APACE

The 10th Conference of Asia-Pacific Association of Chemical Ecologists

Hangzhou, China, Oct. 9-13, 2019

Painted&Designed by Yuebai Zhang

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Welcome from the Local Organizing Committee

It is our great pleasure to welcome all of you, the fellow chemical ecologists all over the world, to participate the 10th Conference of Asia-Pacific Association of Chemical Ecologists (APACE) in Hangzhou, China. This conference is hosted jointly by the Zhejiang University, China Jiliang University, the Tea Research Institute and State key laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences and Zhejiang A & F University.

The conference has received 235 abstracts for oral and poster presentations. The scientific committee has selected 169 abstracts for oral presentations and 66 poster presentations. The topics of 13 symposia represent a broad variety of chemical ecology researches including plant-plant interactions, plant-insect interactions and multiple trophic interactions, which cover both basic and applied researches.

The First World Hotel chosen as the venue is one of the elite conference center in Zhejiang Province and considered as the first five-star tropical rainforest theme hotel in Yangtze River Delta region. Hangzhou has been recognized as one of the most beautiful cities in China and is also the capital of Zhejiang Province. Once upon a time (the southern Song Dynasty), Hangzhou was the capital city of ancient China. It is not only renowned for its historic relics and natural beauty, but also considered as the main hub for innovative modern technologies, 'China's Silicon Valley. We hope that you will all enjoy your stay in this Hangzhou Paradise and Crazy Happy Land with wonderful experiences and extinguished feelings, which certainly will leave you with an unforgettable memory!

We hope that you will find this year's APACE Meeting exciting and inspirational.

Prof. Yonggen Lou

Chair

Prof. Baoyu Han

Co-Chair

Prof. Guirong Wang

Co-Chair

Welcome from the APACE President

It is my great pleasure to welcome all those attending the 10th Conference of Asia-Pacific Association of Chemical Ecologists (APACE) to Hangzhou, China. APACE conferences are held every two years, with every second meeting being held jointly with the International Society of Chemical Ecology: this year we are meeting independently.

Chemical ecology integrates both chemistry and biology to study the ecological interactions among organisms and their environment, and is one of the important disciplines that contribute to our understanding of biodiversity. In this conference, researchers from the Asia-Pacific region (one of the treasure houses of biodiversity) and other regions of the world will share their novel and exciting findings that will significantly influence the future direction of chemical ecology.

I sincerely hope that you will find the conference and your stay in Hangzhou both valuable and enjoyable.

Prof. Junji Takabayashi

President APACE

APACE was officially inaugurated at a symposium meeting held in conjunction with Third Asia-Pacific Conference of Entomology in Taichung, Taiwan on 21 November 1997.

APACE is organized to promote the understanding of interactions between organisms and their environments that are mediated by naturally occurring chemicals. Research areas include the study of structure, function, synthesis and biosynthesis of natural products related to organisms, their importance at all levels of ecological organization, their evolutionary origin and their practical application. The Regular meetings of APACE are held every two years.

1st	1999	Shanghai, China
2nd	2001	Penang, Malaysia
3rd	2005	Jeju, Korea
4th	2007	Tsukuba, Japan
5th	2009	Hawaii, USA
6th	2011	Beijing, China
7th	2013	Melbourne, Australia
8th	2015	California, USA
9th	2017	Kyoto, Japan

Host City

Hangzhou is the capital of Zhejiang Province and the local political, economic and cultural center. As the southern terminus of the Grand Canal, the city is located on the lower reaches of the Qiantang River in southeast China, a superior position in the Yangtze Delta and only 180 Km from Shanghai.

Hangzhou is one of the Seven Ancient Capital Cities. It was the capital of the Southern Song Dynasty from 1127 until the Mongol invasion of 1276. The population is estimated to have been as high as one million in those days, making it the largest city in the world at the time. Even Marco Polo claimed to have passed through, calling it beyond dispute the finest and the noblest in the world.

It is also ranking as one of the most scenic cities in China. As a city of gardens, temples, and lakes, Hangzhou's beauty is praised in all ages. There is an old Chinese saying goes like this: In heaven there is paradise; on earth there are Suzhou and Hangzhou.

