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The 13th World Congress on Parasitic Plants

PROGRAMME & ABSTRACTS

5th–10th July 2015

Kunming, Yunnan Province, China



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The 13th World Congress on Parasitic Plants

“Parasitic plants: the good, the bad, and the mysterious”

5th–10th July 2015, Kunming, China



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FOREWORD

It is our great pleasure to welcome everyone to the 13th World Congress on Parasitic Plants (WCPP13), which brings the WCPP legacy to East Asia for the first time.

With the theme “Parasitic plants: the good, the bad, and the mysterious”, WCPP13 seeks to stimulate a productive exchange of information and ideas among researchers from around the world representing a wide spectrum of disciplines and perspectives, all focusing around the common theme of plant parasitism. The ultimate objectives of WCPP13 can be summarized as “Concern, Control, and Collaboration”, and our meeting activities reflect these three elements: Concern in what we hope to raise more concern on currently non-weedy parasitic plants before they become a problem; Control in the activities that we are developing new technologies and applications for a better management of parasitic weeds; and Collaboration, the hallmark of WCPP13 permeating through all our activities. In addition to an engaging scientific program, attendees will enjoy a range of diverse social events as well as Kunming’s many attractions, including a visit to Yunnan Ethnic Villages that showcase the culture and customs of the ethnic groups in Yunnan Province.

We hope that you will take the opportunity to socialize and network with new acquaintances, and build upon those relationships which have already been established to sustain our collaboration. We sincerely hope you have a pleasant and productive time in Kunming!

Professor Koichi Yoneyama **IPPS President**

Professor Airong Li **Local Organizer**

ACKNOWLEDGEMENTS

I am very grateful to Chinese Academy of Sciences (CAS) and Kunming Institute of Botany, Chinese Academy of Sciences (KIB, CAS) for their sponsorship of the congress and to several National and International fundings for their generous financial support for scientists to attend this congress. I thank KIB for hosting the meeting and Xiaolin Sui (KIB), Weihua Cui (KIB), Ruijuan Xue (KIB), Gelan Yang (Kunming Tonglan Science and Technology Exchange Service Company), and Yi Xiong (Yunnan Dianchi Garden Resort Hotel & Spa) for their invaluable administrative support. I also thank previous WCPP organizers for setting excellent examples to follow.

Many thanks for the time and efforts of the session organizers and wider organising committee who selected and put together an exciting programme and have reviewed all of the abstracts. Particular thanks to Professor Koichi Yoneyama and Professor John Yoder for their tremendous and unconditioned support. Thanks to the delegates who are willing to share their exciting work with the parasitic plant community to make the scientific event possible. Thanks also to all the participants for their kind support and cooperation.

Airong Li

ORGANISING COMMITTEE

President of International Parasitic Plant Society

Prof. Koichi Yoneyama, Utsunomiya University, Japan

Scientific Committee Chair

Prof. John Yoder, University of California, Davis, U.S.A.

Scientific Committee Members

Prof. Hinanit Koltai, Agricultural Research Organization, Israel

Prof. Julie Scholes, The University of Sheffield, U.K.

Prof. Philippe Simier, Nantes University, France

Prof. Ahmet Uludag, Duzce University, Turkey

Prof. Koichi Yoneyama, Utsunomiya University, Japan

Local Organizers

Prof. Airong Li, Kunming Institute of Botany, CAS, China

Prof. Kaiyun Guan, Xinjiang Institute of Ecology & Geography, CAS, China

Session Organizers

Grama Dhanapal	University of Agricultural Sciences (B), India
Yaakov Goldwasser	The Hebrew University of Jerusalem, Israel
Joseph Hershenhorn	Agricultural Research Organization, Israel
Hinanit Koltai	Agricultural Research Organization, Israel
Yongqing Ma	Northwest A & F University, China
Diego Rubiales	CSIS, Spain
Julie Scholes	The University of Sheffield, U.K.
Ken Shirasu	RIKEN, Japan
Philippe Simiere	Nantes University, France
Ahmet Uludag	Duzce University, Duzce, Turkey
John Yoder	University of California, Davis, U.S.A.
Koichi Yoneyama	Utsunomiya University, Japan
Weijun Zhou	Zhejiang University, China

PROGRAMME AT A GLANCE

Sunday 5th July

9:00-19:00 Registration and Poster setup

18:00-21:00 Welcome Reception

Monday 6th July

8:30-10:30 **Session 1: Molecules and biochemistry**

10:30-11:00 *Tea Break*

11:00-12:00 **Session 1: Molecules and biochemistry (continued)**

12:00-12:30 **Poster session 1**

12:30-13:30 *Buffet Lunch*

13:30-15:40 **Session 2: Genes and genomes**

15:40-16:00 *Tea Break*

16:00-18:00 **Session 2: Genes and genomes (continued)**

18:00-20:00 *Buffet Dinner*

Tuesday 7th July

8:30-10:30 **Session 3: Host parasite interactions**

10:30-11:00 *Tea Break*

11:00-12:00 **Session 3: Host parasite interactions (continued)**

12:00-12:30 **Poster session 2**

12:30-13:30 *Buffet Lunch*

13:30-15:30 **Session 3: Host parasite interactions (continued)**

15:30-16:00 *Tea Break*

16:00-17:50 **Session 4: Ecology, phylogeny and evolution-Part 1**

18:00-20:00 *Buffet Dinner*

Wednesday 8th July

8:30-10:00 **Session 4: Ecology, phylogeny and evolution-Part 2**

10:00-10:30 *Tea Break*

10:30-11:30 **Session 4: Ecology, phylogeny and evolution-Part 2 (continued)**

11:30-12:00 **Poster session 3**

12:00-13:00 *Buffet Lunch*

13:00-19:00 *Excursion to Yunnan Ethnic Villages*

19:00-21:00 *Buffet Dinner*

Thursday 9th July

- 8:30-10:00 **Session 5: Control and management**
- 10:00-10:30 *Tea Break*
- 10:30-12:10 **Session 5: Control and management(continued)**
- 12:10-12:30 **Poster session 4**
- 12:30-13:30 *Buffet Lunch*
- 13:30-15:30 **Session 6: Host resistance**
- 15:30-16:00 *Tea Break*
- 16:00-18:00 ***Closing remarks/Awarding Ceremony chaired by
Koichi Yoneyama***
- 18:00-20:00 *Conference dinner*
- 20:00-22:30 *Disco*

Friday 10th July

- All day Departures

DETAILED PROGRAMME

Sunday 5th July

9:00-19:00 Registration and Poster setup

18:00-21:00 Welcome Reception

Monday 6th July

Session 1: Molecules and biochemistry

8:30-8:40 *Welcome address by Professor Yongping Yang, Deputy director of Kunming Institute of Botany*

8:40-8:50 *Welcome by Koichi Yoneyama and Hinanit Koltai*

8:50-9:30 **Keynote lecture: Harro Bouwmeester**

Structural diversity in the strigolactones: biosynthesis and biological significance

9:30-9:50 **Koichi Yoneyama**

Structure- and stereo-specific transport of strigolactones from roots to shoots

9:50-10:10 **Salim Al-Babili**

Caractone: biosynthesis and application

10:10-10:30 **Alessio Cimmino**

Fungal and plant metabolites for the biocontrol of some parasitic plant species

10:30-11:00 *Tea Break*

11:00-11:20 **Rosemary Ahom**

Identification of potential and potency of allelochemicals in velvet bean (*Mucuna cochinchinensis* (Wight) Burck) for the control of *Striga hermonthica* (Del.) Benth.

11:20-11:40 **Kristen Clermont**

Comparative metabolomic analysis of early parasite development of *Phelipanche aegyptiaca* and *Triphysaria versicolor*

11:40-12:00 **Chong Yang**

Physiological and biochemical responses of three sunflower cultivars differing in their sensitivity to *Orobanche cumana* infection

Poster session 1

12:00-12:30 **Chong Yang**

Identification of natural germination stimulants from root exudates of sunflower cultivars differing in tolerance to *Orobanche cumana*

Yongqing Ma

Altitude and location have more effect on contents of germination stimulants for broomrape seeds than extraction methods from the crude extracts of *Houttuynia cordata*

Tadao Asami

Chemicals selectively regulating SL functions

Richard Louden

Can *Striga*-induced changes to strigolactone biosynthesis or signalling pathways explain key alterations in the morphology of its rice host?

Mahdere Shimels

Strigolactone profiles in *Sorghum bicolor*: in relation to arbuscular mycorrhizal fungal symbioses

12:30-13:30 *Buffet Lunch*

Session 2: Genes and genomes

13:30-13:40 *Welcome by Julie Scholes and Ken Shirasu*

13:40-14:20 **Keynote lecture: James Westwood**

Genome level interactions in the parasite-host complex

14:20-14:40 **Gunjune Kim**

Cuscuta gene expression and transcript exchange varies depending on host species

14:40-15:00 **Weishu Fan**

First complete mitochondrial genome from a parasitic plant (*Castilleja paramensis*)

15:00-15:20 **Djibril Yonli**

Genetic diversity of *Striga hermonthica* (Del.) Benth. in Burkina Faso

- 15:20-15:40 **Guangda Liu**
Using transcriptome data to assemble mitochondrial and chloroplast genes of *Cynomorium songaricum*
- 15:40-16:00 *Tea Break*
- 16:00-16:40 **Keynote lecture: Ken Shirasu**
Vascular hijack by parasitic plants
- 16:40-17:00 **Hailey Larose**
Pre- and post-germination transcriptome analysis of two species of parasitic Orobanchaceae
- 17:00-17:20 **Guiling Sun**
Novel Class II hAT transposons were laterally transferred from Brassicaceae to root parasitic Orobanchaceae
- 17:20-17:40 **Zhenzhen Yang**
Comparative transcriptome analyses reveal core parasitism genes and suggest gene duplication and repurposing as sources of structural novelty
- 17:40-18:00 **Xinhua Zhang**
Transcriptome profiling during haustorium development in the root hemiparasite *Santalum album* Linn.
- 18:00-20:00 *Buffet Dinner*

Tuesday 7th July

Session 3: Host parasite interactions

- 8:30-8:40 *Welcome by Philippe Simiere and John Yoder*
- 8:40-9:30 **Keynote lecture: Julie Scholes**
Deciphering the molecular mechanisms of resistance to parasitic plants
- 9:30-9:50 **Suo Qiu**
Understanding the genomic basis of virulence in the parasitic weed *Striga hermonthica*
- 9:50-10:10 **Xiaoyan Jia**
Engineering host cell wall to increase resistance against *Phelipanche aegyptiaca*

- 10:10-10:30 **Loren Honaas**
Risk versus reward: host dependent parasite phenotypes in the facultative generalist *Triphysaria versicolor*
- 10:30-11:00 *Tea Break*
- 11:00-11:20 **Muvari Tjiurutue**
Gypsy moth damage delays parasite attachment to cranberry hosts
- 11:20-11:40 **Jianqiang Wu**
Parasitic plant, *Cuscuta australis*, transmits inter-plant herbivory-induced signals
- 11:40-12:00 **Petra Svetlikova**
The physiological role of hydathode trichomes in parasitic Orobanchaceae

Poster session 2

- 12:00-12:30 **Chun Su**
Identification of parasite effectors mediating *Striga gesnerioides*-host plant interactions
- Yuxia Song**
Comparison of mitochondrial genomes between *Cistanche deserticola* and *Cistanche tubulosa*
- Lei Shi**
A horizontal gene transfer between *Cistanche deserticola* and its host *Haloxylon ammodendron*
- Guilin Chen**
Mitochondrial gene sequence analysis of parasitic plant *Cynomorium* and horizontal gene transfer study
- Yasunori Ichihashi**
Molecular basis for the convergent evolution of parasitism in plants
- Yu Wang**
Evolution and expression profile of transcription factor families in three parasitic plants of the Orobanchaceae
- 12:30-13:30 *Buffet Lunch*

Session 3: Host parasite interactions (continued)

- 13:30-13:50 **Satoko Yoshida**
Genomic and genetic analyses of haustorium formation using *Phtheirospermum japonicum* as a model parasitic plant
- 13:50-14:10 **Pradeepa Bandaranayake**
Functional characterization of haustorial hair development in *Triphysaria versicolor*
- 14:10-14:30 **Songkui Cui**
Haustorial hairs are controlled by root hair genes and involved in parasitism
- 14:30-14:50 **Vincent Goyet**
Towards the understanding of haustorium formation in the obligatory parasitic plant *Phelipanche ramosa*
- 14:50-15:10 **Tilal Abdelhalim**
Effects of mycorrhiza inoculation, nitrogen levels, and sugar cane residue based organic amendments on *Phelipanche ramosa* incidence, and tomato performance in the field
- 15:10-15:30 **Girija Vijayraghavan**
Host parasite interactions and nutrient dynamics of *Dendrophthoe falcata* (L.F.)
- 15:30-16:00 *Tea Break*

Session 4: Ecology, phylogeny and evolution-Part 1

- 16:00-16:10 *Welcome by Grama Nanjappa Dhanapal*
- 16:10-16:30 **Jonne Rodenburg**
The economic losses caused by parasitic weeds in rice in Africa
- 16:30-16:50 **Roshanizah Rosli**
An ecophysiological study of the hemiparasitic *Cassytha filiformis* L. (Lauraceae) in Brunei Darussalam, Borneo
- 16:50-17:10 **Mohamed Zaroug**
Field dodder (*Cuscuta campestris* Yuncker) a new pest of carrot (*Dacus carota* L.) in Gezira Scheme, Sudan

17:10-17:30 **Awad Taha**
Compatibility and incompatibility of some monocotyledonous plant species to field dodder (*Cuscuta campestris* Yuncker)

17:30-17:50 **Bo Xia**
Impact of *Arceuthobium sichuanense* infection on needles and current-year shoots of *Picea crassifolia* and *Picea purpurea* trees

18:00-20:00 *Buffet Dinner*

Wednesday 8th July

Session 4: Ecology, phylogeny and evolution-Part 2

8:30-8:40 *Welcome by Weijun Zhou and Yongqing Ma*

8:40-9:20 **Keynote lecture: Daniel Joel**
Factors affecting host range of weedy Orobanchaceae: the *Orobanche cumana* case

9:20-9:40 **Ahmet Uludag**
How climate change affects host-parasite relations and parasitic plant management

9:40-10:00 **Gensheng Bao**
Effects of the hemiparasitic plant *Pedicularis kansuensis* on plant community structure in a degraded grassland

10:00-10:30 *Tea Break*

10:30-10:50 **Lytton Musselman**
Taxonomy and phylogenetics of Hydnoraceae and a potentially new *Hydnora* from Oman

10:50-11:10 **Nina Hobbhahn**
Pollination ecology of the South African holoparasites *Mystroptalon thomii* and *Sarcophyte sanguinea*, and diversity of pollination systems in Balanophoraceae s.l.

11:10-11:30 **Salman Rahimi**
Explanation of parasite association aspects in plants: game theory application in population dynamics and community structure

Poster session 3

11:30-12:00 **Andy McNally**

Do arbuscular mycorrhizas alleviate the effect of *Striga hermonthica* on host performance?

Airong Li

AM fungi in roots of hemiparasitic *Pedicularis*: friends or foes?

Airong Li

High plasticity in root morphology of two root hemiparasitic *Pedicularis* (Orobanchaceae) species

Yanyan Liu

Influence of soil nutrient status and plant community structure on occurrence and expansion of *Pedicularis kansuensis* in Western China

Wenjun Li

Genetic variation and phylogeographic history of *Pedicularis kansuensis* (Orobanchaceae) inferred from Chloroplast DNA Sequences

Yuchao Chen

Pot culture of an important Chinese medicinal plant *Cistanche deserticola*

12:00-13:00 *Buffet Lunch*

13:00-19:00 *Field Excursion*

19:00-21:00 *Buffet Dinner*

Thursday 9th July

Session 5: Control and management

8:30-8:40 *Welcome by Ahmet Uludag and Joseph Hershenhorn*

8:40-9:20 **Keynote lecture: John Pickett**

Parasitic weed control: management of *Striga* spp. by companion planting with *Desmodium* spp. and opportunities for exploitation via GM

- 9:20-10:00 **Keynote lecture: Joseph Hershenhorn**
 How do amino acid biosynthesis inhibiting herbicides control broomrapes
- 10:00-10:30 *Tea Break*
- 10:30-10:50 **Yongqing Ma**
 A cautious conception for *Orobanche* spp. control by using allelopathy and trap crop
- 10:50-11:10 **Yaakov Goldwasser**
Cuscuta campestris control with granular cell division inhibiting herbicides
- 11:10-11:30 **Joseph Hershenhorn**
 Egyptian broomrape control in processing tomato with maleic hydrazide
- 11:30-11:50 **Musa Kolo**
 Use of some weed species for Witchweed (*Striga hermonthica* (Del.) Benth.) management in maize (*Zea mays* L.)
- 11:50-12:10 **Peter Toth**
 How to detect crop infestation by broomrapes long before than they appear aboveground?
- Poster session 4**
- 12:10-12:30 **Luyang Hu**
 Role of herbicides and salicylic acid in controlling obligate root parasite *Orobanche cumana* growth in host crop sunflower
- Stephane Munos**
 Towards the genome sequence of *Orobanche cumana*
- Philippe Simier**
 Genetic diversity and host preference in the parasitic weed *Phelipanche ramosa* L. Pomel
- Xiaolin Sui**
 Efforts taken in the control of weedy *Pedicularis kansuensis* in China
- 12:30-13:30 *Buffet Lunch*

Session 6: Host resistance

- 13:30-13:50 *Welcome by Diego Rubiales and Yaakov Goldwasser*
- 13:50-14:30 **Keynote lecture: Diego Rubiales**
Resistance to broomrape in legume crops
- 14:30-14:50 **Evgenia Dor**
Broomrape management with a novel tomato mutant line resistant to acetolactate synthase (ALS) inhibiting herbicides
- 14:50-15:10 **Johann Louarn**
Genetic characterization of the interaction between sunflower and *Orobanche cumana*
- 15:10-15:30 **Steven Runo**
Striga/sorghum arms race during domestication as revealed by dual RNA-seq
- 15:30-16:00 *Tea Break*
- 16:00-18:00 **Closing remarks/Awarding Ceremony chaired by Koichi Yoneyama**
- 18:00-20:00 *Conference dinner*
- 20:00-22:30 *Disco*

Friday 10th July

All day Departures

KEYNOTE LECTURES

Structural diversity in the strigolactones: Biosynthesis and biological significance

Harro J. Bouwmeester

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The lifecycle of root parasitic plant species is closely regulated by the presence of their hosts and signaling molecules released by the host play an important role in this interaction. This begins with the first step in the parasites' lifecycle, germination, which is tightly regulated by host-produced stimulants that induce the germination of the parasite seeds. Several classes of germination stimulants have been identified with the strigolactones as the most important class of germination stimulants. An intriguing aspect of the strigolactones is that they play multiple roles in the rhizosphere as well as in the host plant itself. This seems to have resulted in the evolution of an enormous structural diversity in the strigolactones of which we are only just beginning to understand the biological significance. In this presentation the current knowledge on the biosynthesis of strigolactones and strigolactone structural diversification as well as their perception in host plant as well as parasitic plants and the strategy to further elucidate its biological significance will be discussed.

