accumulating populations are found in close proximity on Ni-rich serpentine soils. Having analysed the evolutionary relationships between these populations using neutral genetic markers, we selected four for RNA-Seq analysis. Differential gene expression analysis identified a small subset of genes that are consistently up-regulated in multiple hyperaccumulator versus non-accumulator populations. Our data suggest that Ni hyperaccumulation may have arisen multiple times in this species via modification of the iron homeostatic network.
**P10**

Evaluation of antioxidant content of sunflower and mungbean sprouts

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The aim of this study was to assess the phenolic content and free-radical scavenging activity from sprouts of 3 sunflower (Helianthus annuus L.) varieties (S471, S473, S475) and mung bean (Vigna radiata) at 0, 1, 3, 5, and 7 days-old after germination. Total phenolic content (TPC), Ferric reducing antioxidant power (FRAP), % free-radical scavenging activity by 1,1'-diphenyl-2-picrylhydrazyl (DPPH) assays and HPLC analysis were evaluated. The results showed that the highest levels of TPC, DPPH and FRAP were found in 0 day-old seedlings, and levels then decreased as the days progressed in all varieties of sunflower seedlings. However, in mung bean, FRAP and DPPH antioxidant activities increased, but TPC decreased with increasing time. Moreover, based on the HPLC analysis, gallic acid was found both in sunflower and mung bean. However, sunflower gave higher values than mung bean. The concentration of gallic acid in sunflower seedlings significantly decreased as the days progressed, similar to the TPC, FRAP and DPPH values, indicating that gallic acid could be responsible for the antioxidant capacity, although other chemicals may contribute as well. The present study demonstrates that sunflower sprouts at early ages are a good source of antioxidants.

**P11**

A computational framework for mapping the timing of vegetative phase change

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Phase change plays a prominent role in determining the form of growth and development. Although considerable attention has been focused on identifying the regulatory control mechanisms of phase change, a detailed understanding of the genetic architecture of this phenomenon is still lacking. We address this issue by deriving a computational model. The model is founded on the framework of functional mapping aimed at characterizing the interplay between quantitative trait loci (QTLs) and development through biologically meaningful mathematical equations. A multiphasic growth equation was implemented into functional mapping, which, via a series of hypothesis tests, allows the quantification of how QTLs regulate the timing and pattern of vegetative phase transition between independently regulated, temporally coordinated processes. The mode was applied to analyze stem radial growth data of an interspecific hybrid family derived from two Populus species during the first 24yr of ontogeny. Several key QTLs related to phase change have been characterized, most of which were observed to be in the adjacent regions of candidate genes. The identification of phase transition QTLs, whose expression is regulated by endogenous and environmental signals, may enhance our understanding of the evolution of development in changing environments.
Identifying sex determination genes on the young Asparagus Y chromosome

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Garden asparagus (\textit{Asparagus officinalis}) is a dioecious species with a recently evolved, homomorphic sex chromosome pair which makes it ideal for studying the earliest events in sex chromosome evolution. A proposed evolutionary path from hermaphroditism to dioecy and a sex chromosome pair would involve the origin of a Y chromosome through cessation of recombination between a suppressor of female function and a promoter of male function. We have explored this hypothesis in garden asparagus by genetically mapping sex determination to a 1.8 Mb non-recombining region on the proto-Y chromosome that actively differentiates males (XY) from females (XX). We have identified four independent male-to-hermaphrodite mutants that implicate a single gene in this non-recombining region on the Y as responsible for dominantly interrupting pistil development. Anther development is not affected in these mutants but male to female conversions are seen in two mutants with deletions spanning the 1.8 Mb non-recombing sex determination region. This region contains 14 annotated genes including the sole \textit{Asparagus} homolog for known anther development gene, defective in tapetal development and function 1 (\textit{TDF1}). In support of a model proposed by Charlesworth & Charlesworth (1978), these finding imply that the origin of a non-recombining sex determining region on the \textit{Asparagus} Y chromosome involved the linkage of a male promoting gene with a dominant female suppressor.
 Anthocyanin Gene Expression in *Erica plukenetii*

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*Erica*, with more than 800 species, is the largest genus in the Cape Floristic Region of South Africa, and is ideal for studying the diversification of the Cape Flora. Most species possess small insect- or wind pollinated white or pink flowers. Our phylogeny shows that red, long-tubed, bird pollinated flowers, have evolved independently at least six times. The *Erica plukenetii* clade contains closely related (sub-) species that differ in floral shape and/or colour and should allow the elucidation of the genotypic changes underlying the phenotypic differences. Anthocyanin pigments occur in *Erica*, implying that the anthocyanin pathway determines floral colour.