The West Lake is undoubtedly the most renowned landmark, noted for the scenic beauty that blends naturally with many famous historical and cultural sites. The "Ten West Lake Prospects" selected from the most frequently visited attractions around the lake give travelers a panoramic view of the city's highlights. Take a stroll along the causeway by the lake; you'll feel the peaceful ethos of the city and better understand its time-honored fame as 'Heaven on Earth'.

Venue

The First World Hotel

2555 Fengqing Avenue
Hangzhou, Zhejiang Province
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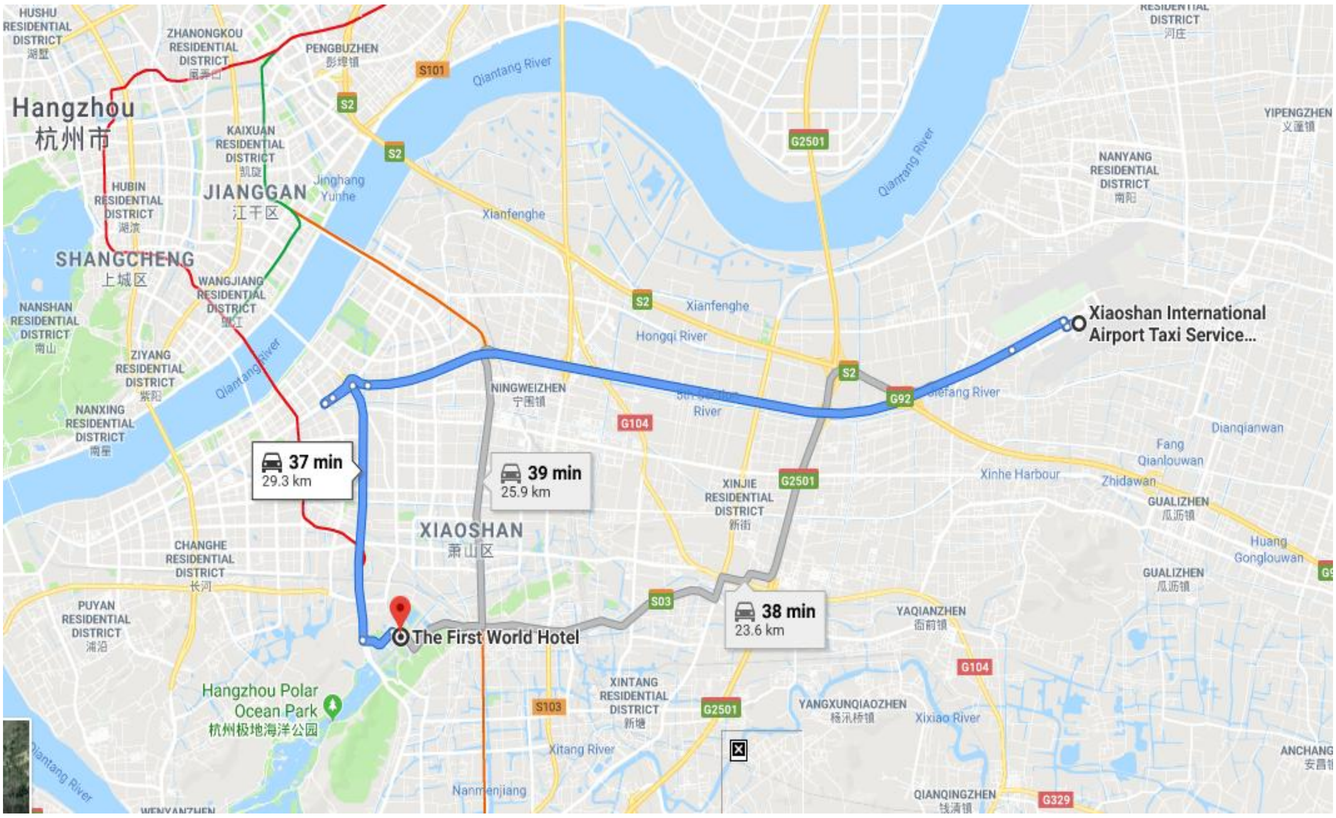
en.first-world.cn