Genome level interactions in the parasite-host complex

James H. Westwood

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Mechanisms by which parasitic plants interact with their hosts have been well documented and comprise some of the clearest examples of plant-plant interactions. Nevertheless, I propose that these are just the tip of the iceberg and that the level of host-parasite integration has deeper implications. All parasites are locked in an arms race with their hosts that drives evolution of both sides. In insects and animals, this has produced remarkable examples of parasite manipulation of host biology and behavior. Similarly, parasitic plants do not merely siphon off host water and nutrients, but rather have sophisticated mechanisms to redirect host resources while simultaneously subverting host defenses. While some of this ability may be accounted for by parasite manipulation of hormone levels and osmotic gradients, recent demonstrations of parasitic plants exchanging macromolecules such as proteins and nucleic acids with their hosts suggests a novel type of interaction that greatly expands the potential mechanisms available to the parasite for host manipulation. This is especially true for *Cuscuta*, where RNA exchange with hosts occurs with high frequency. The concept of exchange is important in this case because the parasite not only acts as a sink, but also transmits its RNA to the host, raising the potential for regulation of host gene expression. One implication of this exchange is the potential for parasite genomes to interact with host genomes, and although little evidence exists for routine exchange of DNA, the epigenetic effects of cross-species RNA movement are intriguing. Extending this beyond the simple one-host model, parasites often interact with multiple hosts simultaneously and can therefore become agents of molecular exchange and modification at the community level. Taken together, it may be appropriate to consider parasites and their hosts as part of a supraorganismal system in which the parasite-host complex is greater than the individual genetics of its members.

Vascular hijack by parasitic plants

Ken Shirasu

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Parasitic plants are unique to have an ability to obtain water and nutrients directly from other plants by hijacking the vasculature system. Several parasitic plant species such as *Striga* and *Orobanche* are serious biological threats to agriculture by infecting crops of high economic values. Thus understanding the mechanism underlying the hijacking process is an important step to develop a strategy to fight against the parasites. The hijacking process is facilitated by a multi-cellular organ called a haustorium, which invades the host plant and connect its vasculature with that of the host. Next-generation sequencing and bioinformatics, as well as genetic analyses revealed the dynamic reprogramming of the parasite cells upon infection. The molecular mechanism behind the uniqueness of parasitic plants will be discussed.

Deciphering the molecular mechanisms of resistance to parasitic plants

Julie D. Scholes

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Rice, sorghum and maize are staple foods for millions of people in sub-Saharan Africa yet the major biotic constraint to crop production and yield improvement is the parasitic weeds of the genus *Striga*. *Striga* species are obligate parasites that invade the roots of their host causing severe stunting and yield losses that range from 40% to total crop failure. Despite this the use of resistant cultivars is still not widespread even as part of an integrated control strategy. This is partly due to, a lack of resistance in farmer-preferred cultivars, an understanding of the molecular genetic basis of resistance (major gene or polygenic), the identity of the gene(s) involved and their relationship to different genetic populations of the parasite (host-parasite specificity). This knowledge is essential as it will allow us to combine appropriate resistance genes in cultivars that are suitable for different agro-ecological zones and to manage the use of cultivars more effectively such that evolution of virulence in the parasite is delayed. Our work is focused on the identification of mechanisms and genes underlying resistance (and susceptibility) in cereal hosts to different ecotypes and species of *Striga* with the ultimate aim of designing novel control strategies and / or breeding durable defence against these parasites. We have known for several years that some rice germplasm shows broad spectrum resistance to different ecotypes of *Striga* and that a common resistance phenotype is an inability of the parasite to invade the host xylem vessels, thus preventing access to host nutrients. I will discuss how the use of mapping populations has enabled us to identify a highly significant Quantitative Trait Locus (QTL) underlying the resistance phenotype that contains many orthologs of disease resistance genes and how we using a range of comparative genomic and molecular approaches to identify which of the candidate gene(s) is/are responsible for the resistance phenotype.

Factors affecting host range of weedy Orobanchaceae: the *Orobanche cumana* case

Daniel M. Joel

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The majority of parasitic Orobanchaceae species are limited in their ability to parasitize crop plants. Only few parasite species, belonging to a small number of genera, adapted to agricultural habitats and became weedy. Parasitic weeds under cultivation are constantly under changing selective pressures, which allow accelerated evolutionary processes that lead to speciation. Globalization contributes to this process by breaking geographical barriers between parasite populations. Furthermore, cultivation brings their seeds to the soil layers in which the crops develop their root systems, thus increasing their chance of parasitizing hosts. While monoculture allows dramatic increase in the parasite seedbank in soil, crop rotation contributes to the parasite polymorphism, which then increases the ability of some parasites to extend their host range. *Orobanche cumana* is predominantly a self-pollinating species, while *O. crenata* is insect pollinated. This reflects on their population diversity. While *O. crenata* is highly polymorphic both in morphology and in DNA profile, *O. cumana* has low population diversity. Nonetheless, both species developed new races that adapt to changing hosts. *O. cumana* is a specific parasite of sunflower that rarely parasitizes other crops. Two major different cases of *O. cumana* heavily parasitizing tomato plants were documented in Israel. The first case was due to an environmental factor while the second case – to genetic factors. *O. cumana* can parasitize tomato plants when grown on sunflower fallow. Lab experiments confirmed that *O. cumana* can germinate when seeds are exposed to tomato root exudates in the presence of soil remains of sunflower root exudates. Once germinated, *O. cumana* seedlings can readily parasitize tomato. The second case emerged when a new race of *O. cumana* heavily infested tomato fields in several different regions. In an inter-SSR DNA analysis, the tomato infesting populations of the parasite clustered into three separate clades, each representing an *O. cumana* infesting tomato population from one region. Offsprings of *O. cumana* originating from tomato fields were able to repeat parasitizing tomato while maintaining their virulence against sunflower. This change in host range was facilitated by seed ability to germinate in response not only to the sunflower sesquiterpene lactones (STLs) that serve as the common stimulants for *O. cumana*, but also to strigolactones (SLs) that are released from tomato roots. A similar ability to respond to both STLs and SLs occurs in segregants of hybrids between *O. cumana* and the weedy *O. cernua* that parasitizes tomato, which may indicate that the virulent race developed in a similar manner. This and other hypotheses regarding the origin of the new virulent race of *O. cumana* are discussed with reference to the current knowledge on the evolution and population diversity of *Orobanche* species.

Parasitic weed control: management of *Striga* spp. by companion planting with *Desmodium* spp. and opportunities for exploitation via GM

John Pickett

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The parasitic weed *Striga hermonthica* (Orobanchaceae) and *S. asiatica* in cereals, can be managed by growing perennial companion legumes in the *Desmodium* genus, also valuable as forage for dairy farm animals. Yields of maize, sorghum, finger millet and upland rice are raised substantially with the control of *S. hermonthica* by intercropping with *Desmodium uncinatum* as the companion crop. There has been a high take-up of this control system in the regions targeted in combination with the use of *Desmodium* spp. Intercrops for repelling stem borer moths and attracting their natural enemies. These intercrops simultaneously provide farm animal forage and fixed nitrogen for the cropping system. The approach is particularly valuable for resource-poor smallholder farmers and it is these farming systems that represent those mainly afflicted by *S. hermonthica*. Very recently, a new programme searching for drought-tolerant companion plants to function in regions experiencing drought, as a consequence of climate change, has demonstrated a similar value for the more drought tolerant *Desmodium intortum*. Other *Desmodium* spp. are being investigated in this context, with *D. intortum* already on-farm in some of the more arid and degraded regions of East Africa. Although far less work has been done on *S. asiatica*, similar control is demonstrated. The mechanism by which *Desmodium* spp. control *Striga* spp. is not fully elucidated but involves a suicidal germination of the parasite which rapidly reduces the seed bank through the growing seasons. Bioassay-guided fractionation has shown that C-linked glycosides of apigenin are mainly responsible for the suicidal aspect of the control mechanism. C-Glycosyl transferases have been isolated and the associated synthesis genes expressed in cowpea in an ongoing attempt to produce a GM legume yielding edible beans incorporating the *Striga*-controlling trait.

How do amino acid biosynthesis inhibiting herbicides control broomrapes

Joseph Hershenhorn

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An effective broomrape control without causing damage to the crop can so far be achieved only with herbicides inhibiting amino acid biosynthesis. Two chemical groups of herbicides inhibit amino acid biosynthesis: a) glyphosate that inhibits the enzyme Enolpyruvylshikimate phosphate synthase (EPSPS), which catalyzes a key step in the formation of the aromatic amino acids phenylalanine, tyrosine and tryptophan; b) aceto lactate synthase (ALS) inhibiting herbicides, which block the formation of the branched chain amino acids leucine, isoleucine and valin by inhibiting the key enzyme aceto lactate synthase also known as aceto hydroxy lactate synthase. The ALS inhibiting herbicides include 5 chemical groups but only sulfonylureas and imidazolinones are used for broomrape control. While the mode of action of the amino acid biosynthesis inhibiting herbicides is well known, the manner by which they successfully control broomrapes is so far not clear. Broomrapes are obligate parasites that draw all their nutritional requirements from the host, including amino acids, and therefore inhibition of amino acid biosynthesis within the parasite should ostensibly not be lethal. It could thus be predicted that these enzymes are not synthesized or active in the parasites. We therefore studied the mode of action of these herbicides in callii of *Phelipanche aegyptiaca* (Pers.) Pomel.. We confirmed that both herbicides inhibited callus growth and demonstrated that there are significant changes in the free amino acid contents of treated callii. We further demonstrated the presence of active EPSPS and ALS in the broomrape callus and in flowering shoots. Inhibition of callus EPSPS and ALS was also demonstrated. Blasting of *A. thaliana* EPSPS and ALS cDNAs against the genomic DNA identified a single DNA fragment of both ALS (*P. aegyptiaca* putative ALS gene) and EPSPS (*P. aegyptiaca* putative EPSPS gene) with about 78% and 75% identity to *A. thaliana* ALS and EPSPS proteins, respectively. It was therefore concluded that broomrape has its own biosynthesis machinery for the production of branched and aromatic amino acids, indicating that these enzymes do have a role in the parasite development. Blocking their activity would therefore lead to shortage in those amino acids and finally - to the death of the parasite.

Resistance to broomrape in legume crops

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Legume crops can be damaged by a number of broomrape species. *Orobanche crenata* is the most widely distributed in the Mediterranean basin and Middle East. *O. foetida* and *O. aegyptiaca* can also be of local importance. Resistance against broomrape in legumes is difficult to access, scarce, of complex nature and of low heritability, and these factors complicate resistance breeding. As a result, only cultivars with moderate levels of resistance are available to farmers. This is further complicated by the fact that several clearly distinct broomrape species can infect the same legume crop, reinforcing the need to search for additional sources of resistance and to test their stability. Available sources of resistance and their underlying mechanisms and genetic basis on the various legume crops will be reviewed and compared with those available in other crops. Implications in resistance breeding will be critically discussed.

SESSION PRESENTATIONS

Session 1: Molecules and biochemistry

Chairs

Koichi Yoneyama and Hinanit Koltai

Structure- and stereo-specific transport of strigolactones from roots to shoots

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It is generally accepted that strigolactones (SLs) mainly produced in roots move acropetally to shoots and inhibit axillary bud outgrowth. In fact, root-applied SLs restore shoot phenotype in SL deficient mutants of *Arabidopsis*, rice, pea, etc. However, SLs were not detected by LC–MS/MS in xylem saps collected from rice (1 L), tomato (13 L), cucumber (20 L), tobacco (7 L), sorghum (1 L), and *Arabidopsis* (2.5 mL), indicating that SLs are hardly transported through xylem at least in these plant species. When shoots of rice plants that had been fed with d₁-orobanchol to roots were harvested 2 and 20 hours after treatment, d₁-orobanchol was detected only in that harvested 20 hours after treatment. In this case, neither d₁-orobanchol nor known SLs were detected in the xylem sap. Similar results were obtained with other plant species. These results imply that both endogenous and exogenous SLs move symplastically in plants. In addition, by using deuterium-labeled SLs, transport of root-applied SLs to shoots was found to proceed in a highly structure- and stereo-specific manner. Details of xylem sap analyses and feeding experiments will be explained and discussed in relation to SL transport in plants.

Carlactone: Biosynthesis and application

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Carlactone is an intermediate of the strigolactone biosynthetic pathway, which is formed from all-trans-carotene by the sequential activity of the all-trans/9-cis-carotene isomerase DWARF27 and the Carotenoid cleavage dioxygenases 7 and 8 (CCD7, CCD8). To explore the potential of this pathway in converting carotenoids other than all-trans-carotene and in producing carlactone-like compounds that might lead to other type(s) of strigolactones. For this purpose, we investigated the substrate specificities of the involved enzymes, using in vitro assays. Our results demonstrate that the rice DWARF27 is highly specific for -ionone ring containing bicyclic carotenoids, i.e. -carotene and -cytotoxanthin, and mediates the isomerization reaction in the -ionone ring containing moiety of the substrate. CCD7 enzymes show a wide substrate- and a very narrow stereo-specificity, converting different 9-cis-configured carotenoids, including 9-cis-carotene, 9-cis-zeaxanthin and 9-cis-lutein. These data indicate the possibility of the formation of hydroxylated carlactones. Initial studies showed that carlactone can induce seed germination in *Striga* at considerable levels but has largely only MAX1-dependent activity in *Arabidopsis*. We designed a new compound, based on carlactone, and tested its biological activity. The carlactone analogue exerted very high activity in inducing seed germination. However, this activity was dependent on the species. In addition, the compound showed strigolactone-like activities in *Arabidopsis*.

Fungal and plant metabolites for the biocontrol of some parasitic plant species

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Broomrapes (*Orobanche* and *Phelipanche* spp.) and dodders (*Cuscuta* spp.), belonging to Orobanchaceae and Convolvulaceae families, respectively, are parasitic weeds infesting a large number of important crops and causing severe yield losses. The main obstacle for long-term management of broomrape infested fields is the durable seed bank with evolved mechanisms of host recognition upon perception of host-derived germination factors. The continuous spread of broomrapes and dodders strongly affect on the farmers work as heavy infestations lead not only to a complete crop failure, but also have a great negative impact over many years, because seeds can survive in soil for a long period of time. Although a large number of certain agronomic practices have been proposed, effective management of parasitic weeds is very difficult to be reached because of their physiological traits and life cycle. Current control relies on the use of resistant crop varieties and herbicides, albeit success has been marginal. Considering that seed germination is a key phase for parasitic plant development and infestation, a further approach proposed for the management of these weeds has been to use microbial or plant metabolites to stimulate, in absence of the host, and/or inhibit the broomrape seed germination. Some metabolites induced a rapid cessation of radicle growth with the promotion of a layer of papillae at the radicle tip hampering the contact of the parasite to the host. The development of herbicides based on natural metabolites from microbial and plant origin, targeting early stages on parasitic plant development, might contribute to the reduction of broomrape seed bank in agricultural soils. Plant and fungal metabolites were also evaluated for their inhibitory effects on germination and growth of dodder species. This communication will illustrates the results obtained in the isolation and chemical characterization of some plants, plant root exudates and fungal metabolites and their effect on the seed germination of different broomrape and dodder species, to develop alternative and ecofriendly strategies for the management of these dangerous parasitic plants.

Identification of potential and potency of allelochemicals in Velvet bean (*Mucuna cochinchinensis* (Wight) Burck) for the control of *Striga hermonthica* (Del.) Benth.

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The Experiment was conducted at the Toxicology laboratory, Faculty of Agriculture, University of Putra Malaysia, Serdang, Malaysia in 2013. The study was to identify plant growth-inhibitory compounds in *M. cochinchinensis* as a step to clarifying the weed-suppressing effect of this plant. The treatments consisted of five concentrations (100, 75, 50, 25, 0 ppm) of plant parts (leaf, root, seed) and extraction solvents (methanol, water). The experimental design was a completely randomized block (CRD) with three replications. In all the treatments, inhibition from root was greater than from leaves. The seed extract showed less inhibition. Six phenolic/flavonone compounds including Gallic acid, caffeic acid, L-dopa, tyrosine, quercetin and isovetexin were isolated and identified in velvet bean leaves, root and seed. Concentration of these phenolic compounds in root was higher than in the leaves. These compounds showed different degrees of inhibition against *Striga hermonthica* and therefore resulted in a stronger allelopathic activity of *M. cochinchinensis*. The identification of these substances might provide chemical basis for the development of bio-herbicides for environmentally friendly sustainable agricultural systems.

Comparative metabolomic analysis of early parasite development of *Phelipanche aegyptiaca* and *Triphysaria versicolor*

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Parasitic weeds of the family Orobanchaceae attach to the roots of host plants via haustoria capable of drawing nutrients from host vascular tissue. The development of the haustorium marks a shift in parasite metabolism from autotrophy to at least partial heterotrophy. Species within the family span the spectrum of host nutrient dependency. This variation is reflected in the physiology of the haustorial attachment, with xylem only versus xylem plus phloem connections in hemi versus holoparasites, respectively. Here we use comparative profiling of primary metabolites to gain insight into carbon and nitrogen assimilation by the obligate holoparasite *Phelipanche aegyptiaca* and the facultative hemiparasite *Triphysaria versicolor*. Metabolic profiles have been generated from key stages of parasitism surrounding haustorial development: before and after haustorial induction, during haustorial penetration, and after haustorial vascularization. For example, during initial growth of *P. aegyptiaca* on *Arabidopsis thaliana* the amino acid pool contained high levels of glutamine, representing 24% of the detectable amino acid. This transitioned to aspartate after further tubercle expansion and development, reducing glutamine to 10% of detectable amino acid and increasing aspartate from 13% to 30%. In contrast, *T. versicolor* grown on *Medicago truncatula* maintained consistent glutamine levels throughout haustorial development, while also maintaining pools of glutamate and asparagine. Previous studies have implicated aspartate/asparagine metabolism in the nitrogen storage and response to host stimuli by parasitic Orobanchaceae. These results provide a rationale for targeting aspartate-family amino acid biosynthesis for disrupting the growth of parasitic weeds. This work also adds metabolome data to current Parasitic Plant Genome Project transcriptome datasets, and will contribute to greater understanding of parasitism in the Orobanchaceae.

Physiological and biochemical responses of three sunflower cultivars differing in their sensitivity to *Orobanche cumana* infection

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Broomrapes (*Orobanche* and *Phelipanche* spp.) are obligate root parasites causing a severe damage to many economically important field and vegetable crops all around the world because of their violent extract of water and nutrients from host. For the development of efficient control strategy, a better understanding of the physiological and biochemical processes underlying the complex host–parasite interaction is required. Keeping the view, we designed the present investigation to study the effect of *O. cumana* inoculation on physiological and biochemical changes in three contrasting cultivars TK0409 (confectionery type and susceptible), S606 (oil type and intermediate) and JY207 (oil type and resistant) of host sunflowers. Infection of broomrape in cultivars TK0409 and S606 reduced plant growth, biomass and produced considerable oxidative stress (MDA, OH⁻, H₂O₂, O₂⁻) as compared to resistant cultivar JY207 and their respective control. Six weeks after the inoculation, significant decrease in photosynthetic and gas exchange parameters were observed in susceptible cultivar TK0409 followed by S606. The significant increase in the activities of SOD, POD and CAT was observed in resistant cultivar JY207 as compared to TK0409 and S606 at both 3 and 6 weeks after inoculation. Compared to susceptible cultivar, enhanced accumulation of phenolic and lignin contents was found in the resistant cultivar JY207. The data suggested that the enhanced plant growth, low oxidative stress, stimulated antioxidant activities, lignin and phenolic contents were associated with improved infection tolerance in cultivar JY207 as compared to TK0409 and S606. Higher concentration of phenolics and lignins in resistant cultivar JY207 is observed under *O. cumana* inoculation that may play a possible role in infection prevention. Further study is needed to clarify the root exudate secretion and molecular mechanism that play a critical role in the infection inhibition in resistant cultivar as compared to susceptible ones.