Illumina NGS sequencing of *Erica plukenetii* generated scaffold sequences that were incorporated into a Local BLAST database. Using sequences from closely related species, the eight anthocyanin pathway genes (*CHS*, *CHI*, *F3H*, *F3’H*, *F3’5’H*, *DFR*, *ANS* and *UDP-GST*) were identified and resequenced, to correct any errors and fill any gaps. The identified genes were annotated with exons, introns, and upstream regulatory sequences. qRT-PCR is being used to determine if expression of the anthocyanin pathway genes differs between red, pink or white flowered *Erica plukenetii*.

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 Heterochrony and patterns of leaf morphology in the Acacieae

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Variation in developmental timing (heterochrony) is an important process in organismal evolution. We are examining the role of heterochrony in the evolution of leaf morphology in the Acacieae, a large tribe of woody legumes. The oldest taxa in this tribe only produce compound leaves, whereas most species in the recently evolved genus, *Acacia*, initially produce compound leaves, but then switch to producing a simple leaf known as a phyllode. Within *Acacia* are 3-6 clades that only produce compound leaves. In many plants, developmental changes in leaf morphology are regulated by a decline in miR156 and miR157. To determine if variation in abundance of miR156/157 may be responsible for these developmental patterns, we examined their expression pattern in species at different phylogenetic positions. This analysis revealed there have been two shifts in the abundance of miR156/157. One shift is associated with the evolution of phyllodes, and the second with the evolution of bipinnate Acacias. We used genome sequencing to identify which MIR156/157 genes contribute to these patterns. Our findings demonstrate that compound-leaf species of *Acacia* are neotenous derivatives of phyllodinous ancestors and suggest that shifts in the duration of the juvenile phase are a major source of morphological diversity in plants.
Breeding system expressed in hybrids between an SI and SC species: characteristics of breeding system in parental species and progeny in Sea rockets.

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The sea rockets, Cakile edentula and C. maritima (Brassicaceae), are closely related and hybrids can be found between the two species. They have contrasting breeding systems: C. maritima is self-incompatible whereas C. edentula is self-compatible. In our study, artificial crossing/backcrossing of parental species and hybrids has been conducted to characterise the breeding systems in parental species, hybrids and backcrossing progeny. We found out that F1 hybrids (both directions) shown complete selfing incompatibility while that of F2s and backcrossing progeny was lost to some extent, which was also supported by the results of pollen ovule ratio. Furthermore, some individuals from backcrossing of hybrids and C. edentula, suffered from male sterility. As a result, SI in hybrids can be inherited from crossing within two close related species while continuous crossing within hybrids and backcrossing with the corresponding SC parent has the potential to break the SI and make its progeny self-compatible.

Evolution of LRR-RLK gene family: ancestral copy number and functional divergence of BAM1 and BAM2 in Brassicaceae

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Gene duplication allows for functional divergence and innovation that provide selective advantages. However in flowering plants, genetic studies have revealed that single-gene mutations affecting one of close paralogs often fail to cause detectable morphological defects, suggesting their functional redundancy. The Arabidopsis BAM1 and BAM2 genes encode highly similar Leu-rich repeat receptor-like protein kinases (LRR-RLKs) and are together essential for normal anther development. We investigated the evolutionary history of LRR-RLK gene family in plants, especially BAM1/2, by phylogenetic analysis and found that BAM1 and BAM2 are two most closely related paralogs resulted from a duplication event before divergence of Brassicaceae. In addition, both BAM1 and BAM2 have accumulated non-synonymous changes compared with their common ancestor, thus possibly have evolved novel functions. We further identified genes that show differential expression in either of the single mutants compared with wild type suggesting that the BAM1 and BAM2 genes, having evolved different functions after their duplication, would eventually exert their own influence upon anther development. Moreover, rechecking of possible anther developmental defects in bam1/bam2 single mutants revealed extra cell division in tapetum cell layers unreported by previous studies. Thus our results showed molecular differences of paralogs that lack visible phenotypes in single mutants.
P17  Genetic correlations with nectar reduction in the evolution of the selfing-syndrome in *Ipomoea lacunosa* (Convolvulaceae)