Registration

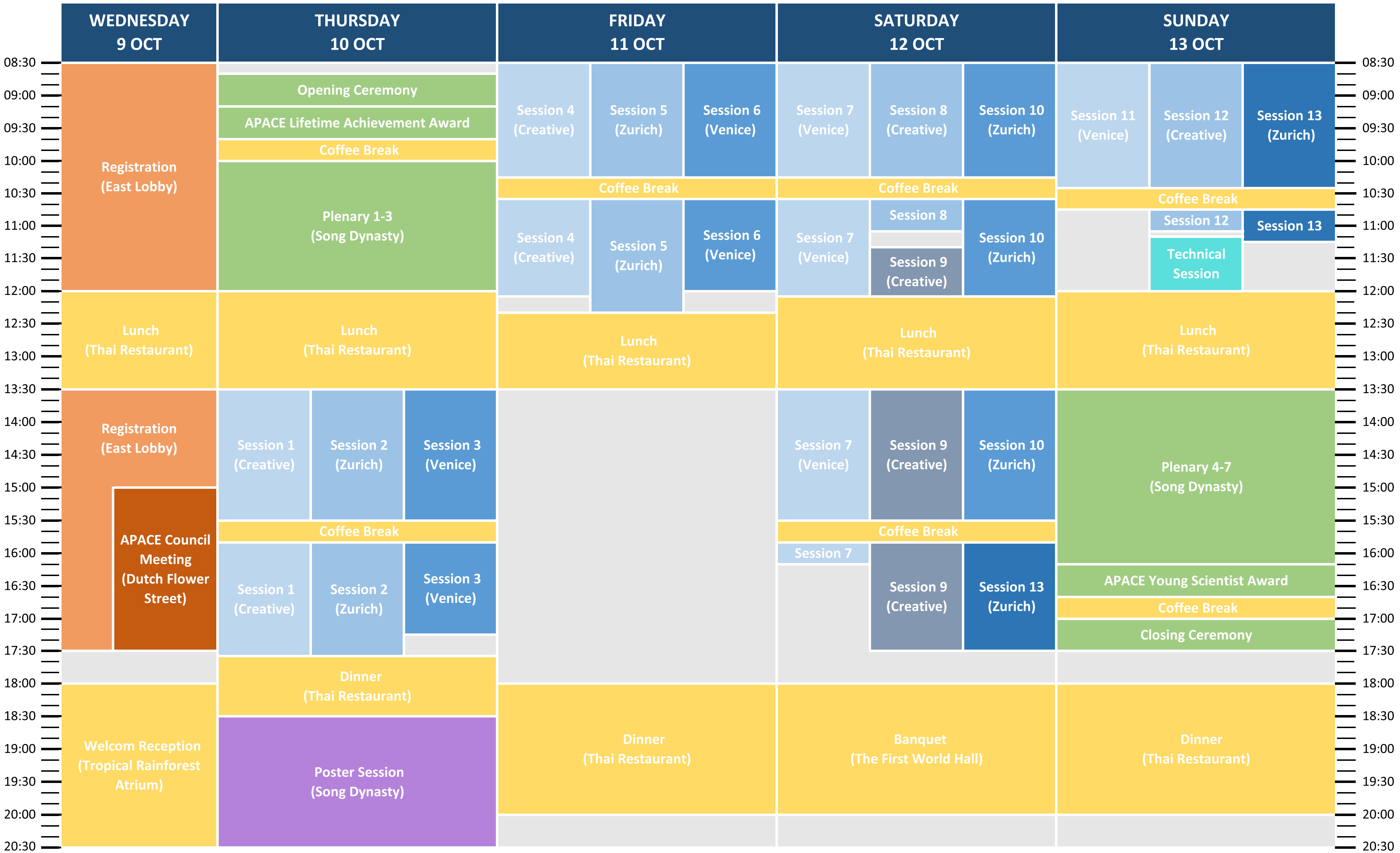
The Registration and Information Desk is located at the East Lobby and will be operational during the following hours:

Wednesday	9 Oct 2019	0830–2100
Thursday	10 Oct 2019	0900–1300
Friday	11 Oct 2019	0900–1300
Saturday	12 Oct 2019	0900–1300



酒店平面图

❶	中国渔村	China Fishing Village
❷	渔人码头	Fisher Whart
❸	乐园厅	Paradise Hall
❹	龙泉山	Longquan Mountain
❺	荷兰花街	Dutch Flower Street
❻	山里人家	Submontane Village
❼	创意城	Creative City
❽	苏黎士	Zurich
❾	威尼斯	Venice
❿	宋城厅	Song Dynasty
⓫	第一世界厅	The First World Hall
⓬	贵宾厅	VIP Hall



WEDNESDAY 9 OCT

- Registration (East Lobby)
- Lunch (Thai Restaurant)
- Registration (East Lobby)
- APACE Council Meeting (Dutch Flower Street)
- Welcom Reception (Tropical Rainforest Atrium)

THURSDAY 10 OCT

- Opening Ceremony
- APACE Lifetime Achievement Award
- Coffee Break
- Plenary 1-3 (Song Dynasty)
- Lunch (Thai Restaurant)
- Session 1 (Creative)
- Session 2 (Zurich)
- Session 3 (Venice)
- Coffee Break
- Session 1 (Creative)
- Session 2 (Zurich)
- Session 3 (Venice)
- Dinner (Thai Restaurant)
- Poster Session (Song Dynasty)

FRIDAY 11 OCT

- Session 4 (Creative)
- Session 5 (Zurich)
- Session 6 (Venice)
- Coffee Break
- Session 4 (Creative)
- Session 5 (Zurich)
- Session 6 (Venice)
- Lunch (Thai Restaurant)
- Dinner (Thai Restaurant)

SATURDAY 12 OCT

- Session 7 (Venice)
- Session 8 (Creative)
- Session 10 (Zurich)
- Coffee Break
- Session 7 (Venice)
- Session 8
- Session 9 (Creative)
- Session 10 (Zurich)
- Lunch (Thai Restaurant)
- Session 7 (Venice)
- Session 9 (Creative)
- Session 10 (Zurich)
- Coffee Break
- Session 7
- Session 9 (Creative)
- Session 13 (Zurich)
- Banquet (The First World Hall)

SUNDAY 13 OCT

- Session 11 (Venice)
- Session 12 (Creative)
- Session 13 (Zurich)
- Coffee Break
- Session 12
- Technical Session
- Session 13
- Lunch (Thai Restaurant)
- Plenary 4-7 (Song Dynasty)
- APACE Young Scientist Award
- Coffee Break
- Closing Ceremony
- Dinner (Thai Restaurant)

Plenary 1

October 10 (Thu.) Room: Song Dynasty

08:40-09:10	**Opening Ceremony**
09:10-09:40	**APACE Lifetime achievement award** Back to the future: bugs, lures and toilet paper **Eric Jang**
09:40-10:00	**Coffee Break**
10:00-10:40	**Plenary 1** How do native plants simultaneously manage complicated ecological interactions? **Ian T. Baldwin**
10:40-11:20	**Plenary 2** Biological production of moth pheromones in plant and cell factories **Christer Löfstedt**
11:20-12:00	**Plenary 3** Functional integration of plant secondary metabolites across three trophic levels **Matthias Erb**

Plenary 2

October 13 (Sun.) Room: Song Dynasty

13:30-14:10	**Plenary 4** New developments in our understanding of the use and misuse of herbivore-induced plant volatiles in insect-plant interactions **Ted Turlings**
14:10-14:50	**Plenary 5** Unexpected origins of defensive compounds in animals **Naoki Mori**
14:50-15:30	**Plenary 6** Sex determination genes and sexual behavior of silkworm **Yongping Huang**
15:30-16:10	**Plenary 7** Something old, something new: caterpillar movement and feeding behaviour on whole plants-traversing a treacherous landscape **Myron Zalucki**
16:10-16:40	**APACE Young Scientist Award** Lepidopteran chemosensory gene repertoires: annotation, evolutionary and functional perspectives **Naiyong Liu**
16:40-17:00	**Coffee Break**
17:00-17:30	**Closing Ceremony**