Identification of natural germination stimulants from root exudates of sunflower cultivars differing in tolerance to *Orobanche cumana*

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The obligate root parasite *Orobanche cumana* has become a severe threat to sunflower production, causing huge economic losses particularly in China's northern and western provinces including the Inner Mongolia Autonomous Region. It is urgent to acquire knowledge about resistance mechanisms for the effective control of this root parasitic weed. Germination of broomrape (*Orobanche* and *Phelipanche* spp.) seeds needs specific stimulants, most of which are called strigolactones, from their hosts, which is considered as the first and critical stage for resistance of hosts against parasites. Canonical strigolactones, which stimulate the germination of the various *Orobanche* species, only weakly elicit germination of *O. cumana*. In our present research, the germination stimulants in the root exudates from three cultivars of sunflowers (confectionery type cv. TK0409, oil type cvs. S606 and JY207, all from Inner Mongolia) with different tolerance capabilities to *O. cumana* (susceptible, intermediate and resistant, respectively) were analyzed using LC-MS/MS. Root exudates were obtained after 18 d of hydroponical culture with 11 d of phosphorus deficiency. Four strigolactone-related compounds including carlactonoic acid, heliolactone, an isomer of zealactone, and a novel stimulant were detected in root exudates from all three cultivars of sunflower. There were no significant differences in the production of these stimulants among the three sunflower cultivars. Data of germination assays with seeds of *O. cumana* and *O. minor* suggested that root exudate from the resistant cultivar JY207 contained germination inhibitors which act at relatively high concentrations. All these sunflower cultivars appear to produce germination stimulants which are more specific to *O. cumana*.

Altitude and location have more effect on contents of germination stimulants for broomrape seeds than extraction methods from the crude extracts of *Houttuynia cordata*

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We have previously reported that the *H. cordata* grown in both China and Japan were able to induce *S. hermonthica* seeds to germinate. It was reported that *H. cordata* grown in different locations have great variations in its chemical components and there are great differences in the contents of flavonoids, quercetin, and methyl-n-nonylketon from different habitats. The results of extraction chlorogenic acid, flavonoids, polysaccharide in *H. cordata* by ultrasonic treatment indicated that the method has high rate and short time of extraction compared with traditional extraction. It was also reported that altitude could affect *H. cordata* production on its secondary metabolites, and the content of bornyl acetate and trans- β -ocimene had significant positive correlation with the altitude. There are controversy reports on dry methods for obtaining active compounds from *H. cordata*. It was reported that the levels of strigolactones in the neutral ethyl acetate solution fractions from freeze-dried *H. cordata* sample were only 1/10 that of fresh sample, indicating that strigolactones were decomposed during the lyophilization. However, crude extracts of both fresh and freeze-dried samples showed a similar level of germination stimulating activity toward *Orobancha minor*. In this report we are aim to induce *P. aegyptiaca* and *O. cumana* seeds germination by *H. cordata* from different locations of China and studied the effect of different pH, temperature, dry methods as well as altitude. Distilled water and methanol extracts from *H. cordata* roots of six different locations by different treatments (drying method, methanol concentration, pH, ultrasonic time, and extraction temperature) were used in this study to stimulate *P. aegyptiaca* seeds and *O. cumana* seeds germination. Extracts of *H. cordata* from Guangxi Province of China has displayed a higher germination rates to stimulate two kinds of broomrape seeds no matter what kinds of drying methods used. In addition, the extracts from Sichuan, Anhui and Hunan had shown a lower germination rates. This indicated that germination stimulant contents between different location and altitude of *H. cordata* have significant differences. When *H. cordata* sample were dried by different drying methods (oven dry 80°C, freeze-drying or dry in the shade) from same location, the germination of broomrape seeds had no significant differences. This indicated that drying methods had a litter impact on effects of stimulation germination of broomrape. Germination stimulant of *P. aegyptiaca* in *H. cordata* is more sensitive to temperature treatment, the germination rate of *P. aegyptiaca* seeds raised with temperature but *O. cumana* seeds was not sensitive to temperature treatment. The germination rate of *O. cumana* seeds was reduced when the pH of extracting solution of *H. cordata* was raised. Seeds of *P. aegyptiaca* can only germinate when the pH of extracting solution of *H. cordata* was at 4.0. The germination rate of broomrape seeds was reducing with ultrasonic time. This might because too long ultrasonic time can extract some germination inhibitor from *H. cordata*.

Chemicals selectively regulating SL functions

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Broad biological activities of SLs have a potential to solve the agricultural problems concerning world food security. As a solution for the problems, we developed chemical tools that can regulate SL signaling, such as biosynthesis inhibitors and mimics, and characterized their functions by using SL mutants. Here, we show the result of structure-activity relationship studies on our SL mimics "debranones" and classify them based on their action spectra. Firstly, we found that chemicals possessing 5-phenoxy-3-methyl-2(5*H*)-furanone skeleton, which is synthesized readily in a cost conscious way, work effectively on inhibiting tiller buds outgrowth of SL deficient mutant rice. So, we called these types of chemicals possessing this skeleton as "debranone" after its structure and activity (de-branching furanone). We screened "4BD" as a representative compound of the first generation debranones by rice tillering inhibition assay. Secondary, we investigated SL functions of 4BD and characterized it as a preferential SL mimic for exerting branching inhibition activity. Next, we tried to develop debranones selectively stimulating seed germination of root parasitic plants. Through the structure-activity relationship study, we found that regioisomeric effect of functional groups on the phenyl group of debranones result in differences in SL functions of each chemical, On the basis of this finding, we characterizes these regioisomers thus synthesized by several SL-related biological assays to identify specific function of each chemical. As a result, we expect that each function of SLs can be mimicked by chemical modification of debranone. In addition, these SAR studies led us to find the most effective debranone that is 1000 times more effective than 4BD in *Striga* germination assay.

Can *Striga*-induced changes to strigolactone biosynthesis or signalling pathways explain key alterations in the morphology of its rice host

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Striga hermonthica is an obligate root parasite that infects a wide range of cereal crops including rice, maize, sorghum and millet in sub-Saharan Africa causing devastating losses in yield. During the infection process, the parasite xylem vessels fuse with those of its host allowing movement of nutrients to the parasite and potentially parasite-derived compounds into the host. Once attached, the parasite causes substantial developmental changes, including stunting of the main stem and a suppression of tillering in rice, both of which contribute to the loss in host yield. While *Striga* infestation is the major biotic stress limiting cereal production for subsistence farmers, little is known about the molecular mechanisms underlying the *Striga*-induced changes in host development. SLs are terpenoid lactone molecules that have been classified recently as a new Plant Growth Regulator (PGR); they were discovered through the isolation of a series of dwarf mutants which display a stunted, high branching/tillering phenotype. The high level of shoot branching in these mutants led to the discovery of SLs role as a key branching regulator. Although the mechanism underpinning this is under discussion the most recent evidence suggests that SLs regulate auxin transport in order to prevent shoot bud outgrowth. In this study we test the hypothesis that *Striga*-induced alterations in host strigolactone biosynthetic or signalling pathways underlie the *Striga*-induced suppression of tillering in rice. Specifically we hypothesised that the rice dwarf mutants which are either compromised in the biosynthesis of strigolactones or in down-stream signalling pathways would not show the characteristic suppression of tillering seen in infected wild-type plants, as both SL presence and signalling are required in order to control auxin transport and prolong shoot bud dormancy. This hypothesis was tested by infecting the d mutants and measuring the changes to above ground morphology including tillering. Our results revealed that all the d mutants showed a significant reduction in tiller number when infected with *S. hermonthica*, compared to uninfected plants. Our data therefore suggest that alterations in strigolactone biosynthesis or signalling alone cannot explain the *Striga*-induced suppression of tillering and that alterations in auxin concentration and signalling are likely to be important. This is currently being investigated.

Strigolactone profiles in *Sorghum bicolor*: in relation to arbuscular mycorrhizal fungal symbioses

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A host driven symbiotic relationship between arbuscular mycorrhizal (AM) fungi and a host plant is common during phosphorus deficient conditions. In this relationship, the AM fungi enhance the phosphorus uptake while relying on the carbon provided by the host plant. To initiate this symbiosis, the host plants' roots release signalling molecules that trigger hyphal branching of the fungal spores. One class of signalling molecules involved in this interaction is represented by the strigolactones. These signalling molecules also function as plant hormone regulating shoot and root architecture. In the rhizosphere, this signal is hijacked by parasitic plants such as *Striga* spp and *Orobanche* spp. Seeds of these parasites use strigolactones as germination stimulants after which they infect the roots of their host and consume its water, assimilates and minerals which can result in serious yield loss of the host. In vitro studies have shown that different strigolactones have different fungal hyphal branching - inducing - and *Striga* germination stimulatory activities. However, the consequence of a difference in strigolactone composition towards AM fungi symbiosis and *Striga* infection in planta has so far not been studied. In this project, we are using a targeted approach where we inoculated sorghum plants with three different AM fungi strains. These sorghum varieties are known to differ in strigolactone profile (both in type and/or amount) and resistance against *Striga* and we decided to study the effect of this on AM fungal symbiosis. Our results suggest that there is specificity for the sorghum cultivar - AM fungi species interaction. Interestingly, the strigolactone profile of some cultivars was changed when inoculated with certain combinations of different AM fungal species. To better understand the effect of different strigolactone profiles on the microbial community assembly in the rhizosphere, including AM fungi, we are currently using an untargeted approach. Hereto, the sorghum genotypes are grown on non-sterile soil and the root system will be subjected to ion Torrent sequencing to determine the fungal community composition. The correlation between strigolactone profile and fungal community composition will be explored.

Session 2: Genes and genomes

Chairs

Julie Scholes and Ken Shirasu

***Cuscuta* gene expression and transcript exchange varies depending on host species**

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Cuscuta species (dodders) are parasitic plants that are able to grow on many different host plants and can be destructive to crops. The connections between *Cuscuta* and its hosts allow movement of not only water and small nutrients, but also macromolecules including mRNA, proteins and viruses. Recent studies show that RNA movement between *Arabidopsis* and *Cuscuta* appears to occur on a large scale as well as in a bidirectional manner. Similar studies using tomato hosts indicated that RNA movement was more limited in this interaction. Given the characteristic ability of *Cuscuta* to attack a wide range of hosts, it is important to characterize RNA movement in a broader range of host-*Cuscuta* combinations. We generated transcriptome data via Illumina sequencing from *Cuscuta* stems near the point of attachment to *Arabidopsis*, tomato, *Medicago* and beet hosts. Analyses demonstrated that *Arabidopsis-Cuscuta* connections are clearly the most efficient in allowing haustorial transfer of host transcripts, whereas tomato, *Medicago* and beet hosts showed fewer transcripts moving. This experiment also provided insight into *Cuscuta* gene expression near the point of attachment. Most parasite genes were expressed consistently regardless of host being attacked, as exemplified by genes related to cell wall modification, which were expressed in all interactions. However, *Cuscuta* also expressed smaller subsets of genes in patterns that were specific for each different host. Taken together, these results indicate that *Cuscuta* interacts with each different host in a specific manner and understanding the dynamics of specific interactions may advance understanding of *Cuscuta* parasitism.

First Complete Mitochondrial Genome from a Parasitic Plant (*Castilleja paramensis*)

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Parasitic plants obtain part or all of their nutrition from their host plant, resulting in the reduction or loss of photosynthetic activity and genes related to photosynthesis in the plastid genome. *Castilleja paramensis* is a perennial herbaceous hemiparasite in the Northern high-Andean Mountains of Colombia. Here we report the complete mitochondrial and plastid genome of *C. paramensis* to investigate changes in the organelle genomes that may result from a parasitic lifestyle. Comparative plastid genome analyses indicate that *C. paramensis* retains nearly all conserved plastid genes, except that *ndhF* has become a pseudogene. This suggests that the NAD(P)H dehydrogenase complex is in the initial stages of degradation, consistent with observations in other hemiparasitic plants. In contrast, the mitochondrial genome, which is the first completed sequence from a parasitic plant, contains a typical set of genes and no evidence for genome degradation. Parasitic plants can facilitate horizontal transfer, and *C. paramensis* appears to be the donor for a transfer event involving the *atp9* and *ccmFn* genes into another Andean plant. The mitochondrial genome also contains the *cox1* intron, which was previously observed to be over-represented in parasitic plants and horizontally transferred among species; however, phylogenetic analysis of the intron indicates that Orobanchaceae parasites have acquired this intron vertically from a non-parasitic ancestor. Collectively, these results are consistent with a reduction in photosynthetic activity but retention of full mitochondria function in *C. paramensis*.

Genetic diversity of *Striga hermonthica* (Del.) Benth. in Burkina Faso

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The parasitic angiosperm, *Striga hermonthica* is a major biotic constrain to cereal production in sub-Saharan Africa by causing huge losses in grain yield. The investigation of the genetic diversity of *Striga* populations is important because it allows identification of strains which is a prerequisite for breeding success. Nineteen simple sequence repeat (SSR) markers were used to estimate genetic variability within and among 95 populations of *S. hermonthica* growing on sorghum, millet, maize, rice and wild grasses from different locations within Burkina Faso. Factorial analysis revealed three distinct clusters of *S. hermonthica* populations. Genetic distances for *Striga* populations ranged from 0.02 to 0.875 with a mean of 0.2817. According to host, genetic distances were 0.3210, 0.4085, 0.1209, 0.1313 and 0.3005 for *Striga* populations collected from sorghum, millet, maize, rice and wild grasses, respectively. The molecular SSR marker analysis of *Striga* populations revealed the existence of genetic variability in *Striga hermonthica* species in Burkina Faso. Despite the means of dissimilarity indexes are not high, both intercrop and intracrop strains of *S. hermonthica* may be present in host crop fields. Cross-inoculation experiments should be carried out to highlight the host specificity.

Using transcriptome data to assemble mitochondrial and chloroplast genes of *Cynomorium songaricum*

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Cynomorium songaricum is a parasitic plant which distributes in China, Mongolia and Central Asia. In China, *C. songaricum* is used as herb drug and its hosts are mainly in the genus of *Nitraria*. *C. songaricum* was placed to different orders in different phylogenetic analyses using nuclear genes, mitochondrial genes and chloroplast genes. The previous studies showed *C. songaricum* had relatively special genetic characteristics, such as horizontal gene transfer of mitochondrial genes, heteroplasmy of plastid gene and recombination of mitochondrial gene *atp1* and chloroplast gene *atpA*. The above genetic characters possibly cause the difficulties in phylogenetic analysis, but also make *C. songaricum* a good material to study these special genetic characteristics. However, plant mitochondrial genome and chloroplast genome includes many genes, it takes too much time to amplify every single gene. In this study, we used the transcriptome data of *C. songaricum* in different growth period to assemble Unigenes; the Unigenes were analyzed with mitochondrial genome and chloroplast genome of *Vitis vinifera* by local blast; the high similarity fragments were analyzed in NCBI to confirm the cDNA fragments of mitochondrial and chloroplast genes. A part of cDNA fragments were verified by PCR and sequencing. RNA editing sites were analyzed by comparing the assembled cDNA and the DNA sequences of *C. songaricum*. In this study, we assembled more cDNA fragments of chloroplast genes than previous study, and classify the genes by functions, we noticed only *clpP* was assembled in all photosynthesis related chloroplast genes, which may indicate a lot of photosynthesis related chloroplast genes were lost or did not transcribe anymore. In this study, the transcriptome data was used to assemble cDNA of mitochondrial and chloroplast genes, this method can also be used for researches on mitochondrial and chloroplast genes in other plants, and the assembled cDNA sequences can also be used to design primers to promote the researches on mitochondrial and chloroplast genes.

Pre- and post-germination transcriptome analysis of two species of parasitic Orobanchaceae

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Seed dormancy is a crucial adaptive trait that allows a species to optimize timing of seed germination to maximize the probability of growing under favorable conditions. The primary dormancy in seeds of *Orobanche*, *Phelipanche* and *Striga* can be categorized as three distinct physiological blocks to germination. These barriers need to be relieved sequentially before germination can occur. This includes: first, a period of dry storage known as dry after-ripening, second, a period of imbibition in water (conditioning) and third, the perception of a host-derived germination signal. The third physiological block is of particular interest, as it prevents seed germination in the absence of an acceptable host. While it is known that gene expression occurs during conditioning, little is known about the genes expressed during the break from dormancy. Transcriptomes of *O. cumana* and *O. cernua* were sequenced at three stages: during conditioning, completed conditioning, and following exposure to stimulant. Transcriptomes of *O. cumana* and *O. cernua* were assembled using Trinity de novo assembler and contain 143,285 and 132,608 contigs respectively. The assembled transcripts were annotated against publically available databases and GO terms were assigned. Differential expression analysis was performed between the various stages for each species and GO enrichment analysis was performed on the differentially expressed genes between the stages. Ongoing analysis of these results aim at elucidating the global changes in gene expression in both *Orobanche* species during release from dormancy to provide insight into the physiological mechanisms governing this process. Ultimately, we plan to apply this system to understanding germination specificity in these species.

Novel Class II hAT transposons were laterally transferred from Brassicaceae to root parasitic Orobanchaceae

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Parasitic plants can acquire foreign genes from their hosts, but the mechanisms for such horizontal transfers (HGT) are still poorly understood. Transcriptome screening in the obligate root parasite *Pelipanche aegyptiaca*, a common pest on crops including *Brassica oleracea*, and detailed gene annotations in Brassicaceae revealed that two genes in *P. aegyptiaca* closely resemble the homologs of Brassicaceae. Homology search against draft genomic assemblies showed that the two genes are also present in *Orobanche austrohispanica* and *O. gracilis*. The domain structure and the unique insertion between two domains indicate that these genes constitute a new group of the hAT superfamily in class II transposable elements, here named *bo* genes. Phylogenetic analysis shows that the *bo* genes evolved into two subfamilies, *bo1* and *bo2*, before the divergence of Brassicaceae. The common ancestor of *Orobanche* and *Pelipanche* likely acquired the *bo1* and *bo2* genes by HGT from Brassicaceae hosts. Given the divergence time of these two genera, the transfer may have occurred 40 million years ago. In Brassicaceae, most *bo* genes are distributed in tandem in the chromosomes, and their flanking genes show strong synteny. The lack of classic boundary structures and transcriptional evidences in Brassicaceae indicate they may have little transposase activity. The high transcriptional levels of the *bo* genes in *Pelipanche* imply they may still possess transposase activity. This is the first case of a class II transposon laterally transferred among eudicots, and it likely involved direct transport of DNAs through haustoria, followed by the insertion catalyzed by the transposase itself.