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In flowering plants, the shift from outcrossing to selfing is one of the most common evolutionary transitions. This transition is associated with changes in several floral characters, collectively known as the selfing-syndrome. While one study demonstrates that natural selection drives reduced flower size in selfers, evidence for other syndrome traits is lacking. We are examining this issue by determining whether nectar reduction is the result of selection or drift in *Ipomoea lacunosa* (Convolvulaceae). This morning glory has a 95% selfing rate and exhibits selfing-syndrome characters (reduced floral size, pigment loss, little nectar) compared to its outcrossing sister species, *I. cordatotriloba*. As an initial step, we are investigating whether other traits are correlated with nectar reduction. We measured the nectar volume, nectar sugar concentration, nectary size, and corolla size in an F3 population created from a cross between *I. cordatotriloba* and *I. lacunosa* and determined that nectar volume is genetically correlated with all three traits. We are in the process of identifying QTLs for these traits via double-digest restriction-site associated DNA (RAD) sequencing. This will lay the groundwork for molecular and field experiments for examining the evolutionary forces driving nectar reduction in the evolution of the selfing-syndrome.

P18  A mechanistic model of stamen filament development that may contribute to mating system evolution in Brassicaceae

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The model species Arabidopsis thaliana has the particular ability to self-pollinate before flower opening. This mating system known as cleistogamy is highly rare among Angiosperms. The molecular evolutionary mechanisms leading to cleistogamy are far from being elucidated. In Arabidopsis, around stage 12 of flower development, stamen filaments acquire their full length reaching the stigmas at the top of the gynoecium in a highly synchronized fashion. Through a functional genetic approach conducted in Arabidopsis, we determined that members of the TCP transcription factor family modulate the elongation of stamen filaments. To do so, TCP factors regulate genes involved in auxin homeostasis, which is the only phytohormone linked to cleistogamy. At the same time, we found that a KNOX transcription factor represses stamen filament elongation acting upstream of TCP factors. We also observed the presence of two adjacent KNOX sites in the promoter of one of the TCP genes, suggesting a direct repression mechanism. Modifications found in the promoter regions of putative orthologues of this TCP gene in other Brassicaceae species suggest that this pathway may differ in the family and this may be related to mating system evolution.
The use of Reconstructing Ancestral State in Phylogenies (RASP) to infer the underlying diversification and biogeography within the family Thymelaeaceae

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Thymelaeaceae is a medium-sized family of approximately 50 genera representing c. 800 species. Geographically, members of this family are distributed across many parts of the tropics and Neotropics, southern Africa, tropical Africa, Madagascar, Australia, New Zealand, the Mediterranean region, South and North America, and the steppes of Asia. There has been a great morphological confusion within the family and most genera were distinguished based on the presence or absence of petals, floral structure and number of stamens. The phylogenetic approach was used to infer the relationships and morphological characters of the family in accordance with biogeography and speciation processes. Biogeographical analyses were conducted using three methods implemented in RASP (S-DIVA, BayArea and DEC model). The result depicted that, by the time Thymelaeaceae family diversified (50 Mya), Gondwanaland, Laurasia and other continents had already separated. S-Diva postulates Madagascar, Sri Lanka, Malesia and Tropical Africa as the origin of the family whereas DEC model suggest Malesia and Tropical Africa as the origin. The Models suggest a complex biogeographical history in which dispersal and vicariance plays a vital role in distribution pattern of the family. The peak diversity of Thymelaeaceae occurred during Miocene and Pliocene. Each clade comprised of taxa with distinguished floral structure and number of stamens, presumably a trait developed as an adaptation to changing climate in the region. Therefore, diversification and morphological dissimilarities among the species within Thymelaeaceae across the globe might have been climatically mediated.
Influence of microspore developmental stage on anther callus induction of sunflower (*Helianthus annuus* L.)

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The production of haploid and doubled haploid plants is important for plant breeding programs, enhancing forward breeding by allowing hybrids to be bred with new traits. However, successful production of these plants is affected by many factors. The objective of this study was to determine whether microspore developmental stages influence anther callus induction in sunflower (*Helianthus annuus* L.). Flower buds at R5.1 stage of Pacific 22 cultivar were sterilized and their anthers were carefully removed from the three outermost rings of disk florets, namely, 1, 2 and 3. Twenty five anthers were cultured on MS medium supplemented with different combinations of hormones (NAA, 2,4-D, BAP) and additive substances (coconut water and casein hydrolysate) for callus induction. In addition, microspore developmental stages were observed under an optical microscopy. The results showed that anthers of the ring no. 2 had the highest percentage of uninucleate microspore stage. However, the best calllogenesis frequency was about 78% found from ring no. 1 in the MS medium supplemented with 2 mg l⁻¹ of NAA, 1 mg l⁻¹ of BAP and 500 mg l⁻¹ of casein hydrolysate.