Session 1

Understanding the mechanism and behavioural ecology of olfaction for improved control of fruit fly pests

October 10 (Thu.) Room: Creative City

Organizer	**Paul Cunningham** and **Alvin Kah-Wei Hee**
13:35-13:55	**Keynote Lecture** Field evaluation of a new attract-and-kill trap for mated female Queensland fruit fly **Paul Cunningham**
13:55-14:15	**Keynote Lecture** Scents from the wild: The vinegar fly *Drosophila suzukii* prefers volatiles from wild than cultivated blueberries **Cesar Rodriguez-Saona**
14:15-14:35	**Keynote Lecture** An improved understanding on male fruit fly-phytochemical lure interactions benefitting fruit fly control **Suk Ling Wee**
14:35-14:55	**Keynote Lecture** Functional characterization of olfactory receptors in Dacini fruit flies (Diptera: Tephritidae) that respond to semiochemicals **Hajime Ono**
14:55-15:15	**Keynote Lecture** Identification of the odorant receptors responsible for methyl eugenol perception in the oriental fruit fly, *Bactrocera dorsalis* **Li Xu**
15:15-15:30	Proteome-transcriptome analysis of maxillary palp and antenna of male Oriental fruit fly following strong attraction to methyl eugenol **Anna Chui-Ting Chieng**
15:30-15:50	**Coffee Break**
15:50-16:05	Cross-species comparison of fruit fly olfactory sensitivity to host fruits as a way of exploring new attractive blends **Vincent Jacob**
16:05-16:20	Monitoring individual fruit fly responses to attractants using radio frequency identification **Matthew Siderhurst**
16:20-16:35	Olfactory learning and memory in the polyphagous frugivore, *Bactrocera tryoni* **Rehan Silva**
16:35-16:50	Olfactory cues of predators influence vital life processes of *Bactrocera tryoni* **Vivek Kemparaju**
16:50-17:05	Identification and field evaluation of male-produced sex pheromone of *Neoceratitis asiatica* (Becker) **Yan Liu**
17:05-17:20	Gut microbiota affects development and olfactory behavior in *Drosophila melanogaster* **Huili Qiao**
17:20-17:35	Identification of odorant binding proteins which binding with methyl eugenol and their function research in *Bactrocera dorsalis* **Xiaofeng Chen**

Session 2
Plant-mediated insect interactions

October 10 (Thu.) Room: Zurich

Organizer **Ted Turlings** and **Yunhe Li**

13:30-14:00	**Keynote Lecture** Effects of crop nutrition on anti-herbivore resistance **Rensen Zeng**
14:00-14:15	*Diabrotica virgifera virgifera* females can sequester multiple plant toxins to protect their eggs against predators **Carla Arce**
14:15-14:30	Plant volatiles as mate finding cues for insects **Hao Xu**
14:30-14:45	Volatiles from un-infested rice plants enhance the spread of the major rice pest, brown planthopper *Nilaparvata lugens* Stål **Jingjiang Zhou**
14:45-15:00	Chemical responses in plant-insect interaction of plant gall **Shihong Luo**
15:00-15:15	Understanding the dynamics of wheat chemical and physical defense mechanisms against aphids **Vered Tzin**
15:15-15:30	Ecological and biochemical mechanisms that determine the preference of *Nilaparvata lugens* for Bt over nonBt rice plants **Yunhe Li**
15:30-15:50	**Coffee Break**
15:50-16:05	Root herbivores require intact carbon dioxide and sugar perception for optimal foraging **Ricardo Machado**
16:05-16:20	Feeding preferences and taste responses to plant substances in two species of Helicoverpa caterpillars **Qingbo Tang**
16:20-16:35	Detoxification of Brassicaceae glucosinolates in multi-trophic interactions **Ruo Sun**
16:35-16:50	Aphid-borne viral spread is enhanced by virus-induced accumulation of plant reactive oxygen species **Yucheng Sun**
16:50-17:05	What omnivores don’t eat: nonconsumptive ecological effects of phytophagy by Macrolophus pygmaeus **Xiaoning Zhang**
17:05-17:20	Anabolism of homoterpenes involved in indirect defense of *Gossipium hirsutum* **Danfeng Liu**
17:20-17:35	ER-body system in plant is involved in production of volatile compounds to suppress feeding motivation of insect: a model study using *Arabidopsis thaliana* and *Phormia regina* **Mamiko Ozaki**