Comparative transcriptome analyses reveal core parasitism genes and suggest gene duplication and repurposing as sources of structural novelty

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The origin of novel traits is recognized as an important process underlying many major evolutionary radiations. We studied the genetic basis for the evolution of haustoria, the novel feeding organs of parasitic flowering plants, using comparative transcriptome sequencing in three species of Orobanchaceae. Around 180 genes are upregulated during haustorial development following host attachment in at least two species, and these are enriched in proteases, cell wall modifying enzymes, and extracellular secretion proteins. Additionally, about 100 shared genes are upregulated in response to haustorium inducing factors prior to host attachment. Collectively, we refer to these newly identified genes as putative “parasitism genes.” Most of these parasitism genes are derived from gene duplications in a common ancestor of Orobanchaceae and *Mimulus guttatus*, a related nonparasitic plant. Additionally, the signature of relaxed purifying selection and/or adaptive evolution at specific sites was detected in many haustorial genes, and may play an important role in parasite evolution. Comparative analysis of gene expression patterns in parasitic and nonparasitic angiosperms suggests that parasitism genes are derived primarily from root and floral tissues, but with some genes co-opted from other tissues. Gene duplication, often taking place in a nonparasitic ancestor of Orobanchaceae, followed by regulatory neofunctionalization, was an important process in the origin of parasitic haustoria. This study illustrates the power of detailed spatial sampling and genome scale data, coupled with powerful bioinformatic and evolutionary analysis, to produce new insights into parasite biology and a collection of specific target genes for experimental analysis.

Transcriptome profiling during haustorium development in the root hemi-parasite *Santalum album* Linn.

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Santalum album (sandalwood) is one of the economically important plant species in the Santalaceae for its production of highly valued perfume oils. Sandalwood is also a hemi-parasitic tree that obtains some of its water and simple nutrients by tapping into other plants through haustoria which are highly specialized organs in parasitic angiosperms. However, an understanding of the molecular mechanisms involved in haustorium development is limited. In this study, a combination of next-generation sequencing and cytomorphological studies was used to identify changes in gene expression and metabolic pathways associated with the development of the *S. album* haustorium. A total of 56,011 non-redundant contigs with a mean contig size of 618bp were obtained by *de novo* assembly of the transcriptome of haustoria and non-haustorial seedling roots. A substantial number of the identified differentially expressed genes were involved in cell wall metabolism and protein metabolism, as well as mitochondrial electron transport functions. Phytohormone-mediated regulation also played an important role during haustoria development. Especially, cytokinin and gibberellins metabolism were involved in haustorial development and auxin signaling might be essential for haustorial initiation. This provides a vital clue for artificially increasing the number of haustoria to improve growth by exogenous application of plant growth regulators in beneficial parasitic plants. In addition, genes encoding nodulin-like proteins might be important candidate genes for haustorial morphogenesis in *S. album*. The obtained sequence data will become a rich resource for future research in this interesting species. This information improves our understanding of haustorium development in root hemi-parasitic species and will allow further exploration of the detailed molecular mechanisms underlying plant parasitism.

Session 3: Host parasite interactions

Chairs

Philippe Simiere and John Yoder

Understanding the genomic basis of virulence in the parasitic weed *Striga hermonthica*

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Striga species are parasitic weeds that infect the roots of the staple cereal crops of Africa causing devastating yield losses. Much research is focussed on identifying genes underlying resistance in different crops with the aim of utilising this knowledge for crop improvement. However, the extensive *Striga* seed bank, the fact that *S. hermonthica* is an outbreeding parasite and that parasite populations/ecotypes are highly genetically variable, pose a great risk to the durability of host resistance thus making sustainable management of resistant cultivars difficult. In fact, even the most resistant cultivars are often parasitized by a few *Striga* individuals that possess the 'virulence' loci/genes to overcome host resistance. Therefore, it is essential for us to understand the virulence mechanisms and the genetic variation for virulence in *Striga* populations to manage the use of cultivars such that evolution of virulence in the parasites is delayed. In this study, we are taking population genomic approaches to locate virulence loci within the *S. hermonthica* genome that allow parasites to overcome host resistance genes in rice cultivars. Specifically, we infected two rice cultivars with contrasting resistance profiles (one very susceptible and one strongly resistant) to the same ecotype of *S. hermonthica* collected from Kibos, Kenya. We hypothesise that the few individuals of *S. hermonthica* that are able to grow successfully on the strongly resistant cultivar will possess virulence gene(s) to overcome the resistance genes of this rice cultivar and that the allele frequencies of these genes will differ markedly from those of the *Striga* plants growing on the very susceptible cultivar. Three replicate samples each composed of 100 *S. hermonthica* individuals were collected from each rice cultivar and DNA was then extracted from each sample for Next Generation Sequencing. The sequences from each sample were then independently mapped to both genomic (*Striga asiatica*) and transcriptomic (*S. hermonthica*) reference sequences. Differences in allele frequencies between the *Striga* plants growing on the two contrasting rice cultivars were then compared at Single Nucleotide Polymorphism (SNP) level and at the gene level. These analyses revealed that many genes were highly significantly differentiated between the *Striga* individuals growing on the susceptible and resistant cultivars and are therefore excellent candidates for virulence determinants. Blast analysis of the gene sequences predicts that they have a variety of functions.

Engineering host cell wall to increase resistance against *Phelipanche aegyptiaca*

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The intrusive cells of root parasite *Phelipanche aegyptiaca* push their way between host cells rather than break down and penetrate them. Pectin methylesterases (PME) have been shown to be secreted by parasitic plant intrusive cells during invasion and were hypothesized to facilitate penetration. From transcriptomic data analyses of our Parasitic Plant Genome Project (PPGP), two orthogroups of Pectin methylesterase inhibitor (PMEI) unigenes were identified showing specific upregulation in the penetration stage (stage 3) of all three parasitic species, *Phelipanche aegyptiaca*, *Triphysaria versicolor* and *Striga hermonthica*. We hypothesized that parasite PMEI plays a protective function to prevent degradation of its own pectin during parasitism and that expression of the protein in host cells may impede haustorial intrusive growth. To test this idea, we generated transgenic hosts expressing parasite PMEI. Neither gene was predicted to contain an intron, and full-length coding regions of *PaPMEI1* (*OrAeBC5_21049*) and *PaPMEI2* (*OrAeBC5_9410*) genes were amplified from *P. aegyptiaca* genomic DNA. Nucleotide sequences of cloned *PaPMEI1* and *PaPMEI2* matched perfectly with corresponding PPGP assembled transcript sequences except for one SNP in each gene. *PaPMEI1* and *PaPMEI2* genes were then cloned into binary vectors for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. These were used to generate transgenic *Arabidopsis* overexpressing the *PaPMEI1* gene driven by the 35S promoter. We performed qRT-PCR for 12 T1 transgenic lines to determine the relative transcript levels of *PaPMEI1* and confirmed that the transgene was expressed. Preliminary data showed that *PaPMEI1* ectopic expression *Arabidopsis* plants exhibited an aerial rosette phenotype when grown under short day condition. We then examined the growth of *P. aegyptiaca* on *PaPMEI1*-OX lines versus WT *Arabidopsis*. *PaPMEI1*-OX lines retained ability to host *P. aegyptiaca* growth and no significant morphological difference was observed in parasite development compared to those inoculated on WT plants. We are currently working on the expression and purification of *PaPMEI* protein in bacteria to test its inhibiting activity against known PMEs. We also plan to examine whether *Orobanchae* PMEI can affect the degree of pectin methylesterification of host cell wall. The *PaPMEI1*-OX lines will also be challenged by other plant pathogens (e.g., bacteria and fungi) to assess how PMEI overexpression impacts plant defense.

Risk versus reward: host dependent parasite phenotypes in the facultative generalist *Triphysaria versicolor*

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Triphysaria versicolor is a true facultative generalist parasite and a model plant for parasitic Orobanchaceae. The weedy Orobanchaceae are destructive crop pests that cause \$US billions of damage to cereal and legume crops each year in Africa and the Mediterranean where the severity and scope of damage is increasing. Towards understanding the genetic foundation of parasitism in the pernicious, weedy Orobanchaceae, we explored host-dependent growth patterns of the generalist *Triphysaria*. We grew *Triphysaria versicolor* on a wide array of host plants spanning flowering plant diversity and the parasite's host range. We discovered host-dependent phenotypes displayed by the parasite that provide insight into reproductive strategies and host choice mechanisms of *Triphysaria*. The methods developed in the course of this work provide tools to quantify parasite phenotypes, increase throughput, and more accurately estimate parasite success. Finally, these approaches can be applied in different and broader experimental contexts aimed at characterizing the parasitic plant-host plant interaction.

Gypsy moth damage delays parasite attachment to cranberry hosts

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Plants experience a myriad of interactions with other species that often occur sequentially. Herbivory may induce defenses involving jasmonic acid (JA) and salicylic acid (SA) signaling pathways that can directly affect preference and performance of subsequent herbivores, pathogens and even parasitic plants. Parasitic plants are present in most ecosystems, and can alter community dynamics and cause major economic damage in agricultural systems. For example, in heavily infested cranberry patches, the parasite dodder (*Cuscuta* sp.) can cause 80-100% yield loss. Although host plant nutritional quality can affect dodder foraging preference, the effects of herbivore damage to host plants on dodder preference remain unknown. Such information could potentially be used to simulate herbivory if previous herbivory confers resistance to dodder parasitism, offering producers an alternative management strategy for dodder control. Understanding how herbivore damage affects parasite preference also adds to our understanding of how single interactions structure subsequent community dynamics. Cultivated cranberry is genetically very similar or identical to native wild genotypes, making research with agricultural cultivars very relevant to understanding ecological interactions in native systems. We conducted a greenhouse study to ask (1) Does gypsy moth damage (*Lymantria dispar*) affect subsequent dodder (*Cuscuta pentagona*) preference on cranberry hosts? (2) Do cranberry cultivars differ in levels of phytohormones and phenolics, and does such variation correspond with dodder preference? and (3) Does gypsy moth damage induce phytohormones or phenolics in cranberry cultivars that may affect dodder preference? We used three cranberry cultivars: Mullica Queen, Stevens and Howes, to assess dodder preference. We measured dodder preference as the number of dodder stems attached and number of days to attachment. In a separate experiment, we measured overall and induced chemical defenses for each cultivar, including phenolics and phytohormones, using HPLC and LC-MS/MS. Gypsy moth damage reduced the number of dodder that attached by more than 50%, and also delayed attachment of dodder to cranberry host by approximately 2 days. Cultivars varied in overall levels of some phenolics but not in phytohormone levels. Gypsy moth damage marginally increased induced changes in the flavonol galactoside-3-quercetin, suggesting a possible mechanism of cranberry defense to dodder parasitism. These results indicate that a host plant's single interaction with one herbivore species alters subsequent interactions with a prevalent parasitic plant, broadening our knowledge about community dynamics.

Parasitic plant, *Cuscuta australis*, transmits inter-plant herbivory-induced signals

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Insect herbivory poses a major threat to plants. Accordingly, plants have evolved sophisticated defenses to counteract insect attack. In addition to the defense responses in the tissues that are damaged by insects, distant undamaged (systemic) tissues and organs also deploy defense responses (systemic defenses). However, systemic signaling in plant resistance to insects is still poorly understood. About 1% of angiosperms are parasitic plants, which draw water, nutrients, and other molecules from their hosts. Plants in from the genus *Cuscuta* (dodder) are widely distributed and holoparasitic. They parasitize host plant shoots and when growing vigorously they could cover most of the host canopy and may reach and parasitize the neighboring plants. Recent findings indicate that host mRNAs and proteins can be translocated to *Cuscuta*. To examine the possibility that *Cuscuta* also mediates herbivory-induced systemic signaling between plants, *Cuscuta australis* was used to connect two soybean (*Glycine max*) plants. We show that, when one soybean plant (local plant) is attacked by chewing insects (*Spodoptera litura*), certain systemic signals are induced and transmitted to both *C. australis* and the other soybean host (systemic plant) through *C. australis*. These signals induce increased levels of jasmonic acid-isoleucine conjugates in the systemic soybean plant but not in *C. australis*. RNA-seq analysis revealed that 572 genes were up- or down-regulated in leaves of the systemic plants, and strikingly, among these, 358 were unique genes that were not regulated in the treated plant. These results indicate that the parasitic plant *Cuscuta* mediates inter-plant signaling in plant-insect interactions, and may provide hosts with certain fitness advantages by sending “insect attack” alerts from infested to non-infested systemic plants.

The physiological role of hydathode trichomes in parasitic Orobanchaceae

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Root hemiparasites from the Rhinanthoid Orobanchaceae were repeatedly shown to possess metabolically active glandular trichomes. These trichomes were suggested to function as hydathode trichomes actively secreting water and thus facilitating resource acquisition from host root xylem. Direct evidence relating the trichomes to water secretion and the carbon budget of the assumingly energy-demanding water secretion were, however, missing. Here, we combine macro- and microscopic observations of the leaves of hemiparasitic *Rhinanthus alectorolophus* with gas-exchange measurements to find a correlation among guttation, respiration, and transpiration, a pattern attributable to active water secretion. In addition, the carbon budget of the trichome activity is quantified. We provide the first direct evidence on the physiological role of the hydathode trichomes in active water secretion in parasitic plants. Our observations reveal water secretion from the glandular trichomes present on the abaxial leaf side. The presence and size of guttation drops are positively correlated with night-time respiration and transpiration in young (non-flowering) plants. No such correlation is found in mature (flowering) plants, which suggests the peak activity of hydathodes in the juvenile stage of the hemiparasitic plants. Based on the carbon budget calculations, a potential role of the trichomes in the evolution of holoparasitism within the clade is proposed.

Identification of Parasite Effectors Mediating *Striga gesnerioides*-Host Plant Interactions

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Striga gesnerioides (Willd.) is a root hemiparasitic weed that is a significant constraint to agricultural productivity throughout sub-Saharan West and Central Africa. Among the primary host for the parasite is cowpea (*Vigna unguiculata* L. Walp.), by far the most important food and forage legume grown in this region and a major source of dietary protein for humans and fodder for animals. Genotyping and host differential response studies have established that the parasite exhibits a high level of host specificity and that at least seven distinct races of *S. gesnerioides* parasitic on cowpea exist in West and Central Africa. Host resistance is race-specific and current evidence implicates a gene-for-gene mechanism characteristic of effector-triggered immunity as operating in *Striga*-cowpea interactions. The cowpea accession B301 is resistant to all races of *Striga* identified in West Africa with the exception of SG4z a hypervirulent race from Benin. In order to identify potential candidate parasite effectors proteins and avirulence factors in the parasite that specifically suppress host defense responses allowing parasite ingress or trigger a hypersensitive response in resistant hosts, we have carried out transcriptome profiling using high throughput RNAseq analysis in parasite haustorium during compatible and incompatible response of resistant (B301) and susceptible (Blackeye) cowpea cultivars with three races of *S. gesnerioides* (SG3, SG4 and SG4z). Subsequent de novo transcriptome assembly and bioinformatics screening reveals more than thousand candidate effector genes that are expressed at late and early attachment stages of cowpea-*Striga* interactions. Comparisons among transcriptomes of three *Striga* races distinguish race-specific effector candidates that are responsible for susceptible and resistant response in different host cultivars. We are currently validating a subset of those race-specific candidates in host root using ex vitro composite plants. These studies will enhance our understanding of how parasitic plants identify potential hosts, overcome the host's innate defense mechanisms, and establish themselves via haustorial connections to successfully complete their life-cycles. Importantly, our studies have the potential to contribute knowledge that will fulfill the practical goal of alleviating the burden of *Striga* and other parasitic weeds from the backs of subsistence farmers in Africa.

Comparison of mitochondrial genomes between *Cistanche deserticola* and *Cistanche tubulosa*

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Cistanche deserticola and *Cistanche tubulosa*, belonging to the family Orobanchaceae, are both root parasitic plant that distribute in Northwest China. We have obtained the mtDNA of *C. deserticola* and *C. tubulosa* by combining sucrose density gradient centrifugation and differential centrifugation, then sequenced the Mitochondrial genomes of these two species. We finally obtained five complete fragment sequences of mtDNA of *C. deserticola* and also five complete fragment sequences of mtDNA of *C. tubulosa*, with the length of 462162bp and 570980 bp. There are 44 functional genes in sequenced *C. deserticola* mtDNA, including 30 protein coding genes and 14 tRNA genes; 32 functional genes in sequenced *C. tubulosa* mtDNA, including 22 protein coding genes and 10 tRNA genes. There are 16 homologous genes in these two mitochondrial genomes, in which the sequence similarity of 9 genes up to 97%, *cox1*, *nad4L* and *rps4* are even 100% sequence identity. All the protein-coding genes of the two species shows a strong A+T bias, with contents both about 55%; the G+C content of tRNA gene is 50.13% and 51.74%. Among the protein coding genes in these two mitochondrial genomes, there exists a consistent pattern of T> A> G> C at the second position and the third position, while the pattern for first position is A> G> T> C. The AT content of the third position of codons of these genes in mitochondrial genomes of *C. deserticola* and *C. tubulosa* are 63.11% and 62.63%. We have detected 24 tRNA genes in these two mitochondrial genomes, all of them can be folded into the cloverleaf secondary structure, and have some base pair mismatches, while tRNA^{Ser (GGA)}, tRNA^{Leu (CAA)}, tRNA^{Ser (GGA)} and tRNA^{Tyr (GTA)} of mitochondrial genomes of *C. deserticola* containing variable arm. This work can enrich the database of mitochondrial genome, help us to make clear the expression and regulatory mechanisms of genes of *Cistanche*, the interaction of extranuclear and intranuclear genetic information, and the evolution of mitochondrion of *Cistanche*.

A horizontal gene transfer between *Cistanche deserticola* and its host *Haloxylon ammodendron*

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Cistanche deserticola, commonly known as desert-broomrape and traditionally used as an important tonic herb in China and Japan, is distributed in Inner Mongolia, Gansu, Ningxia and Sinkiang provinces in Northwest China and the Mongolian People's Republic, and is also considered to be an endangered wild species in recent years due to increased consumption by humans. *C. deserticola* is parasitized on the roots of psammophyte *Haloxylon ammodendron* (Chenopodiaceae), which mainly inhabit deserts and semi-deserts due to its high tolerance to drought and salinity. A number of studies about the chemical components or pharmacological effects of *C. deserticola* have been reported. However, the research about molecular biology, evolution and the interaction with its host of this species is very little. There are many studies indicated that plant mitochondrial genomes experience frequent and evolutionarily widespread horizontal gene transfer(HGT). In this study, we use *Cistanche tubulosa* and *Cistanche salsa*, in the same genus with *C. deserticola*; and *Haloxylon Persicum*, in the same genus with *H. ammodendron* as control, to test whether there are some HGT between mitochondrial genomes of *C. deserticola* and its host. According to a homology search and phylogenetic analysis, We found that *C. deserticola* has a copy of Mt gene matR (encoding Maturase), being horizontally acquired from its host *H. ammodendron*, and very likely becoming a pseudogene. The length of the complete ORF sequence of matR of *H. ammodendron* is 1968bp, the copy of *C. deserticola* is 1926bp, which is shorter. We detected the 1286bp upstream sequence of the initiation codon in matR of *H. ammodendron*, found the transcription start site A in upstream 362bp of ATG, and the TATA Box is located in upstream 26bp of the transcription start site. Also, a large number of resistance regulatory elements were found in the promoter sequence. However, there is no evidence that there exists a promoter in the upstream sequence of the matR copy of *C. deserticola*.