Investigation of *MSR1* in glutathione redox-dependent root development

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Glutathione is involved in thiol redox signaling and acts as a major redox buffer against reactive oxygen species, helping to maintain a reducing environment in planta. The crucial role of glutathione redox status in root growth has been revealed. We have previously shown that root apical meristem (RAM) and root stem cell niche were maintained by glutathione redox status in plastids, which was controlled by glutathione reductase 2 (GR2). The loss-of-function GR2 mutant *miao*, exhibited remarkable defects in root developmental. However, the downstream factors regulated by glutathione redox status in root development remains elusive. Here, by using forward genetic approach, we screened miao suppressors (*msr*) from an ethyl methanesulfonate-mutagenized miao population. We isolated *msr1*, whose root growth and RAM length was obviously rescued. With the combination of whole-genome sequencing and rough mapping, we identified *MSR1* gene. The aim of this study is to uncover the molecular mechanism how *MSR1* acts in glutathione redox-dependent root development.
Concerted neofunctionalization of duplicated gene products in the Brassicaceae PRC2 complexes rewiring the regulatory pathways in seed development

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As a major contributor to genome evolution in eukaryotes, the divergence of individual duplicated genes is well documented; however, we studied PRC2 (Polycomb Repressive Complex 2) in the Brassicaceae, to describe the co-divergence of duplicated genes whose products function together in a complex. The VRN-PRC2-complex comprises VRN2 and SWN, and both genes are duplicated to generate FIS2 and MEA, which form the Brassicaceae-specific FIS-PRC2-complex. The VRN-complex regulates vegetative tissue differentiation and controls flowering, but the FIS-complex regulates seed development. We found that FIS2 and MEA have reproductive-specific expression patterns, which are correlated, and derived from the broadly expressed Arabidopsis VRN2 and SWN and outgroup orthologs. In the Arabidopsis vegetative tissues, repressive marks are enriched in FIS2 and MEA, while active marks are associated with all their paralogs; this change in the epigenetic features explains the loss of vegetative expression. FIS2 and MEA also became imprinted in the endosperm. We detected comparable accelerated amino acid substitution rates and structural rearrangements in FIS2 and MEA. We conclude that FIS2 and MEA have neofunctionalized in concert to create a new PRC2-complex in the Brassicaceae. This FIS-PRC2, coupled with the functional divergence of some Brassicaceae-specific duplicated genes, rewired the regulatory pathways in seed development.

Nitric oxide induced changes in antioxidant metabolism and in vitro evaluation of NO biosynthesis in Brassica juncea under elevated concentration of Cu

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Nitric Oxide (NO) is a multifunctional gaseous signal molecule in plants system. Nitrate reductase (NR) is one of the imperative enzymes for NO generation; nitrite has been used as a substrate for NO synthesis mediated by the enzyme nitrite reductase (NiR) which is localized in various compartments of the plant cell. In plant system major sources of NO production include nitric oxide synthase (NOS), NR and NiR. In this study, effect of NO and enzymes involved in NO production has been monitored under Copper (Cu) stress and sodium nitroprusside (SNP) treatment. For the experiment B. juncea was cultivated under Cu stress for 72hr and it was supplied with NO donor SNP to determine the physiological mechanisms of NO on B. juncea. Treatment of 100µM SNP resulted in alleviated level of Malondialdehyde (MDA), proline and stimulated level of antioxidant where as increased level in nitrate and nitrite reductase activity was observed. The effect of Cu on NADPH-diaphorase (NADPH-d) activity, commonly employed as a marker for nitric oxide synthase (NOS) activity and nitric oxide (NO) production were investigated in root sections of Brassica juncea. Increase in NO activity was observed under elevated concentration of copper stress which was decreased by SNP treatment. The results are suggested that exogenous NO could effectively induce plant to adjust physiological and biochemical effect against copper toxicity and maintain normal metabolic capacity and growth under adverse condition of heavy metal stress.
Unveiling the molecular basis of floral zygomorphy in Lamiales: *Torenia fournieri* as a model species