Session 3
Signaling and perception in plant-herbivore interactions

October 10 (Thu.) Room: Venice

Organizer	**Matthias Erb** and **Yonggen Lou**
13:30-13:55	A ligand-receptor pair for plant recognition of orally secreted elicitor peptides **Adam Steinbrenner**
13:55-14:15	The systemin receptor SYR1 enhances resistance of tomato against herbivorous insects **Lei Wang**
14:15-14:35	Integration of herbivore-induced plant volatiles into plant defense and resistance **Lingfei Hu**
14:35-14:55	Getting tuned: Understanding specificity in plant volatile signaling **Silke Allmann**
14:55-15:15	The oriental armyworm (*Mythimna separata*) feeding induces local and systemic defense responses within and between maize leaves **Jinfeng Qi**
15:15-15:35	Chemical cues linked to risk: plants and insect herbivores respond to chemical cues from entomopathogenic nematodes **Anjel Helms**
15:35-15:50	**Coffee Break**
15:50-16:15	Insights from the JA signaling cascade and down-stream defense responses into herbivore perception through AMF networks in the *Nicotiana attenuata* system **Ian Baldwin**
16:15-16:35	Expressing *OsMAPKb* increases rice resistance to BPH but accelerate rice senescence **Xiaoli Liu**
16:35-16:55	Systemic stomatal closure induced by herbivores is dependent on jasmonic acid-mediated synthesis of H_2O_2 in guard cells **Yibin Lin**
16:55-17:15	Solar UV-B radiation and ethylene play a key role in modulating effective defenses against herbivore insects in field-grown soybean **Jorge Zavala**

Session 4
Molecular mechanism of pheromone detection in insects

October 11 (Fri.) Room: Creative City	
Organizer	**Chenzhu Wang** and **Shuanglin Dong**
08:30-09:00	**Keynote Lecture** A novel lineage of pheromone receptors for sex communication in moths **Jacquin-Joly Emmanuelle**
09:00-09:15	CRISPR/Cas9 mediated gene knockout reveals different contribution of three PBP genes in female sex pheromone perception in *Spodoptera litura* **Shuanglin Dong**
09:15-09:30	An odorant receptor mediates pheromone to regulate locust density **Long Zhang**
09:30-09:45	Genome-wide identification and functional study of chemosensory genes in three notorious rice planthoppers **Peng He**
09:45-10:00	Physicochemical basis and comparison of two type II sex pheromone components binding with pheromone-binding protein 2 from tea geometrid, *Ectropis obliqua* **Hongliang Li**
10:00-10:15	Identification and chemoreception of sex pheromone in *Athetis lepigone* **Yanan Zhang**
10:15-10:35	**Coffee Break**
10:35-11:05	**Keynote Lecture** Olfactory coding of sex pheromone blends in Heliothine moth species **Chenzhu Wang**
11:05-11:20	Putative neural network within a S. basiconoica for nestmate and non-nestmate CHC discrimination in the Japanese carpenter ant: The ultrastructure and mathematical simulation **Mamiko Ozaki**
11:20-11:35	Identification and function researches of Dendrolimus specific pheromone receptor genes **Sufang Zhang**
11:35-11:50	Comparison of Chemosensory Receptor Genes in the Antennae Transcriptome of *Sirex noctilio* and *S. nitobei* (Hymenoptera: Siricidae) **Weiwei Wu**
11:50-12:05	Identification and functional study of the pheromone receptors in *Apolygus lucorum* **Yang Liu**