Mitochondrial gene sequence analysis of parasitic plant *Cynomorium* and horizontal gene transfer study

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Cox1 gene group I intron in angiosperm has the phenomenon of horizontal gene transfer (HGT). We have amplified and analyzed the sequences of mitochondrial genes *cox1*, *cox2* and *nad1* in medicinal parasitic plant *Cynomorium songaricum*. Using the maximum likelihood method to analyze the introns and exons of *cox1* and *cox2* gene, we found that the phylogeny of *cox1* gene intron were not consist with phylogenetic position, which suggested the *cox1* intron may have HGT phenomenon. We compared the average distance of exon and intron sequences of mitochondrial genes *cox1*, *cox2* and *nad1* from six different populations of *C. songaricum*, finding that the genetic distance of *cox2* and *nad1* genes are relatively high between populations, and the genetic distance of *cox1* gene was relatively low between differences populations, the homology of *cox1* intron from different populations had reached to 100% , the results suggested the intron of *cox1* gene may have function. Bioinformatics analysis showed that the intron most likely coded endonuclease, and endonuclease is thought to promote the intron to transfer. 3'Co-conversion tracts (CCT) is traces of angiosperm intron metastasis. 3'CCT analysis testing showed *C. songaricum* contained a 35bp 3'CCT. RT-PCR indicated *cox1* intron can be transcribed to mRNA independently. We have amplified and analyzed the sequences of mitochondrial genes *cob*, *nad5*, *nad7*, *rps3*, *nad6*, *nad9*, *rpl5*, *ccmC* and *cox3* in medicinal parasitic plant *Cynomorium songaricum* and its host. The phylogeny analysis of *nad9* showed that *songaricum* and its host *Nitraria* were in the same branch, which suggested the *nad9* genes of *songaricum* and *Nitraria* may have HGT phenomenon; the similarities of *nad9* gene sequences and amino acid sequences between *songaricum* and *Nitraria* were high, which indicated that *nad9* genes of *songaricum* and *Nitraria* may have similar functions.

Molecular basis for the convergent evolution of parasitism in plants

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Convergent evolution is the independent evolution of similar traits in species of different lineages, but the molecular basis remains largely unknown. Parasitic plants, which have originated independently at least 11 times in angiosperms, have the ability to obtain nutrient directly from other plants through a multi-cellular organ called a haustorium. What molecular basis had allowed the ancestral angiosperms to evolve parasitism? Our transcriptomics of phylogenetically independent parasitic plants revealed that similar molecular pathways have been leveraged in the evolution of parasitism in plants.

Evolution and expression profile of transcription factor families in three parasitic plants of the Orobanchaceae

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The Orobanchaceae is one of the largest and most diverse groups of parasitic angiosperms in existence today and includes among its members individuals that constitute significant constraints to agricultural productivity worldwide including *Triphysaria versicolor* (a facultative hemiparasite), *Striga hermonthica* (an obligate hemiparasite), and *Phelipanche aegyptiaca* (syn. *Orobanche aegyptiaca*; an obligate holoparasite). We have used comparative transcriptomics over a series of developmental stages from parasites and outgroups to uncover genes that might be important to the parasitic life-style and host selection. A well-designed bioinformatical pipeline based on the computational prediction of conserved domains and the experiential rules of presence/absence of certain domains was employed to discover the transcription factors (TFs) and transcriptionally-active (TAPs) protein coding genes represented in *T. versicolor*, *S. hermonthica*, and *P. aegyptiaca* using RNAseq data from different stages during parasite development. Total of 1,885, 2,119 and 1,673 non-redundant unigenes from *T.versicolor*, *S. hermonthica*, and *O. aegyptiaca* were identified within about 110 TF families. The predicted parasite TF genes were compared with TFs and TAPs genes from 22 representatives of sequenced land plant genomes (Amborella Genome Project 2013) and analysis of the number and phylogenetic variation between parasitic and non-parasitic plants was determined. Expression profiles based on developmental stage-specific reads counts were used to identify differently expressed TF genes in different developmental stages particularly in post-attachment haustorial stages. The comparable amounts of TF genes at genomic level in *S. asiatica* and the significant reduction of TF genes in the three parasites at transcriptomic level compared with the 22 reference plants revealed that parasitic plants may retire partial pathways by expropriating either the nucleotide sequences or protein products from hosts after infection. A wide range of gene duplication was detected in many TF families. The functional analysis of these duplicated genes illustrated gene duplication and the followed neofunctionalization may play important role during haustorial evolution. Many TF genes from the three parasites were significantly up-regulated during the post-attachment haustorial stages. These results revealed the important roles and evolutionary process of TF genes in parasitic plants and provided special angle to uncover the formation and origination of parasitism.

Genomic and genetic analyses of haustorium formation using *Phtheirospermum japonicum* as a model parasitic plant

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The Orobanchaceae family contains a range of parasitic plants from facultative parasites to obligate parasites, including the world most devastating pests *Striga*, *Orobanche* and *Phelipanche* spp. One of the key features in plant parasitism is the formation of a haustorium, an organ specialized for host invasion and nutrient transfer, in response to host signals. During such response, the root tip or lateral parts of the root form a haustorium, which penetrates into the host root and forms a vascular connection with the host. However, the molecular and genetic basis for the haustorium formation remains poorly understood. Molecular analyses of plant parasitism have been hampered by the lack of analytical tools and molecular information. To overcome these problems, we have developed a model plant system using the facultative parasite *Phtheirospermum japonicum*, which also belongs to Orobanchaceae. *P. japonicum* is an annual herb, which is self-compatible, and has a short life cycle. The hairy root transformation system has enabled us to visualize expression of cell marker genes and plant hormone responsive genes by *in vivo* imaging. We have performed transcriptome analyses to identify genes expressed during haustorium formation. Reverse genetic studies using RNAi techniques revealed that auxin-biosynthesis gene *YUC3* is involved in the haustorium formation. Furthermore, the genome of *P. japonicum* was sequenced for comparative analyses with the obligate parasites and non-parasitic plants. Mutant collections from *P. japonicum* ethyl methanesulfonate (EMS)-mutagenized lines also revealed possible genetic components involved in plant parasitism.

Functional characterization of haustorial hair development in *Triphysaria versicolor*

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Haustorial hairs attach and bind the parasitic Orobanchaceae to their host roots. Similar to root hairs, haustorial hairs develop as extensions of epidermal cells. But unlike root hairs, haustorial hairs secrete adhesive substances, described as petinaceous or hemicellulosic mucilage that chemically bind the tips of the haustorial hairs to host root cells. Haustorial hairs are also unique in that they are induced to develop in response to contact with host roots or host root factors, and only grow at positions overlying the developing haustoria. We hypothesize that the development of haustorial hairs requires some of the genes used in normal root hair development while also recruiting additional host genes that provide attachment specific functions. Our current work is on understanding the genetic basis of haustorial hair development in the hemiparasitic plant *Triphysaria*. Twenty-two genes whose mutations in Arabidopsis lead to changes in root hair phenotypes, including hairless roots and changes in root hair number, morphology, position and length, were selected for this study. The Arabidopsis coding sequence for each selected gene was used to search the Parasitic Plant Genome Database for homologous *Triphysaria* sequences. Approximately 300 nts fragments of each gene were cloned into pHG8-YFP, a Gateway compatible RNA interference (RNAi) transformation vector containing the yellow fluorescence protein (YFP) reporter gene for selection in parasite roots. The RNAi constructs were then transformed into *T. versicolor* roots by *Agrobacterium rhizogenes* transformation. *Triphysaria* roots transformed with empty parent vector were used as controls. Two months old transgenic roots were exposed to the haustoria inducing factor DMBQ and the number of haustoria and the haustorial hair phenotypes recorded 24h later. We will discuss our current results identifying parasite genes that function in haustorial hair development using RNAi technology.

Haustorial hairs are controlled by root hair genes and involved in parasitism

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Haustorial hair formation is one of the earliest events during haustorium development. Although they exist in a wide range of root parasitic plants in Orobanchaceae, including *Striga* spp., their developmental regulation and physiological functions are not well understood. Here, we show the characterization of haustorial hair defective (*hhd*) mutants in *Phtheirospermum japonicum*, a facultative root parasitic plant, which also belongs to Orobanchaceae. We conducted a forward genetic screening with EMS (ethyl methanesulfonate)-mutagenized *P. japonicum* seeds and isolated three lines of mutants lacking haustorial hairs. These mutants also lack root hairs, suggesting that haustorial hairs are controlled by genetic components involved in root hair development. Indeed, *PjEXP18*, the orthologous gene to *Arabidopsis* root hair specific EXPA18, was expressed in both root hairs and haustorial hairs, suggesting similar genetic identity between them. All three mutants show reduced number of haustoria upon host rice root infection. This phenotype is restored when we force the roots of the host and the parasite to grow together in a narrow pathway, suggesting a role of haustorial hairs on the efficient host detection or host attachment. Interestingly, these mutants differentially react to various haustorium-inducing factors (HIFs), indicating that the genes responsible for the mutants may be involved in host signal perception, or that the haustorial hairs may be important for efficient perception of HIFs. Furthermore, their response to host root extract is not fully explained by any of single HIF application, implicating the complexity of haustorium induction signals in roots. Next generation DNA sequencing was performed and the identification of genetic mutations in these mutants are undergoing.

Towards the understanding of haustorium formation in the obligatory parasitic plant *Phelipanche ramosa*

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The genera *Orobanche* and *Phelipanche* (“orobanche”) represents the biggest group of non-chlorophyllous root parasitic plants. Some species such as *Phelipanche ramosa* are known to be serious agricultural pests in many agrosystems. Key steps of plant parasitism include seed germination in response to germination stimulants that are exudated from the host roots, and haustorium formation during early events of infection. Haustoria are structures of main importance in the parasitic behavior from facultative parasites such as *Trypthisaria versicolor* to obligate chlorophyllous parasitic plants such as *Striga* spp. or achlorophyllous parasitic plants such as *Orobanche* and *Phelipanche* spp. Haustoria establish a vascular bridge between the host and the parasite. Its development starts with the differentiation of attachment structures ie. haustorial hairs in *Striga* or papillae in *Orobanche*. Although several decades of research have focused on deciphering the molecular events leading to the haustorium establishment, still few actors have been clearly identified. It has for instance been shown in *T. versicolor* and *Striga* spp. that compounds present in host root exudates including quinone 2,6 dimethoxy-1,4-benzoquinone (DMBQ) induce haustoria formation and are therefore be considered as Haustorium Inducing Factors (HIFs). At the molecular level, although DMBQ treatment induced the overexpression of circa 100 putative parasitism genes in *T. versicolor* and *S. hermontica*, it failed to induce haustorium formation in *Phelipanche* spp. and in consequence neither HIFs nor haustorium-related genes have yet been clearly identified in *Phelipanche* spp. Interestingly we have been able to induce papillae in *P. ramosa* germinating seeds upon treatment with biological extracts. In our experiments up to 50% of the treated seeds were showing papillae. Treated germinating seeds harboring these structures showed a significantly higher infection rate during co-cultivation experiments on *Brassica napus* roots using minirhizotron system in comparison to untreated germinating seeds. Moreover, upon similar treatment, *S. hermontica* germinating seeds displayed hairs identical to those formerly described as pre-haustorium structures. No HIF treatment have ever been described before to be effective on *P. ramosa* germinating seeds, thus we used it to produce *P. ramosa* seeds displaying pre-haustorium structures for transcriptomic approaches using a *P. ramosa* microarray. As a complementary approach, we developed a functional validation approach based on fast calli generation from *P. ramosa* germinating seeds, calli transformation via *Agrobacterium rhizogenes*, and selection using antibiotics. We successfully used these transgenic calli to infect tomato roots. It yielded healthy transgenic tubercles that were able to grow flowering spikes which produced seeds.

Effects of mycorrhiza inoculation, nitrogen levels, and sugar cane residue based organic amendments on *Phelipanche ramosa* incidence, and tomato performance in the field

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Parasitic flowering plants are significant constraints to agricultural production worldwide. The present work was undertaken to investigate the possibilities of combining the use of AMF, organic residues from the sugar industry, and N fertilization for the management of *Phelipanche ramosa* in tomato plants. The experimental design was a split plot design with four replications. AMF (*Glomus intraradices*, *G. mosseae*, or control), sugarcane filter mud (FM) (10 t ha⁻¹ or none), and nitrogen doses (Urea 0, 36, or 72 kg ha⁻¹) were assigned to main, sub, and sub-sub plots, respectively. In un-inoculated control plants, AMF colonization ranged between 13 to 22 % with no significant differences among FM and N treatments. AMF colonization levels in inoculated plots ranged from 31 to 49%. Adding AMF or FM resulted in a significant increase of branching in the tomato plants with no additive effects. Dry weights were slightly increased through FM application when no N was applied and significantly at 36 kg N ha⁻¹. There was no effect of FM on the time until the first *P. ramosa* emerged while AMF and N application interacted. Especially AMF inoculation resulted in a tendency to delayed *P. ramosa* emergence. The marketable yield was extremely low due to a heavy fruit infestation with insects. Adding AMF led to a significant decrease the level of titrable acidity. Tomato plants inoculated with *G. mosseae* produced significantly higher total yield than inoculated with *G. intraradices*; however, the insect damage to *G. mosseae* inoculated plants was also significantly higher.

Host parasite interactions and nutrient dynamics of *Dendrophthoe falcata* (L. F)

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Mistletoes do not produce functional roots but obtain water and nutrients from the xylem sap of the host plant. The dynamics of nutrient movement from the host to parasite and from parasite to host was studied in *Dendrophthoe falcata* with labeled ^{14}C . Sodium carbonate solution containing 0.5 mCi of ^{14}C was mixed with 20ml of non radioactive sodium carbonate; 5 ml of this solution was applied with a syringe to dilute hydrochloric acid kept in a sealed chamber into which a twig of the parasite and the host were both inserted separately. In each case the chamber was kept closed for half an hour. The chemical reaction led to the evolution of CO_2 . The experiment was undertaken between 10 am and 2 pm when maximum sunlight was available for photosynthesis. Leaf samples were collected from different locations of the parasite and the host after 2, 4, 6 and 14 days. The samples were dried, powdered and fed to a biological oxidizer at a temperature of 950°C . The CO_2 evolved was collected in a ^{14}C cocktail and the radioactivity was counted in a liquid scintillation counter. About 4 % of ^{14}C fixed by the parasite was seen in the host plant and 2-3% of the ^{14}C fixed by the host was observed in the leaves of the parasite. The study showed that there is a two way movement of carbon both from the host to the parasite and from the parasite to the host. Studies on nutrient accumulation in the parasite revealed that among the minerals Ca, K and N were found in large concentrations in the parasite than that of the host species. All other elements were either on par or lower in the parasite than that of the host plant. The results call for further studies on the role of Ca and K on signaling between the host and the parasite.

Session 4: Ecology, phylogeny and evolution

Chairs

Gramma N. Dhanapal, Yongqing Ma and Weijun Zhou

The economic losses caused by parasitic weeds in rice in Africa

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Parasitic weeds are increasingly important as production constraint in rainfed rice systems in Africa. The main parasitic weeds species are *Striga asiatica*, *S. aspera* and *S. hermonthica* in rainfed uplands, and *Rhampficarpa fistulosa* in rainfed lowlands. Affected areas accommodate some of the world's poorest farmers. The extent to which parasitic weeds impact the region's rice production is unknown. Information on the regional spread and economic importance of parasitic weeds in rice production systems would however greatly serve priority setting of future research and development undertakings. From various herbaria, seed collections and literature sources, data on the regional distribution of the most important parasitic weeds were obtained and used to generate maps. These were overlapped with the best available rainfed rice distribution maps. The estimated probability of occurrence of parasitic weeds in rice fields was derived from this and used in a simple, stochastic economic loss model with rice production figures and yield loss estimates from literature as additional main input parameters. The model simulates parasitic weed damage and weed control by farmers to obtain an aggregate estimate of the total production losses inflicted by parasitic weeds in Africa. *Rhampficarpa fistulosa* was found in at least 35 African countries, 32 of which produce rice in rainfed lowlands where the species thrive. Based on our model, the maximum annual regional economic losses caused by *R. fistulosa* in rice are estimated at US \$ 569 million. *Striga* spp. (*S. asiatica*, *S. aspera* and *S. hermonthica*) were found in 34 countries, 33 of which produce rice in the rainfed uplands where these species can be encountered. Based on our model, the maximum annual regional economic losses caused by *Striga* spp in rice are estimated at US \$169 million. Parasitic weeds occur in at least 33 rainfed rice producing countries in Africa and affect an estimated 2.5 million rural households. Maximum total annual economic losses caused by parasitic weeds in rice in Africa are estimated at US \$728 million. Based on the country-specific importance of rice production and parasitic weeds (the abundance, number of occurring species and estimated losses), investments in innovations for parasitic weed management will have the highest potential impact in Guinea, Cote d'Ivoire, Nigeria, Uganda, Tanzania and Madagascar. While stakeholder awareness, preparedness and collaboration should be increased to address this emerging problem, research should focus on the development of locally adapted and acceptable innovations such as resistant varieties and agronomic management practices.

An ecophysiological study of the hemiparasitic *Cassytha filiformis* L. (Lauraceae) in Brunei Darussalam, Borneo.

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Cassytha (family-Lauraceae; woe vines) is the only parasitic genus in the family. It is often confused with *Cuscuta* spp. of the Convolvulaceae, mainly due to the remarkable parallelisms between the two genera of parasitic vines. *Cassytha filiformis* is a pantropical species common in Brunei especially in strand vegetation. The aims of this pilot study were to determine the biology of *C. filiformis* including the establishment of its host attachment, and its implications on the biology of hosts especially in relation to photosynthesis and the synthesis of selected bioactive compounds. Germination studies indicated positive results (28.86 ± 4.4 %) albeit relatively low, only when *C. filiformis* seeds were mechanically scarified at exactly opposite to carpellary micropyle. Other treatments such as sulfuric acid and random mechanical scarification showed no radicle development. Field observations over two years show that this parasite is most common along the coastlines of Brunei, parasitizing 24 species that can be divided into “starter host” and “primary woody hosts”. The haustorial penetration of *C. filiformis* is primarily enzyme mediated rather than mechanical based on a lack of collapsed host cells at the haustorial interface. Xylem-xylem, parenchyma-xylem and parenchyma-parenchyma tissue fusions in the haustorial-host interface were observed, hence sustaining both selective (cross membrane) and mass flow of solute uptake *via* xylem tissue grafts. The infection of *Cassytha* negatively impacted the photosynthetic rates of hosts as well as their chlorophyll content. Suppressed photosynthesis of nationally significant hosts such as *Melastoma malabathricum* and *Dillenia suffruticosa* implied eventual decrease in host vigour, with a potential negative impact upon the native flora of Brunei. The reduced photosynthetic rates of an exotic host, *Acacia mangium* suggested the prospective use of *Cassytha* as a possible biocontrol agent. Findings on the bioactivity of hosts affected by *Cassytha* parasitism revealed that the antioxidant (total phenolic and flavonoid) contents of parasitized hosts *M. malabathricum* and *D. suffruticosa* were higher than that of non-parasitised hosts. Antioxidant activities measured by 2,2-diphenyl-1-picrylhydrazyl (DPPH) and Ferric Reducing Ability of Plasma (FRAP) assays were positive with infected hosts compared to uninfected. This also indicated the presence of total phenolics and flavonoids as well as antioxidant activity in *C. filiformis* stems that infected these respective hosts, although their values were lower than those of their infected and uninfected hosts.