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Focusing on the mechanisms that control patterns of floral symmetry, botanists have found *CYCLOIDEA*-like transcriptional factors being independently recruited multiple times during the parallel evolution of floral zygomorphy. In Lamiales species *Antirrhinum majus*, *CYC* homologs with their downstream factor *RADIALIS*, regulate dorsal–ventral asymmetric floral development. Distinct from this *CYC-RAD* module, our previous work in Fabaceae dissected zygomorphy into dorsal–ventral (*DV*) asymmetry and organ internal (*IN*) asymmetry, established by *CYC*-like factors and *SYMMETRIC PETALS1* (*SYP1*), respectively. Selecting a well transformable Lamiales plant *Torenia fournieri* as a model, we have explored how these factors coordinate determining floral zygomorphy. Using petal spots and shape ratios as major indicators, we found that all petals become dorsalised or partially dorsalised in ectopic expressed *TfCYC1/2* and *TfRAD* plants. Normal development of dorsal petals was disrupted when down-regulating the expression of *TfCYC1* or targeted deleting of *TfRAD*, suggesting a conserved *CYC-RAD* module in Lamiales. Two *SYP1*-like genes *TfSYL1/3* were isolated with distinct expressional patterns in the junction between SAM and floral organs. Floral zygomorphy in 35S::*TfSYL1* plants was influenced with decreased *TfRAD* mRNA level indicating possibly combinatory actions among these factors. Altogether, we developed a model Lamiales species to unveil the molecular basis of floral zygomorphy.

The genetic architecture of heterochrony in *Prunus mume*

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By exploring the mechanistic influence of developmental processes on phenotypic novelties, synthesizing development into evolution and ecology has been a major focus in modern biology. This synthesis can be accelerated by identifying QTLs that determine the process of development. More recently, we have developed a computing framework by which to map unique QTLs that modulate key timing events, known as heterochrony, during development. The QTLs identified by this framework can interpret how heterochrony takes place in a precisely regulated spatial and temporal context, facilitating our understanding of evolutionary origins of developmental events. In this study, we applied this approach to map heterochrony QTLs (*h*QTLs) that determine the pattern and process of development in an ornamental woody plant – *mei* (*Prunus mume*). Different sets of *h*QTLs for growth rate and the timing of inflection point illustrate a quantitative picture of the genetic architecture underlying stem growth and development in woody plants.
Floral bilateral symmetry enhances shape variation revealed through morphometric and genetic analysis

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Floral shape is a complex trait and is probably controlled by a sophisticated developmental process. The evolution and development of flower bilateral symmetry has been suggested to facilitate floral shape variation yet no concrete evidence is available to demonstrate this due to the complexity of shape. We have successfully quantified the extent of shape variation with flower 2D and 3D images using geometric morphometric analysis. The result showed that major changes of shape from zygomorphic wild type to actinomorphic peloria in Sinningia speciosa are increased flower opening and decreased corolla asymmetry, the characters which related to floral display and pollinator attraction. To further dissect the genetic control of flower shape, we found SsCYC plays a major role on flower opening and corolla tube asymmetry, as well as all major traits affecting shape. This indicates SsCYC has pleiotrophic effect on shape changes. In addition, correlating genotypic effects with traits morphometric measurement, the interactions between SsCYC and SsRAD, together that SsDIV-SsMYBML or SsRAD-SsMYBML interaction also affect traits related to lobe size and throat opening. Traits correlation data indicated zygomorphic flowers can be clustered into more morphologically distinct subgroups than actinomorphic ones. This demonstrates that zygomorphic flowers can generate more shape variations than actinomorphic flowers, which support the hypothesis that the development of bilateral symmetry may help to generate more shape changes allowing flowers to evolve.

Combining Bulked Segregant Analysis (BSA) and Maize SNP3K BeadChip Mapping Carbon Partitioning Defective (cpd) genes in Maize