Field dodder (*Cuscuta campestris* Yuncker) a new pest of carrot (*Dacus carota* L.) in Gezira scheme, Sudan

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Field dodder *Cuscuta campestris* Yuncker is an obligate holoparasitic weed species belonging to the family Cuscutaceae. During weed survey in November and December 2014, field dodder was abundantly found parasitizing carrot (*Dacus carota* L.) in a field cultivated in carrot, in Taiba block of the Gezira scheme, Sudan. This field was previously sown in onion infected with field dodder. The impact of field dodder infection on the new host was evaluated. Field dodder infection reduced single root fresh weight, and root diameter by 84.26% and 48.48%, respectively. Whereas the carbohydrates, proteins, calcium, and potassium were reduced by 46.30%, 12.60%, 87.90% and 63.39%, respectively. In conclusion, field dodder in Gezira could be considered as an important pest that can affect vegetable crops of economic and nutritional values to a wide range of low income farmers. To prevent new dodder infestation, planting carrot in soils known to be infested should be avoided, and use of certified seed free of field dodder is recommended.

Compatibility and incompatibility of some monocotyledonous plant species to field dodder (*Cuscuta campestris* Yuncker)

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Microscopic examinations were performed to study the response of four monocotyledonous plant species to the parasitism of the stem parasite field dodder (*Cuscuta campestris* Yuncker). The studied plants were Bermuda grass (*Cynodon dactylon* L.) and sorghum (*Sorghum bicolor* L.) which belong to family Poaceae, onion (*Allium cepa* L., family Liliaceae) and ginger (*Zingiber officinale* L., family, Zingiberaceae). Members of family Poaceae were found to be resistant hosts, while onion and ginger were found to be susceptible hosts. In this study, the haustorium of field dodder exhibited different developmental stages that varied from initiation of haustorial meristem only in members of family Poaceae, to the formation of functional endophyte which connected to the host tissues in onion and ginger. This variation may be attributed to the behavior of the parasite's epidermal cells in both groups (resistant and susceptible hosts). In onion and ginger, the epidermal cells of field dodder were modified into secretory trichomes and shapes adjusted to conform the shape of host plants' surface cells for attachment, thus stimulating the haustorial meristem to trigger the development of functional haustoria (endophytes) that connect the host vascular tissues. In members of family Poaceae (Bermuda grass and sorghum), the epidermal cells of the parasite kept their normal structures and were not attached to the host surface cells. Likewise, the haustorial meristem in the parasite's stem kept its normal structure without further development. Thus, it failed to trigger the development of functional haustorium. The results of this study indicate that the tested monocotyledonous plant species could be classified as either compatible (onion and ginger) or incompatible (Bermuda grass and sorghum) hosts to field dodder. The incompatible hosts could be used as trap crops or incorporated in a suitable rotation system in order to combat the menace of this obnoxious weed.

Impact of *Arceuthobium sichuanense* infection on needles and current-year shoots of *Picea crassifolia* and *Picea purpurea* trees

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Arceuthobium sichuanense is an aerial parasite plant that infects primarily *Picea crassifolia* and *Picea purpurea* in Qinghai province, China, and causes severe damage to spruce forests in Qinghai-Tibet Plateau. The two main hosts, *P. crassifolia* and *P. purpurea* are main native tree species in Sanjiangyuan area, forming mixed forests at the altitude from 2900 m to 3100 m in Maixiu Forest occasionally. In the present study, the effects of *A. sichuanense* infection on *P. crassifolia* and *P. purpurea* trees were evaluated by examining needle and current-year shoot morphology, needle water and nitrogen use efficiency and needle nitrogen concentration. The most apparent effect of *A. sichuanense* infection was a significant reduction in both needle size distal to infection and current-year shoot length in the infected branches ($P < 0.001$). Percent reductions in needle and current-year shoot length were smaller in *P. purpurea* than in *P. crassifolia* (41.21% vs. 57.18%; 46.8% vs. 63.68%). Using isotopes to trace nutrient transfers, the high degree of correlation in foliar $\delta^{15}\text{N}$ values between dwarf mistletoe and the two species of host trees ($R^2=0.7179$, $P < 0.001$) suggested that mistletoe nitrogen was derived entirely from hosts. The dwarf mistletoe infection also resulted in a significant decrease in host needle N concentration and $\delta^{13}\text{C}$ values ($p < 0.001$). The percent reductions in needle nitrogen concentration and $\delta^{13}\text{C}$ values were larger in *P. purpurea* than in *P. crassifolia* trees (15.73% vs. 9.21%; -2.47‰ vs. -1.25‰). These results suggest that the growth reduction of needle and current-year shoot of both two host species may result from the limitation of nitrogen and water. We suspect that *P. purpurea* may suffer more nitrogen and water stress compared to *P. crassifolia* in our field (ca. 3072 m elevation), especially in drought years.

How Climate Change Affects Host-Parasite Relations and Parasitic Plant Management?

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The main results of global climate change are global warming, drought coming after reduction of precipitation, and increasing of CO₂ and O₃ rates. These changes negatively affect many aspects of agricultural production and it is expected to show itself seriously in the next 50-60 years. The parasitic weeds threaten agricultural production has also inevitably affected by this change. However, the impact of these climatic factors on parasitic plants is not fully understood today and it is very hard to give an overall estimate in this regard because the climatic factors can affect the development of the parasitic and host plants in a positive or negative direction. On the other hand, it is estimated that negative factors coming with climate change can effect to control methods of parasitic plants negatively. More accurate estimations should be done by doing more research and model studies on this issue and the most appropriate decision should be made according to these studies. This presentation prepared based on studies conducted in response of parasitic weeds, belong to *Orobanche-Phelipanche*, *Striga*, *Alectra*, *Cuscuta*, *Viscum*, *Arceuthobium*, *Rhinanthus* and *Epifagus* genus, and their host plants to the factors of climate change. It is considered that *Orobanche-Phelipanche*, *Striga* and *Viscum* species would be more troublesome in future because of their high adaptation capacity, and therefore controlling of them would be more difficult.

Effects of the hemiparasitic plant *Pedicularis kansuensis* on plant community structure in a degraded grassland

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Species-rich grasslands have high conservation value because they support diverse floral and faunal assemblages. Alpine grassland is an important and characteristic ecosystem of the Qinghai-Tibet Plateau, but ca. 30% has been severely degraded by the combined effects of climate change, human activity, overgrazing and rodent damage. One potential method to restore grassland diversity involves using hemiparasitic plants to modify the competitive relationships among neighboring species. A possible candidate is *Pedicularis kansuensis*, a hemiparasitic plant found in grasslands throughout the Qinghai-Tibet Plateau, but more information on its host associations and its effects on surrounding vegetation is required to assess its suitability. Thus, we examined host associations of *P. kansuensis* by direct root excavation at a selected site on the Qinghai-Tibet Plateau and found that haustoria formation is non-randomly distributed among host species, with preferential bias for members of Poaceae, Rosaceae and Fabaceae. We also found that aboveground biomass of grasses and legumes was higher in quadrats from which the parasite had been removed than in intact controls, while the biomass of sedges and forbs was unaffected by parasite removal. However, removal significantly decreased plant species richness and Shannon–Wiener diversity. These results suggest that *P. kansuensis* modifies the competitive balance in grassland communities of the Qinghai-Tibet Plateau, allowing for colonization by subordinate species and thereby enhancing species diversity and contributing to restoration of these degraded grasslands.

Taxonomy and Phylogenetics of Hydnoraceae and a Potentially New *Hydnora* from Oman

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The Hydnoraceae is a small family of holoparasites within the Piperales comprising two genera, *Hydnora* and *Prosopanche*. The under-collection and the poor preservation of fertile material have contributed to taxonomic confusion within the family. We recognize seven old world *Hydnora* taxa and synonymize 11 additional names. Within *Prosopanche* we accept four new world taxa and synonymize 5 other names. Our taxonomy is based in part on a three loci (*accD*, *nad6*, ITS) phylogeny. *Hydnora* and *Prosopanche* were resolved as sister clades in rooted (with *Piper nigrum*) maximum parsimony and Bayesian analyses. *Hydnora* are parasites on three rosid lineages. The ancestral *Hydnora* hosts seem to be members of the Fabaceae and *Commiphora* (Burseraceae) followed by a single host-shift to *Euphorbia* spp. Significant work may be needed to revise the taxonomy of the Fabaceae-*Commiphora* parasitizing (FCP) clade of *Hydnora*, where only three species are currently recognized, but at least six descriptions of species from east and northern Africa remain unevaluated. Among the FCP clade is a *Hydnora* from the southern region of the Arabian Peninsula represented by a handful of herbarium specimens and initially misidentified as *Hydnora africana*. We review the poorly known Arabian *Hydnora* and present new taxonomic data from 2014 field work in the Dhofar region of Oman.

Pollination ecology of the South African holoparasites *Mystropetalon thomii* and *Sarcophyte sanguinea*, and diversity of pollination systems in Balanophoraceae s. l.

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The pollination ecology of most parasitic plants is unknown, despite the evolutionary and potentially conservation or control relevance of the requirements for successful plant reproduction. The holoparasitic Balanophoraceae s. l. comprise 50 species in 17 genera, yet the reproductive ecology of only six species has been studied. We studied the pollination ecology of the monospecific South African genera *Mystropetalon* and *Sarcophyte*. *Mystropetalon thomii* is a rare endemic to the Kleinmond area in the Western Cape, and the inflorescences' dark red colour, weak scent, and copious nectar production suggested bird pollination. *Sarcophyte sanguinea* is rare in eastern South Africa, and the putrid smell and flesh-like appearance of the inflorescences suggest pollinator attraction by carrion mimicry, a pollination system not previously recorded in the Balanophoraceae. We assessed pollinator fauna with observations, motion-sensor video cameras, and capture of visitors. We determined presence of nectar and standing-crop volume by absorbing nectar onto filter paper, and assessed nectar sugar concentration with hand-refractometers. Floral scent was sampled using thermodesorption of adsorbent cartridges and analysed using gas chromatography-mass spectrometry. In *M. thomii* we used fluorescent dyes to examine spatial patterns of pollen dispersal. We demonstrate that *M. thomii* is pollinated by several species of rodents, while birds only extremely rarely interact with inflorescences. The scent bouquet reminiscent of crushed berries is chemically complex but curiously several of the major components appear not to be attractive to rodents. Rodents transfer copious pollen in their facial fur while licking nectar from the inflorescences. Pollen transfer mostly within clusters of inflorescences suggests little outcrossing, yet extremely high seed set suggests absence of quantitative or qualitative pollen limitation. The pungent scent of *S. sanguinea* is dominated by sulphides, a scent profile consistent with generalist carrion mimicry. It attracts flies from several families and carrion beetles (Silphidae). Inflorescences produce no rewards for pollinators. Large differences in pollen loads, commonness, and mobility between beetles and flies suggest significant quantitative and qualitative differences between pollination services provided by beetles and flies. From our results and previous studies of Balanophoraceae pollination ecology we extrapolate pollination syndromes for unstudied species and discuss the diversity of pollination systems in the Balanophoraceae in the context of the phylogenetic relationships in the family. We conclude that Balanophoraceae s. l. exhibit a remarkable diversity of pollination systems despite the extreme reduction of individual flowers and limited inflorescence diversity. Further studies are needed to understand the diversity of pollination systems and the relevance of pollinator-driven speciation in the Balanophoraceae.

Explanation of parasite association aspects in plants: game theory application in population dynamics and community structure

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Alongside of abiotic interactions, modeling the behaviour of parasitic plants in contrasting to hosts and other biotic set, is playing a critical role to determine their effects on plant communities. Game theoretical models could be applied to describe interactions among parasites and other biotic agents that behave strategically, to predict pay-offs of these interactions, and to illustrate ecological and evolutionary processes which are affected by parasites together that shape plant communities. In this way, models can predict the effects of different strategies profiles between the co-occurring host species that are parasitized on their population dynamics and community structure. Here parasite-mediated competition in host-parasite systems with density-dependent interactions is the main factor. Game theoretical models, which describe co-infection interactions between parasite and herbivore as intrahost competitors, suggest that players select selfishness in spite of the greater pay-offs in cooperation in this strategy, which refer to “Coordination Failure”. Repeated games, which are continuing again and again, could be applied to describe how host-parasite coevolution is reached to stable equilibrium in the population dynamics. To sum up, the evolution of the strategies of parasitic plants shows that evolutionary stability will change the multiple equilibria in system to efficient equilibrium by which prevents “Self-Fulfilling Prophecy” in plant community, and finally strategies will become stable throughout the population.

Do arbuscular mycorrhizas alleviate the effect of *Striga hermonthica* on host performance?

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Plants release chemicals to recruit beneficial organisms to their roots, particularly under nutrient-limited conditions. For example, strigolactones (SLs) induce hyphal branching and enhance colonisation by mutualistic arbuscular mycorrhizal (AM) fungi, symbionts that supply their host with phosphorus (P) and nitrogen (N) in return for host carbon. SL biosynthesis and exudation are down-regulated due to improved host nutrient status as a result of AM colonisation. The SL signalling mechanism is also vital to initiate seed germination of the root parasitic weed *Striga hermonthica* that devastates crops in sub-Saharan Africa. Soils in Africa are generally nutrient poor thus creating an ideal environment for *S. hermonthica* infection and for AM colonisation. Individually, both *S. hermonthica* and AM fungi manipulate the physiology of the host roots, including altering SLs and host defensive compounds, and thus have the potential to influence the relative fitness of each other. However, the consequences of co-infection by *S. hermonthica* and AM fungi for host, AM and parasite performance remain poorly understood. In this study we tested the hypothesis that colonisation by AM fungi will lower infection of host roots by *S. hermonthica* and thus reduce the negative effects of the parasite on host performance. To test this, we grew rice alone (control), with the AM fungus *Rhizophagus irregularis* alone (+AM), with *S. hermonthica* alone (+*Striga*), and with both together (+AM+*Striga*) under field relevant nutrient conditions. Levels of *S. hermonthica* infection, AM colonisation, and host growth were measured along with host tissue N and P levels. Unsurprisingly, colonisation of host roots by AM fungi increased host biomass and increased tissue P concentrations in both the roots and the shoots. In contrast, infection by *S. hermonthica* massively decreased host biomass, whilst slightly increasing N and P concentrations. Contrary to our hypothesis, co-infection of roots by AM fungi and *S. hermonthica* resulted in significantly increased number and biomass of the parasite on the host. We are currently investigating the hypothesis that this effect can be explained by transient alterations in either host nutrient status or defence chemistry.

AM fungi in roots of hemiparasitic *Pedicularis*: friends or foes?

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Arbuscular mycorrhizal (AM) fungi and parasitic plants are two ubiquitous and important components in terrestrial ecosystems. Both groups impose direct impacts on their host plants as well as consequent influences on community structure of their ecosystems, though in very different ways. Despite their opposite influence on host plants (with parasitic plants often being parasitic and AM fungi mostly mutualistic), recent findings suggest that colonization by AM fungi and infection by root parasitic plants may be modulated by similar molecular mechanisms, and interesting parallels between plant parasitism and AM associations have been indicated. In addition, a limited but growing number of studies have found that the AM status of host plants significantly influences growth of parasitic plants. However, most root parasitic plants do not form mycorrhizal associations and studies experimentally addressing interactions between parasitic plants and AM fungi are very limited. As a consequence, roles of AM fungi for plant communities in which root parasitic plants occur remain largely unknown. Using root hemiparasitic plant species of the genus *Pedicularis* (Orobanchaceae) that harbor AM fungi in their root systems, we investigated possible roles of these fungi in the root hemiparasites as well as in the plant communities where both partners occur. The results showed that AM fungi had significant influence on survival and biomass of the root hemiparasites, though robust variation was observed in terms of the outcomes of AM inoculation, depending on plant and fungal identity as well as growing conditions. In addition, AM fungi played important roles in regulating interactions between the root hemiparasites and their host plants. Damage to host plants by parasitism of the root hemiparasites was generally alleviated by inoculation with AM fungi. However, the mechanisms involved in the alleviation were quite different between different host-parasite pairs.

High plasticity in root morphology of two root hemiparasitic *Pedicularis* (Orobanchaceae) species

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As an effective adaptation strategy, root modification has been reported in many plant groups, giving these species more plasticity in nutrient acquisition in response to different conditions. Root hemiparasites often have poorly developed root systems and are generally non-mycorrhizal, which puts them at a disadvantage in terms of nutrient uptake from soil. As a consequence, root hemiparasitic plants depend largely on their hosts for acquisition of inorganic nutrients and water via specialized structures called haustoria. Despite variations in host dependency and duration of the pre-parasitic phase prior to the development of functional haustoria, all root hemiparasitic plants can grow for a period of time without attachment to a host. A few facultative root hemiparasitic plants can complete their life cycle in the absence of a host, showing a retained capability for nutrient acquisition through their own root systems. We hence hypothesize that root hemiparasites may retain the plasticity in response to heterogeneous environments as observed for autotrophic plants. In contrast to numerous investigations of root morphological plasticity in autotrophic plant species in the past decades, little is known about morphological plasticity in root hemiparasitic plants. In this study, plasticity in root morphology of two *Pedicularis* species was studied both in the field and in manipulated pot cultivation experiments. The results showed that both *P. rex* and *P. tricolor* maintained high root morphological plasticity. Host plant identity, soil nutrient status and texture, arbuscular mycorrhizal fungi, and vegetation density all had robust influence on root morphology of the hemiparasites. We presume that the plasticity contribute greatly to their adaptation to disadvantage environments, including nutrient deficiency, strong host defense responses, and strong intra-specific competition.

Influence of soil nutrient status and plant community structure on occurrence and expansion of *Pedicularis kansuensis* in Western China

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As an endemic species of China, root hemiparasitic *Pedicularis kansuensis* has been expanding in Bayanbulak Grassland of Xinjiang Uygur Autonomous Region and some areas of Qinghai Province in the past decade, threatening the local livestock industry. In order to understand why this damaging species expands in some areas but not in other, we compared soil nutrient status and plant community structures between the heavily infected and non-infected sites. We hypothesized that soil nutrient levels and plant species composition would be more beneficial to spatial expansion of *P. kansuensis* in heavily infected areas than in non-infected ones. Quadrat (1 m*1 m) surveys were carried out in Qinghai Province (MaiXiu, NingXiu and ChengDuo) and Xinjiang Uygur Autonomous Region (Bayanbulak Grassland). Species number, percent vegetation cover, aboveground plant biomass, plant height and relative frequency were recorded. Three soil samples were taken at 0-10 , 10-20, and 20-30 cm depths, respectively from each quadrat, and nutrient status determined. The results showed that (1) influence of soil nutrient status did not have a clear pattern on occurrence and expansion of the root hemiparasite, (2) total aboveground plant biomass in heavily-infected areas were generally higher than non-infected areas, despite of the parasitism by a large number of *P. kansuensis*, (3) aboveground biomass of *P. kansuensis* negatively correlated with graminoid aboveground biomass, but positively correlated with that of forbs, (4) *P. kansuensis* occurred more frequently in graminoid-dominated areas. More studies are required for a better understanding of the driving forces for spatial expansion of the damaging root hemiparasite.

Genetic variation and phylogeographic history of *Pedicularis kansuensis* (Orobanchaceae) inferred from Chloroplast DNA Sequences

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Pedicularis kansuensis Maxim., a root hemiparasitic plant species endemic to China, is disjunctly distributed in Qinghai-Tibetan Plateau (QTP) and Tianshan. In this study, we investigated the genetic diversity and phylogeography of this species, aiming to understand how the Quaternary climatic oscillations influenced the range shifts and intraspecific genetic variation. Two chloroplast DNA spacers (*rpl32-trnL* and *trnL-trnF*) were sequenced for 319 individuals from 34 populations covering the whole distribution range of this species. Seventeen haplotypes were identified in total. The level of genetic diversity was high (HT=0.882, HS=0.559), but genetic differentiation among populations was relatively low (GST=0.326). Based on Bayesian Evolutionary Analysis Sampling Trees (BEAST) analysis, the divergence times among four main lineages can be dated back to early Pleistocene, indicated that *P. kansuensis* had experienced the Quaternary major glaciations. Mismatch distribution analyses showed that none of those four lineages had experienced a recent range expansion. Compared with the present distribution range, we found *P. kansuensis* did not obviously shrink in QTP, but disappeared in Tianshan during the last glacial maximum (LGM). We propose that *P. kansuensis* may have survived *in situ* in QTP during glacial periods, and the Quaternary climatic oscillations promoted its intraspecific differentiation. In addition, its current distribution in Tianshan might be due to dispersal by animals moving through the wide arid region after LGM.

Pot culture of an important Chinese medicinal plant *Cistanche deserticola*

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Cistanche deserticola, which parasitized on root of *Haloxylon ammodendron*, was an important Chinese herb, and could be used to treat asynodia, senile dementia and constipation. *C. deserticola* was endangered species because of being affected by factors such as over excavation, growing environment deterioration and so on. In this study, potting parasitic technology including the host age, inoculation time, inoculation seed weight and watering frequency were studied. The result showed that 1 year-old, 2 year-old and 3 year-old *H. ammodendron* plants could all be parasitized by *C. deserticola*. The parasitism rate of 2 year-old *H. ammodendron* plants, which was the highest, was 87%. However, the parasitic body weight of 3 year-old *H. ammodendron* after parasitized 120 days, which was the highest, was 14.9 g. The *C. deserticola* could all parasitize *H. ammodendron* plants when inoculation in the late ten days of April, the middle ten days of May, the first ten days of June and the middle ten days of September. The parasitism rate of the late ten days of April, which was the highest, was 87%. The inoculation seed weight had significant effect on parasitism rate and parasitic body number, and 0.03 g was the appropriate. The appropriate watering frequency was 2~3 times per month. And the appropriate water content of base material in pot was 60~80%. The potting parasitic technology of *C. deserticola* had advantages of high parasitism rate, low inoculation seed weight and simple operation process, would provide support for resources protection and efficient scale production of *C. deserticola*.

Session 5: Control and management

Chairs

Ahmet Uludag and Joseph Hershenhorn

A Cautiously Conception for *Orobanche* spp. Control by Using Allelopathy and Trap Crop

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Orobanche spp. has caused huge damage to the farmland ecosystem of the world, which was difficult to control because of their special life cycle. Researchers have proposed a number of methods for controlling broomrapes. These methods include hand-weeding, adjustment of sowing dates, herbicide application, selection and breeding of resistant crop cultivars, and use of trap or catch crops. Among these methods, the use of trap crops is most promising. Trap crops induce *Orobanche* spp. seeds to germinate without being parasitized themselves. The *Orobanche* seedlings die for lack of nutritional support, a process termed “suicide germination”. Strigolactones (SLs) are a group of compounds that trigger germination of *Striga* spp. Most SLs are also able to induce *Orobanche* spp. germination. The ability to produce SLs has been observed in many other plant species under laboratory conditions, including both hosts and non-hosts of *Orobanche* spp.. Our research group has conducted researches on trap crop for *Orobanche* spp. by using wheat, maize, cotton, soybean, rice, switchgrass, and millet (Unpublished data). However, it was observed that not all crop varieties were able to induce *Orobanche* spp. seeds to germinate under the pot and field conditions and also why *Orobanche cumana* plants were only parasitized on the horizontal layer of the sunflower seeding depth under field condition both in Spain and China. Since the discovery of the SLs could stimulates the AMF fungi branch and inhibit shoot branch of plants most of the researchers have believed that the most of the plant producing SLs (80% of land vegetation), which could be used as trap crop for *Orobanche* spp.. People have to aware that SLs inducing *Orobanche* spp. seeds germination is an allelopathic phenomenon. The produced SLs have to be released into soil in suitable quantity and have to have enough concentration to arrive to *Orobanche* seeds in order to stimulate the germination under various environmental stresses. People may understand the term of allelopathy and trap crop, but it is also true that the way ahead is much longer than that already walked down. As we get more in-depth knowledge about allelopathy and trap crop for *Orobanche* spp. and their environments, new questions arise. The knowledge of how SLs from host or non-host plants are released into the environment, their concentration and isomers and also stability in the given environment, translocated, degraded into soil, fixation in soil organic matter, the stage of host and/or host plant, soil temperature and moisture, minerals, and adsorbed by *Orobanche* spp. is of paramount importance. In addition, how we could recommend the crop varieties to farmers as trap crop for *Orobanche* spp. because each crop have thousands of varieties and among them most of it may not able to inducing *Orobanche* spp. seeds to germinate. We have to be very serious on popularization of our knowledge on trap crop and allelopathy for individual farmers for *Orobanche* spp. control. The varietal differences among different trap crops (wheat, maize, cotton, soybean etc) for *Orobanche* spp. and in different growth stages will be discussed in the presentation and the reasons why the millet data were stopped to be publish will also be pointed out.

***Cuscuta campestris* control with granular cell division inhibiting herbicides**

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Field dodder (*Cuscuta campestris*) is an obligatory aboveground plant parasite that causes severe damage in field crops and vegetables worldwide. In most cases there are no selective and effective measures to control the parasite. In recent studies, we have suggested that the window of opportunity for efficient dodder control is the phase between parasite germination and host attachment. The aim of the present study was to examine granular formulations of herbicides applied before dodder germination for effective and selective control. In laboratory experiments we applied Granular Treflan (5% trifluralin, G), Snapshot (2.5% trifluralin + 0.5% isoxaben, G) and Corral (2.68% pendimethalin, G) on dodder seeds in Petri dish. The cell division inhibiting herbicides reduced dodder seedling elongation from 10 cm in the untreated control to 1 cm only. Snapshot was the most effective growth inhibitor and in addition reduced 30% of parasite germination rate, compared to the untreated control. In net-house and greenhouse experiments we applied the granular herbicides on three week old tomato, chickpea and watermelon plants grown in pots inoculated with dodder seeds. Snapshot decreased dodder emergence four-fold at 1/2X (X =recommended rate=3.0+0.6 kg ai/ha), while the X rate completely eliminated parasite growth on chickpea and watermelon with no damage to the host plant even when treated at 2X. Granular Treflan applied at 2X (X=3.0 kg ai/ha) did not totally prevent dodder parasitism but its growth was halted at the host stem penetration phase. Corral was more effective than Granular Treflan and eliminated dodder parasitism on both hosts at 1/2X (X=3.22 kg ai/ha). These studies indicate that cell division inhibiting herbicides can be efficient and selective for dodder control in tomato, chickpea and watermelon. In future studies we will investigate the efficacy of dodder control and crop selectivity with granular herbicides applied under field conditions.

Egyptian broomrape control in processing tomato with maleic hydrazide

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Broomrapes (*Phelipanche* and *Orobanche* spp.) are root holoparasitic plants that cause severe damage to many crops in Israel. The most damaging species is Egyptian broomrape (*P. aegyptiaca*) that is the main limiting factor in processing-tomato production in Israel and some countries of the Arabian Peninsula. The only control measure for this weedy root parasite in tomato in Israel is based on a complicated chemical control protocol. The complexity of the protocol, the need for precise application timing, the upper irrigation system and water cost and above all the long soil residual effect of the herbicides that jeopardizes effective crop rotation was the driving force for searching other control options. Maleic hydrazide (Himalaya) is a plant growth regulator used to prevent potato and onion sprouting during storage. Egyptian broomrape control efficacy of maleic hydrazide in pots under greenhouse conditions was impressive. Based on the initial protocol developed in the greenhouse we conducted numerous field experiments during the years 2009-2012. The final protocol for successful Egyptian broomrape control includes 5 maleic hydrazide applications. The first and second applications of 270 ai h⁻¹ each should be applied 100 and 200 growth degree days (GDD) after tomato planting. The third and fourth applications of 540 ai h⁻¹ should be applied at 400 and 700 GDD and the last application of 540 ai h⁻¹ should be applied at 1100 GDD. The method proved to be highly effective in controlling broomrape and increased the yield in fields with moderate to high broomrape infestation levels. On March 2014 Himalaya was registered for a commercial use and was extensively and successfully used by the Israeli tomato growers in the last two growing seasons. We will present data on the development and optimization of maleic hydrazide as a broomrape control agent and the results of observations on its efficacy in full scale of commercial use.

Use of some weed species for Witchweed (*Striga hermonthica* (Del.) Benth.) management in maize (*Zea mays* L.)

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Three weed species, bush tea (*Hyptis suaveolens* (L.) Poit.), greenleaf (*Desmodium intortum* (Mill.) Urb. and sicklepod (*Senna obtusifolia* (L.) Irwin & Barneby) were planted in alternate stands on the top or the slope of the ridge (furrow) simultaneously with maize (*Zea mays* L.) sown at 50 cm apart on 6 July, 2013. Sole maize was the control treatment. The treatments were arranged in a randomized complete block design and replicated four times. Results revealed that days to first *S. hermonthica* shoot emergence was earliest in the sole maize control treatment. However, it was not significantly different from that of furrow planted *S. obtusifolia*. *Striga* shoots emerged 7-24 days later in the inter-planted plots than the control treatment. On the contrary, furrow planted *Desmodium* delayed *Striga* shoot emergence most, which was at par with alternate *Desmodium* and *Hyptis* inter-planting. *S. hermonthica* shoot density m⁻² was significantly higher in the sole maize plots, while all the inter-planted maize treatments were statistically similar. Sequel to early *Striga* shoot emergence and higher shoot density in sole maize, grain yield was significantly lower than in all other treatments, except *Hyptis* interplant. Maize grain yield was 48.3-65.9% greater in the inter-planted maize compared with the control sole maize. We infer that these weed species could be used for *S. hermonthica* management.

How to detect crop infestation by broomrapes long before than they appear aboveground?

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Holoparasitic plants from the genus *Orobanche* and *Phelipanche* considerably damage crop plants due to withdrawal of water, minerals and carbohydrates. The weedy species of these parasites are almost uncontrollable under field conditions, also because a lot of damage has already been inflicted to the host once the parasite appears above ground. The growth of the hosts is retarded and yield losses range from 5 to 100%. Successful control would be greatly advanced if infestation could be detected well in advance of emergence. In our study we explored whether volatiles organic compounds (VOCs) produced by the host plant can be used for this early detection. Hereto, dynamic headspace analysis was carried out on model system - sunflower, *Helianthus annuus*, infested by *Orobanche cumana*. Volatiles were collected from the host plant during various stages of infestation and the samples analyzed using Gas chromatography-Mass Spectrometry. The results show that infection of sunflower by *O. cumana* indeed induces volatile emission from the sunflower plants. Moreover this occurs already in a very early stage of infection, few days after sunflower sowing, long before the parasite emerges. An early change in plant volatile emission upon infection with parasitic plants could be developed into an early warning system by using sensors that can detect the difference between healthy and broomrape infected plants, such that selective herbicide application can be used. These findings will be discussed in the context of plant protection against the root parasitic plants.

Role of herbicides and salicylic acid in controlling obligate root parasite *Orobanche cumana* growth in host crop sunflower

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Sunflower broomrape (*Orobanche cumana* Wallr.) is an obligate holoparasitic weed that causes severe damages to the sunflower crops worldwide. In the present study, an attempt was made to investigate the efficiency of different herbicides and salicylic acid (SA) to control the *O. cumana* infection on specific sunflower plants. For this purpose, two groups of sunflower seeds were used; one presoaked with SA in germination stage, while other group was treated by three herbicides trifluralin, butralin and S-metolachlor with three different concentrations (50% of recommended rate, recommended rate, and 200% of recommended rate) in pot experiment. Among three herbicides, trifluralin showed the best effect followed by butralin and S-metolachlor. The present study is also proposed that all these three herbicides could restrain infection into sunflower by *O. cumana*. Moreover, results revealed that lower concentrations of trifluralin (50% and 100%) showed better effects than higher concentration (200%). Meanwhile, for butralin, 200% concentration was the optimal concentration. The effect of three gradients of S-metolachlor did not show any significant difference. The plants soaked with SA showed enhanced growth, higher chlorophyll contents, efficient antioxidant defense system and less oxidative stress as compared to untreated SA plants. This study proposed that application of SA helped the sunflower seedlings to relieve the harm caused by *O. cumana* parasitism. *O. cumana* usually would attach to sunflower root in one month in normal pot experiment; while, in the present study, before moving to the greenhouse, no parasitism was found in sunflower roots, which implied that low temperature might also have significant inhibitory effect, though the influence of herbicides could not be ruled out. Further research is planned to investigate the effect of these herbicides and SA on the *O. cumana*-sunflower interaction under various environmental conditions.

Towards the genome sequence of *Orobanche cumana*

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Few genomic data are available for *Orobanche cumana*. Two projects, HeliOr and Resorobanche, aim at sequencing the genome of *O. cumana* and to produce a reference transcriptome respectively. The objectives of the projects will be detailed.

Genetic diversity and host preference in the parasitic weed *Phelipanche ramosa* L. Pomel

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Phelipanche ramosa L. (Pomel) is a holoparasitic plant from the Orobanchaceae family. Unlike most species of this family, *P. ramosa* is an annual weed parasitizing a large range of cultivated crops, and especially in the Mediterranean area. The genetic diversity of this species relative to its different host plants has not been extensively studied. For this study, sampling in a large geographic scale was organized through a network of scientific and agronomic experts belonging to the International Parasitic Plants Society, agronomic institutes and breeder companies. Samples corresponded to dried shoots or seeds. In this last case, DNA was extracted from tubers which developed on host roots in mini-rhizotron systems (artificial infestation). Potential SSR markers were identified from a 454 sequencing program. Twenty SSR markers were selected from preliminary genetic analyses using a set of *P. ramosa* individuals harvested on different hosts in the largest geographic scale. Then over 100 populations of *P. ramosa* and close species (*P. aegyptiaca* and *P. mutelii*) were genotyped, half of which coming from different geographical regions and different host plants in France. The remaining half corresponds to international populations coming from three continents and different host plants (tomato, tobacco, mustard and weeds). Genetic diversity analyses show low intra population variation and high and significant inter population variation. From the PCA analysis, all the analyzed populations can be partitioned in four groups - Type 1 for populations harvested on WOSR and melon in Western France which are highly differentiated from the remaining *P. ramosa* samples; Type 2 for populations harvested on hemp and WOSR in North Eastern France; Type 3 for populations harvested on tobacco in France (any regions) and in Europe, and an intermediate genetic group parasitizing different host crops in France, Europe and Western Asia. These results suggest the existence of different genotypes that could also differentiate by their degree of plasticity or host preference. To test this hypothesis, a core collection of 16 genotypes covering the genetic variability of *P. ramosa* serves for aggressiveness tests towards a range of seven host species (WOSR, hemp, tobacco, tomato, melon, sunflower and red clover) in order to clarify to what extent do genetic differentiation and phenotypic plasticity influence the adaptation of *P. ramosa* to different hosts on different geographic scales. Mini-rhizotron experiments are in progress.

Efforts taken in the control of weedy *Pedicularis kansuensis* in China

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Pedicularis L. (Orobanchaceae) is a large linkage of root hemiparasitic species widely distributed in the temperate zone of Northern Hemisphere, with about 800 species worldwide (2/3 of the species distributed in China). In most cases, they show patchy distribution patterns and do not cause significant reduction in plant community productivity at a large scale. However, dense occurrence in large scales and rapid expansion of *P. kansuensis* recently in the west of China are severely reducing plant community productivity in grasslands, hence threatening the local livestock industry. Previous studies attributed the population expansion of *P. kansuensis* to overgrazing. As a result, grassland fencing has been currently used as a primary practice for management of the hemiparasitic weed. Unfortunately, fencing practice seems not to be so successful as expected, as *P. kansuensis* plants grow much better and are more often found in large populations inside fences than those left outside (N.B. animals tend to avoid the hemiparasite when foraging). Chemical control has also been tested against the hemiparasite using a couple of herbicides such as 2,4-D butyl ester. However, because herbicides could damage other non-target species and are not environmental friendly, the implement of chemical control has been greatly limited. Manual or mechanical eradication has been used but are less successful in terms of the large scale of infested areas and the mixture of the hemiparasite with forage grasses. For a more effective and sustainable management of *P. kansuensis*, a better knowledge of the driving forces and underlying mechanisms for rapid spatial expansion of the weedy species is essential. We are now studying the key ecological and genetic factors influencing population dynamic of the parasitic species and relevant ecophysiological mechanisms.

Session 6: Host resistance

Chairs

Diego Rubiales and Yaakov Goldwasser

Broomrape management with a novel tomato mutant line resistant to acetolactate synthase (ALS) inhibiting herbicides

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One of the most destructive pests in agriculture are broomrapes (*Phelipanche* and *Orobanche* species), which are a limiting factor in the production of many crops, including processing tomatoes. Acetolactate synthase (ALS) inhibiting herbicides and glyphosate are the only herbicides known to control broomrapes. ALS inhibiting herbicides inhibit the enzyme acetolactate synthase, a key enzyme in the branched chain amino acid biosynthesis pathway leading to the formation of leucine, valine and isoleucine. Tomato plants are sensitive to all ALS inhibiting herbicides but tolerate several members of the sulfonylurea group. These herbicides may be used for broomrape control, but their application is based on a complicated protocol that includes 5 herbicide applications that the first 3 should be followed by upper irrigation of $300 \text{ m}^3 \text{ ha}^{-1}$. The development of a tomato variety resistant to the imidazalinone herbicides could serve as a practical solution to control the parasite. Those herbicides are readily absorbed by leaves, translocated to the roots and accumulated in broomrapes until it die. Using chemical mutagenesis, we developed a tomato line (HRT1) that is resistant to several groups of ALS inhibiting herbicides including imidazolinones. The ability of the imidazolinones to control broomrape parasitizing HRT1 plants was tested in greenhouse and under field conditions. In greenhouse experiments one application of imazapic (cadre) and imazapyr (arsenal), each at a rate of $12 \text{ g. a. i. ha}^{-1}$ almost completely prevented the emergence of broomrape shoots above soil and significantly decreased broomrape biomass. Three applications of 4.8, 9.6 or $12 \text{ g. a. i. ha}^{-1}$ at three-week intervals of each of these herbicides decreased broomrape biomass attached to the roots by 60-90%. In field experiments, 4 imazapic or imazapyr applications at the rates of 4.8, 9.6 or $12 \text{ g. a. i. ha}^{-1}$ or three applications of $24 \text{ g. a. i. ha}^{-1}$ completely prevented broomrape shoot emergence above soil. In field experiments we demonstrated that imazapic even at a rate as high as $144 \text{ g. a. i. ha}^{-1}$ did not cause any visual damage or yield loss of HRT1 plants. Effective broomrape control without yield loss of HRT1 can be achieved by four imazapic applications of 24-36 g. a. i. ha^{-1} , a total of 96-144 g. a. i. ha^{-1} per growth season.

Genetic characterization of the interaction between sunflower and *Orobanche cumana*.