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During the photosynthesis, carbon partitioning (CP) is the process that sugars or starch are transformed from CO\(_2\) in the leaves of the plants and moved to the other parts of the plants (e.g. roots, flowers and fruit). Carbon partitioning (CP) is directed toward biomass increase, cell propagation and survival. In this experiment, the source of materials are cpd-like phenotype by natural mutation. It found that the leaf tips accumulated abundant starch and anthocyanin pigments and lacked the exporting competence. The height of cpd mutant was lower and the maturity period was later than those of normal. The ear of mutant was smaller even had no seeds. There was significant difference between the leaves of mutant and normal by Photosynthesis meter LiCOR-6400. Using the results of KI starch staining, separate the plant into mutant and non-mutant. Build the mutant and non-mutant pools of DNAs for BSA. This Bead Chip contains 3172 validated markers derived from the B73 reference sequence. We found cpd candidate genes in Chromosome 5.
Distinct regulatory changes underlying differential expression of TCP genes associated with petal variations in zygomorphic flowers of *Petrocosmea* (Gesneriaceae)

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The morphological diversification of zygomorphic flowers is universal in several angiosperm lineages with predominantly zygomorphic flowers. However, the underlying molecular mechanism is still obscure. To address this question, we selected two closely related species, i.e. *Petrocosmea glabristoma* and *P. sinensis*, from the family Gesneriaceae to conduct hybridization, expression, mutant, and allele-specific expression (ASE) analyses. The results show that the size change of dorsal petals between the two species is mainly explained by the differential expression of two *CYCLOIDEA*-like TCP genes (*CYC1C* and *CYC1D*), while the shape variation of all petals is related to the expression change of one *CINCINNATA*-like TCP gene (*CIN1*). In reciprocal F1 hybrids, the additive expression of *CYC1C*, *CYC1D*, and *CIN1* is consistent with the intermediate petal phenotypes. ASE analyses show that the expression differentiation of these TCP genes is underlain by distinctly different regulatory mechanisms, and that the highly redundant *CYC1C* and *CYC1D* are controlled by remarkably different regulatory pathways. Therefore, natural selection may favor distinct regulatory modifications rather than structural changes in the coding sequence of key developmental genes in generating morphological diversity.

The making of elaborate petals through developmental repatterning

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As a special type of floral organ, petals show tremendous diversity in shape, structure, color/coloration, and function, and have increasingly been used as a model for studying plant organogenesis and evolution. Petals of *Nigella* (Ranunculaceae) species are of particular interest because they are highly elaborate, bilabiate structures with extensive modifications. To understand how *Nigella* petals become elaborated and diversified, we investigated the morphology, micro-morphology and development of petals in seven representative species (i.e. *N. integrifolia*, *N. nigellastrum*, *N. orientalis*, *N. damascena*, *N. sativa*, *N. hispanica*, and *N. arvensis*). We found that the degree of petal complexity increased gradually during evolution, involving both modification of existing characters (e.g. the elongation of stalk and the alteration of the upper and lower lips in shape) and *de novo* origination of new features (e.g. pseudonectaries, short trichomes, and conical cells). By investigating and comparing the processes of petal morphogenesis in these species, we also demonstrated the duration of important developmental events that led to the diversification of mature petals in gross morphology and micro-morphology. We found that developmental repatterning has played key roles in generating petal complexities during evolution.
Gain of an auto-regulatory site led to divergence of the *Arabidopsis APETALA1* and *CAULIFLOWER* duplicate genes in the time, space and level of expression and regulation of one paralog by the other

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How genes change their expression patterns over time is still poorly understood. Here, by conducting expression, functional, bioinformatic and evolutionary analyses, we demonstrate that the differences between the *Arabidopsis thaliana APETALA1* (*AP1*) and *CAULIFLOWER* (*CAL*) duplicate genes in the time, space and level of expression were determined by presence or absence of functionally important transcription factor-binding sites (TFBSs) in regulatory regions. In particular, a CArG box, which is the auto-regulatory site of *AP1* that can also be bound by the *CAL* protein, is a key determinant of the expression differences. Because of the CArG box, *AP1* is both auto- and cross-regulated (by *AP1* and *CAL*, respectively), and its relatively high-level expression is maintained till to near-mature sepals and petals. The observation that the CArG box was gained recently further suggests that the auto- and cross-regulation of *AP1*, as well as its function in sepal and petal development, is a derived feature. By comparing the evolutionary histories of this and other TFBSs, we further indicate that the divergence of *AP1* and *CAL* in regulatory regions has been markedly asymmetric and can be divided into several stages. Specifically, shortly after duplication, when *AP1* happened to be the paralog that maintained the function of the ancestral gene, *CAL* experienced certain degrees of degenerate evolution, in which several functionally important TFBSs were lost. Later, when functional divergence allowed survival of both paralogs, *CAL* remained largely unchanged in expression whereas the functions of *AP1* were gradually reinforced by gains of the CArG-box and other TFBSs.
A High-Dimensional model charts a global view of genetic control on secondary growth trajectories in a forest tree