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Sunflower is an important crop and is mainly used for oil production. *Orobanche cumana* is a major disease in cultivated areas around the black sea and in Spain. The pathogen spread more recently to several other countries (France, China ...). During the last ten years, several new *O. cumana* races have emerged but very few efficient methods were available to control their development. Genetic resistance was the more efficient and introgression of major resistance loci was successfully used to produce new resistant sunflower varieties (from races A to E). With the recent emergence of new virulent races (called F and F+), novel resistance loci need to be mapped and characterized. A recombinant inbred line population, derived from the cross between the lines HA89 and LR1, has been developed by INRA. It has been previously characterized for the resistance to the race E of *O. cumana*. We used this population to map QTLs controlling quantitative resistance to race F. The phenotyping has been conducted on the 107 lines of the population at different stages of the interaction. We evaluated each line for (i) the capacity of their root exudate to induce germination of *O. cumana* seeds, (ii) their ability to induce incompatible attachment, (iii) the number of broomrape tubercles in growth chamber, and (iv) the number of broomrape emergences in the field. Different response profiles were observed at these 4 stages of development, indicating several resistance mechanisms in sunflower. Interestingly, even if the two parental lines showed a close resistant phenotype, we observed a large diversity of the resistance level in the population. Combined with this detailed phenotyping analysis, we performed the genotyping of the sunflower recombinant inbred lines using an AXIOM array of 586 985 SNPs. QTLs will be mapped for the different traits.

Striga/sorghum arms race during domestication as revealed by Dual RNA-seq

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Transformation of wild species into elite cultivars through domestication entails narrowing the genetic diversity in crop plants. For sorghum in Eastern and Central Africa, continued selection has greatly contributed to more susceptible sorghum as well as increased virulence of the parasitic weed *Striga*. An efficient strategy to build new resistance against *Striga* in cultivated sorghum is to reclaim resistance lost during domestication, while preventing increasing virulence from the parasite. We sought to harness *Striga* resistance genes from wild sorghum cultivars as well as compare the profile of *Striga* virulence between cultivated and wild sorghum. We carried out dual RNA sequencing (both host and parasite tissue) of wild and cultivated sorghum using Illumina HiSeq. We then profiled genes – in wild sorghum – that are differentially expressed at early and late *S. hermonthica* infection and compared their profile to those of susceptible sorghum. In addition, we compared the profile of differentially expressed genes between *S. hermonthica* infecting wild sorghum and cultivated sorghum. Finally, we compared the profile of differentially expressed genes between *S. hermonthica* and *S. asiatica* in cultivated sorghum. Our results will make available genes/loci that will provide a platform enhancing resistance of sorghum to *Striga* using a genetic modification (GM) or a non-GM approach. We will also be able to understand how *Striga* is able to evade surveillance from its host and overcome resistance. These two outcomes are of fundamental importance to developing durable and broad-based resistance against *Striga* and have far reaching applications in developing resistance in other important cereal crops in SSA.

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NOTES

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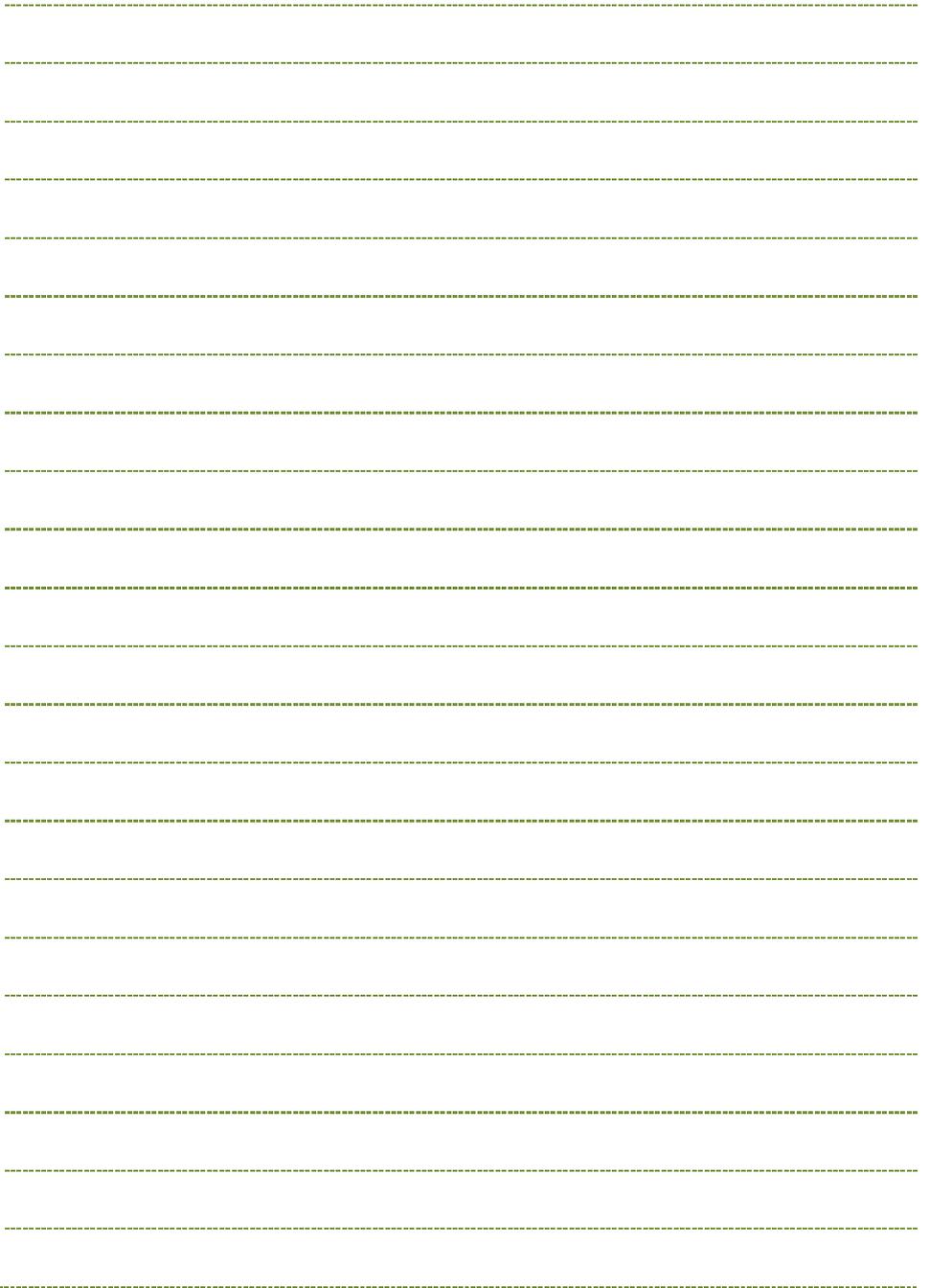
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Biography of Keynote speakers

(In session order)



Professor Harro Bouwmeester, Department of Plant Science, Wageningen University, The Netherlands

Harro Bouwmeester is chair of the Laboratory of Plant Physiology of Wageningen University, the Netherlands. The work in his group is centered around the elucidation of the biosynthesis of terpenoids and strigolactones in plants and their role in plant-environment interaction. In this work a number of different expertises are integrated, such as analytical chemistry, plant physiology, biochemistry, molecular biology and biology to study the importance of plant metabolites in the interaction of plants with parasitic plants and insects. With regard to parasitic plants his main interests are the structural diversity in the strigolactones and the importance of this structural diversity in biological specificity, such as parasitic plant host specificity. The research in the Bouwmeester lab has resulted in many publications in international peer-reviewed journals and an international position and extensive network in the field of terpenoid biosynthesis and strigolactones. At the end of 2005, he was awarded a Vici-grant of 1.2 M€ for his work on underground chemical communication of plants with parasitic plants and arbuscular mycorrhizal fungi and in 2007 a professorship in The Physiology of Plant Communication. From June 2008 he is full chair of the Laboratory of Plant Physiology of Wageningen University.

More information at: <http://www.wageningenur.nl/pph>



Professor Jim Westwood, Department of Plant Pathology, Physiology and Weed Science, Virginia Polytechnic Institute and State University, USA.

James Westwood's primary research interests center on parasitic plants, and specifically on their interactions with hosts. Parasitic plants have evolved amazing adaptations that enable them to locate suitable hosts and then establish physiological connections in order to feed on these hosts. His research explores multiple levels of plant-plant communication and aims to dissect these interactions at the molecular and genomic levels. His program focuses on broomrapes (*Phelipanche* and *Orobanch* spp.) and dodders (*Cuscuta* spp.), both of which are obligate parasites and pose serious threats to global agriculture. With respect to the broomrapes James Westwood is interested in how the haustorium functions inside the host, influencing host defenses and promoting the transfer of nutrients. In recent years James Westwood has been a leader of the Parasitic Plant Genome Project, a large collaborative project to develop gene sequence resources for parasites and explore the genetic bases for the evolution of parasitism in the Orobanchaceae. His research on dodders has characterized the exchange of messenger RNA between hosts and parasite and revealed remarkably open connections between species. The Westwood group is currently working to understand the biological significance of this phenomenon, and whether RNAs are used as information or a means of host manipulation by the parasite. James Westwood is active in the International Parasitic Plant Society (Past President and Honorary Member) and the Weed Science Society of America. He is a Professor of Plant Pathology, Physiology and Weed Science at Virginia Tech, Blacksburg, VA. He earned his Ph.D. at Purdue University, M.S. at the University of Minnesota, and B.A. at Concordia College, Moorhead, MN.

For details: <http://www.ppws.vt.edu/people/faculty/westwood-james.html>



Professor Ken Shirasu, RIKEN Center for Sustainable Resource Science, Japan.

Ken Shirasu's current interest is to understand how plants defend themselves against pathogens and how the pathogens break the immunity. His lab has been studying the parasitic plant *Striga*, an Orobanchaceae plant that is a serious agricultural threat in Africa. His group developed a model system to understand the parasitism using the hemiparasite *Phtheirospermum japonicum*, a Japanese native Orobanchaceae plant. *P. japonicum* can be easily grown in the lab and is amenable for various genetic analyses, such as crossing, mapping and transformation. Genome and transcriptome data on these plants provide important resources towards understanding molecular and evolutionary aspects of plant parasitism. Ken Shirasu graduated from the Department of Agricultural Chemistry of the University of Tokyo in 1988, and was awarded his PhD in genetics at the University of California, Davis, USA, in 1993. His thesis focused on molecular characterization of virulence factors of the plant pathogen *Agrobacterium*. He continued research as a Salk-Noble postdoctoral fellow at the laboratories of the Salk Institute and the Noble Foundation, USA, where he started to study plant immunity. In 1996, he joined the Sainsbury Laboratory, UK, as a researcher, and in 2000 became a group leader in the laboratory. He then joined RIKEN as a Group Director in 2005, and since 2008 has also held a position of adjunct professor in the Department of Biological Sciences, the University of Tokyo.

More information at:

http://www.riken.jp/en/research/labs/csrs/plant_immun



Professor Julie Scholes, Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK.

Julie Scholes is Professor of Plant and Microbial Sciences at the University of Sheffield UK. Her research interests are focused on understanding the physiological and molecular interactions between plants and their symbionts (parasitic weeds, fungal pathogens and mycorrhizal fungi).

A specific focus of her research is the root parasitic witchweed *Striga* that infects the staple cereal crops of sub-Saharan Africa causing devastating losses in yield. At present her research group are exploiting genomic, comparative genomic and quantitative genetic approaches to identify mechanisms (and genes) underlying resistance and susceptibility in cereal hosts to different ecotypes and species of *Striga hermonthica* and *S. asiatica* with the aim of breeding durable defence against these parasites. She is also taking a population genomics approach to identify virulence loci in *Striga* in order to understand the basis of host-parasite specificity. Her work encompasses both laboratory-based studies and field trials in Kenya, Tanzania and Uganda. Professor Scholes currently leads a BBSRC-DfID-funded consortium called "STRIGA" (STriga Rice resistance Genes for Africa)" involving scientists from Africa, France and the UK and a Leverhulme Trust Programme to elucidate mechanisms of resistance and virulence in the cereal-*Striga* interaction. She also has collaborative research projects with Syngenta, focused on understanding the metabolic basis of resistance and susceptibility in a variety of crops to the root parasitic Orobanchae species. Professor Scholes obtained her PhD in Physiological and Molecular Plant Pathology at the University of Wales in 1986 and then moved to Sheffield University to take up a Royal Commission for the Exhibition of 1851 Research Fellowship. In 1987 she was awarded a Royal Society University Research Fellowship that she held until 1995. She then accepted a position in the Department of Animal and Plant Sciences where she is Professor of Plant and Microbial Sciences.

For details: <http://www.shef.ac.uk/aps/staff-and-students/acadstaff/scholes>



Professor Daniel M. Joel, Department of Weed Research of the Agricultural Research Organization (ARO), Israel.

Danny Joel specialized on the biology and control of parasitic weeds, with focus on the root parasites *Orobanche* and *Phelipanche* (the broomrapes). In addition to writing reviews, book chapters and numerous research publications on parasitic plants, he recently edited the book 'Parasitic Orobanchaceae – Parasitic Mechanisms and Control Strategies' (Joel et al. 2013). His early ultrastructural and immunocytochemical studies demonstrated the mode of *Orobanche* attachment to the host and haustorium penetration, revealing the *in situ* release of wall-degrading enzymes and the resulting changes in host cell walls. His group established physiological and ultrastructural aspects of *Orobanche* seeds in relation to germination, and identified dehydrocostus lactone as the specific germination stimulant of sunflower root exudates. He achieved the first effective broomrape control with transgenic herbicide-resistant crops, and demonstrated the use of resistant rootstocks in providing host resistance to the parasites. Further to demographic studies of various broomrapes around the Mediterranean, his group developed markers of the different species for molecular diagnosis of soil-borne seeds. Joel's lab developed a variety of *in vitro* methods for host root infection and protocols for genetic studies of these parasites, which are currently used in genetic and genomic studies related to germination specificity and virulence mechanisms. Danny received his PhD from the Hebrew University of Jerusalem and was post-doc in Oxford University (UK) where he studied mechanisms of carnivory in plants, resulting in co-authoring the book 'The Carnivorous Plants' (Juniper et al. 1989). After lecturing botany at the Hebrew University he joined the ARO and became Head of the Department of Weed Research and of the Parasitic Plant Research Group. He was co-founder and President of the International Parasitic Plants Society (IPPS), Secretary of the Botanical Society of Israel and President of the Israeli Weed Science Society.

More information at <http://www.agri.gov.il/people/741.aspx>



Professor John Pickett, Rothamsted Research, UK.

John Pickett studies the chemical ecology of interactions between plants, including crops and weeds, and insects together with some other animals. This specifically involves the chemical characterisation of molecular structures for natural products that influence the development or behaviour (semiochemicals) of plants, insects and other organisms. He was the first to identify aphid, mosquito and sand fly pheromones. Research extends to the biochemistry and molecular biology of secondary plant metabolites for plant defence. The long term objectives are to develop semiochemicals for new methods of pest control. This is exemplified particularly by his work in Africa using companion crops to deliver plant secondary metabolites for pest and parasitic weed management and new approaches using genetic modification of crop plants to release protective metabolites.

John Pickett was appointed Head of the Insecticides and Fungicides Department (later the Department of Biological Chemistry) in 1984 and, concurrently in 2007, Scientific Director of the Rothamsted Centre for Sustainable Pest and Disease Management. In 2010, he relinquished these positions on being awarded the first Michael Elliott Distinguished Research Fellowship at Rothamsted. As well as fulfilling this prestigious new role, he continues to contribute to chemical ecology research and is still very much involved with such activities around the world. He has over 480 publications and patents. John's scientific work has been acknowledged with the 1995 Rank Prize for Nutrition and Crop Husbandry, election to Fellowship of the Royal Society in 1996, appointment to CBE for services to Biological Chemistry in 2004, and the Wolf Foundation Prize in Agriculture in 2008, among many other international measures of esteem. In April 2014 he was elected Foreign Associate of the National Academy of Sciences (US).

More information at:

<http://www.rothamsted.ac.uk/bch/PersonalWebpage/JohnPickett.html>



Professor Joseph Hershenhorn, Department of Weed Research of the Agricultural Research Organization (ARO), Israel.

Joseph Hershenhorn is a research scientist at the Department of Phytopathology and Weed Research at Neve Ya'ar Research Center, Agricultural Research Organization of Israel. His main research objectives are focused on control and management of the root parasites *Orobanche* and *Phelipanche* collectively known as broomrapes. Broomrape control is extremely difficult, therefore the strategy of his research group is to integrate several control measures applied together or in a sequence in an optimized manner. These control methods include biological control with fungi that are highly specific and attack only Egyptian and sunflower broomrapes. The research in this area is concentrated on optimization of a formulation that is suitable to be applied through drip irrigation systems. Using mutagenesis techniques and sophisticated screening procedures the group developed a broomrape resistant tomato line. The resistant mechanism is based on the inability of the plant to produce strigolactones. The group also developed a mutant that is highly resistant to the imidazolinone herbicides known for their ability to control broomrapes. Field experiments demonstrated excellent control efficacy without any damage to tomato plants or yield. Currently these two lines are crossed together in order to produce two defense layers. The group also developed a unique Egyptian broomrape control system in tomato based on the application of a plant growth regulator (Maleic Hydrazide). The method proved to be highly effective and safe and was registered for use in Israel in 2014. Joseph Hershenhorn earned his PhD. in botany at The Tel Aviv University, Tel Aviv. He joined the ARO and became Head of the Department of Weed Research and of the Chemical Control Research Group. He was Secretary and President of the Israeli Phytopathology Society and Secretary and President of the Israeli Weed Science Society.

More information at: <http://www.agri.gov.il/people/729.aspx>



Professor Diego Rubiales, CSIC, Institute for Sustainable Agriculture, Córdoba, Spain.

Diego Rubiales is Professor and leader of the Stress Resistance Group at the Institute for Sustainable Agriculture, CSIC, Córdoba, Spain. His research interest is resistance to diseases in cereals and legumes. He performed a PhD in Plant Breeding at the University of Cordoba in 1991 and then was postdoc in Holland. In 1993 got a permanent position as scientist at CSIC at Cordoba, then as senior scientist and then as Professor.

During the first 10 years of his career Diego worked on resistance to fungal diseases in cereals and then slowly moved to legumes. Although his background was on resistance to fungal diseases, when trying to contribute to solving legume problems in a Mediterranean country he faced the *Orobanche crenata* problem. No way to avoid this... Resistance to broomrape became then a central part of his research in the past 20 years. This was not an easy task. Everything started with coordination of COST action 849 “Parasitic Plant Management in Sustainable Agriculture” what allowed proper contacts and collaborations. Since then he has been quite successful in coordinating a substantial number of national and international projects on resistance to diseases on legumes. Unfortunately, in spite of his wishes, broomrape was not the major target of any of them. Fortunately, thanks to a lot of motivation and enthusiasm he managed to maintain some continuity on broomrape research. This was possible only thanks to huge efforts, a lot of luck and excellent collaborations.

As a result, he published 265 articles in journals with IF, 82 of which are on parasitic weeds, besides a substantial number of book chapters, dissemination articles and congress presentations, compiling h=35. However, what he feels most proud is on the number of excellent students that were trained (24 PhDs, 8 of which were on resistance to broomrape) and particularly, the registration of the first pea cultivars resistant to broomrape.

For details: https://www.researchgate.net/profile/Diego_Rubiales



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