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Despite their paramount importance to regional economy and environmental protection, forest trees have not been well studied in terms of their genetic control. Here, we identified a pool of genetic loci associated with stem radial growth trajectories in poplar trees by scanning the whole Populus genome. We implemented a two-side high-dimensional variable selection model, 2HiGWAS, to analyze a full-sib family derived from P. deltoids and P. × euramericana clones. For poplar, the first 24 years of growth present an early stage of its ontogeny, but which can be clearly split into two phases, juvenile and early adult. The QTLs detected by 2HiGWAS exhibit different temporal patterns of inheritance for stem growth; for example, some loci affects stem radial growth in the juvenile phase, some exert its influence in the early adult phase, and the others display an oscillating pattern of genetic effect during ontogeny. Many QTLs detected determine stem growth trajectories through mediating the heterochronic variation of development in the timing and duration of developmental events. Analysis of gene annotations shows that a majority of QTLs detected by 2HiGWAS are located in the regions of candidate genes with known functions in biochemical and physiological aspects of growth. Our results may be useful for charting an overall picture of the genetic architecture underlying stem growth and building up the genotype-phenotype map toward tree production breeding.
Comparative analysis of patterning gene expression with localized cell proliferation in *Juncus prismatocarpus* (Juncaceae) using a novel EdU method

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Unifacial leaf (leaves lack adaxial side) has evolved repeatedly in monocot. We previously showed that in *Juncus prismatocarpus* (Juncaceae), *DROOPING LEAF* (*DL*) is responsible for the flattened abaxialized leaf blade development in towards the shoot apical meristem (SAM) and *PRESSED FLOWERb* (*PRSb*) is responsible for the secondary margin development. However, how these genes affect local cell proliferation is unknown. In the present study, we have examined whether the spatio-temporal expression patterns of *DL* and *PRSb* play a direct role in localized cell proliferation using 5-ethynyl-2’-deoxyuridine (EdU). We have developed a novel EdU method to quantify the directionality of cell division in *J. prismatocarpus*. The novel EdU method is a quick and powerful method and can be also applied to Arabidopsis. Preliminary analysis indicated that cell division direction seemed to be random at P1 to P2 stage to generate the precursors of cell files and exclusively vertically (within the cell file) at P3 stage. Our analysis also indicated that the effect of *DL* on cell division seemed to be non-cell-autonomous. Our combined analyses of gene expression patterns and local cell proliferation do not support the classical concept “adaxial meristem” and gives insight on monocot leaf development.
The potential output and long-term stability in agricultural ecosystems are mainly referred to as the preservation and strengthening measures of biodiversity in all its aspects. Contemporary farming systems that are highly accentuating on constant and definite diversity of species and excessive utilization of high-yielding crops in a mono-culture paradigm are responsible for the current menace to stable production and sustainability of agroecosystems. Wild and semi-domesticated plant species, mostly possessing medicinal and industrial properties, have a key role in the biodiversity of conventional agricultural systems that can be introduced as novel crops to commercial and ecumenical markets. The required data pertaining to the number and planting area of aromatic/medicinal plants were gathered from 183 counties belonging to 27 provinces distributed across the Iranian territory. Results demonstrated that roughly 56 traditional species, being principally medicinal/ aromatic, are under cultivation with Shannon diversity index (H) of 0.64. The proportion of their cultivated land area to the total arable lands was found to be around 0.87%; 44.5 percent of which devoted to cumin (Cuminum cyminum L.) and Saffron (Crocus sativus L.) species. Multipurpose medicinal plants received 43.5 percent, while only 12 percent of the total area under cultivation of medicinal/aromatic plants was allocated to species that were particularly cultivating for their medicinal properties. Taken together, Khorasan province ranked first among provinces in terms of total cultivated land area and diversity of medicinal/aromatic plants.
P34 Dissecting the functions of SEPALLATA-like genes in patterning of the pseudanthium-type inflorescence of *Gerbera hybrida* (Asteraceae)

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The evolutionary success of Asteraceae (the sunflower family) has long been attributed to their inflorescence type, the capitulum. A capitulum compresses hundreds of morphologically different florets on a single receptacle, but superficially mimics a showy, solitary flower. Patterning of the capitulum also bears resemblance to a single flower, with regard to the sequence of lateral primordia, meristem determinacy as well as the histological configuration of the inflorescence meristem. The ornamental plant *Gerbera hybrida* harbors a duplicated family of the SEPALLATA-like genes that has been recently extended to 8 members (namely as GRCD1-8). Unlike the *Arabidopsis SEP* orthologs conferring redundant E-functions in floral patterning, expression pattern of the GRCDs has been broaden at both the flower and inflorescence levels, occurring sequentially from reproductive transition, floral initiation, floral patterning, to the determinacy of reproductive meristems. Combining the data from studies in phylogeny, gene expression, protein-protein interaction, and phenotypes of transgenic Gerberas, sub-functionalization of the GRCDs genes are claimed accordingly. A model for GRCDs functions is thus proposed and their linkages with the other shoot/flower identity genes will also be presented. Our data suggest that evolution of the Asteraceae SEP-like genes may play an indispensable role in shaping the unique pseudanthium-type inflorescences.

P35 A gene evolved with regulatory variations optimizes cotton fiber elongation

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During evolution, novel phenotypes could emerge through changes in gene expression pattern. Many crops are allopolyploids and bias gene expression is a distinct feature to allopolyploid species. The allopolyploid cottons (AADD) represent typical nature-originated allopolyploids through interspecies hybridization followed by diversification and domestication. Cotton cultivars have been evolved to produce extreme long seed-born fibers important for textile industry. We identified a cotton bHLH transcription factor named PRE1. We show that *PRE1* is preferentially express in fast growing fiber to promote cell elongation and that fiber length is correlated with the *PRE1* expression level. *PRE1* expression in cotton has evolved cumulatively over time under both natural and human selections and, consequently, shows A-homoeolog bias expression in allotetraploid fiber cells. We found that natural variations of the canonical TATA box, a regulatory element in *PRE1* core promoter, is sufficient to potentiate the peculiar *PRE1* expression, representing a mechanism underlying the homoeolog-specific gene expression. Thus, the cell elongation regulator *PRE1* is a target of evolution that has contributed spinnable fiber formation in cotton. Genetic editing of the *PRE1* genome may provide an option for engineering of desirable crop trait.
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Plants possess enormous morphological variation in nature. As the ancient, plant specific proteins, TCP domain regulatory proteins are known to control many important morphological traits by modulating cell proliferation patterns. Phylogenetic analysis has uncovered two subfamilies of TCP transcription factors: PCF (class I) and the CYC/TB1 clade and CIN clade proteins (class II). In angiosperms, the CYC/TB1 clade has experienced duplications and can be divided into three subclades in core eudicots: CYC1, CYC2 and CYC3. The functions for CYC1 and CYC3 clade genes are poorly understood in any species, only the Arabidopsis homologs BRC1/2 known to control shoot branching. Most of the studies have focused on the CYC2 clade genes showing specific roles in regulating flower symmetry and inflorescence development in diverse plant species. To understand the ancestral functions and how CYC/TB1-like genes have evolved, a comparative study of TCP genes from phylogenetically important species of bisymmetrical and radial symmetrical representatives in Ranunculales (Eschscholzia californica, Aquilegia coerulea, Cysticapnos vesicaria), a lineage basal to all other eudicots was carried out. Expression analysis by qPCR and in situ hybridization show the divergent expression pattern of the duplicate homologs. Phylogenetic analysis of duplication events, gene losses and lineage-specific expansions will be discussed.

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Phenotypic novelties are critical to macroevolutionary patterns of diversity, but the molecular changes underlying these novelties remain poorly understood. In the mega-diverse angiosperm lineage of eudicots, the evolution of fused petals (sympetaly) is considered to be an important innovation that has repeatedly led to increased pollination efficiency, resulting in accelerated rates of plant diversification. Although little is known about the underlying regulation of sympetaly, genetic pathways involved in organ boundary establishment are strong candidates. As a first test of this hypothesis, we functionally characterized orthologs of CUP SHAPED COTYLEDON (CUC) organ boundary genes in sympetalous Petunia, following the establishment of a functional shoot apical meristem. Our results demonstrate that NO APICAL MERISTEM (NAM), and its closely related paralog NH16, have retained a role in inter-floral-whorl organ boundary establishment, but have evolved a novel role in the growth and fusion of petals. We suggest that CUC-like genes play a central role in the evolution of corolla patterning, either through context-specific protein–protein interactions and/or downstream targeting of effector genes.
Participants

To be included.