Session 5
Chemical information flow among organisms

October 11 (Fri.) Room: Zurich

Organizer	**Li Chen** and **Wei Xu**
08:30-09:00	**Keynote Lecture** Info-chemical flows among plants, flies and microbial communities of larval growth and oviposition environments **Jerry Zhu**
09:00-09:15	Neighbours matter: Community effects on plant-volatile emissions **Andrea Clavijo-McCormick**
09:15-09:30	A practical technique for EAG recording from lamellated antenna of scarab beetle **Li Chen**
09:30-09:45	Volatile production by banana plants infected with *Fusarium oxysporum* f.sp. *cubense* **R Andrew Hayes**
09:45-10:00	Provisioning pheromone: Parents regulate larval begging by the pheromone in a burying beetle **Yuki Mitaka**
10:00-10:15	Regulation of aphid population and distribution on host plants by tending ants: benefits to mutualistic insects with a sacrifice of host plants **Tian Xu**
10:15-10:35	**Coffee Break**
10:35-11:05	**Keynote Lecture** Aposematic signal and antipredator defense in locusts **Jin Ge**
11:05-11:20	Detection of chemical signals from host and non-host organisms in insects **Kye Chung Park**
11:20-11:35	Mechanism of methyl eugenol perception in *Bactrocera dorsalis* : A molecular approach **Hongbo Jiang**
11:35-11:50	A phylogenomics approach to characterizing sensory neuron membrane proteins (SNMPs) in Lepidoptera **Huijie Zhang**
11:50-12:05	Transcriptome analysis of priming defense between and within *Brassica nigra* **Jichang Zhang**
12:05-12:20	Responses of *Tribolium castaneum* to infested wheat and aggregation pheromone **Wei Xu**

Session 6
Chemical ecology of forest ecosystem

October 11 (Fri.) Room: Venice

Organizer	**Zhen Zhang** and **Qinghe Zhang**
08:30-08:55	**Keynote Lecture** Host selection in bark beetle *Ips typographus* : Understanding anti-attractants like NHV and their possible use for mitigation in the Anthropocene **Fredrik Schlyter**
08:55-09:15	Bacterial volatile ammonia regulates the consumption sequence of D-pinitol and D-glucose in a fungus associated with an invasive bark beetle **Min Lu**
09:15-09:35	Facile and efficient syntheses of (11Z, 13Z)-hexadecadienal and its derivatives key sex pheromone and attractant components of notodonfidae **Fu Liu**
09:35-09:55	Phylogeographical analysis of *Dendrolimus punctatus* based on the whole mitochondrial DNA and ITS markers **Huicong Du**
09:55-10:15	Functional analyses of chemosensory proteins in the apple buprestid beetle *Agrilus mali* **Deguang Liu**
10:15-10:35	**Coffee Break**
10:35-11:00	**Keynote Lecture** Mating behavior and attractiveness of male cuticle extracts based on electroantennogram and behavioral assay in *Sirex noctilio* Fabricius **Pengfei Lu**
11:00-11:20	Molecular and functional characterization of candidate sex pheromone receptors in Dendrolimus punctatus Walker **Sifan Shen**
11:20-11:40	Two trace volatiles released from living adult of *Aromia bungii* Faldermann (Coleoptera: Cerambycidae) as minor component of pheromone **Jianrong Wei**
11:40-12:00	Chemical ecological mechanism of conexistence among three *Tomicus* species **Zhen Zhang**

Session 7
From basic science in chemical ecology to commercial pest control products: alternative semiochemical-based insect pest management

October 12 (Sat.) Room: Venice

Organizer	**Jerry Zhu, Yinzhong Cui** and **Jianyu Deng**
08:30-09:00	**Keynote Lecture** A to Z: The journey from synthesis to global commercialization of semiochemicals **Lacey Cole**
09:00-09:15	Rescue® dual bait technology for common household ants **Qinghe Zhang**
09:15-09:30	Identification of the sex pheromone of the spherical mealybug *Nipaecoccus viridis* **Anat Levi-Zada**
09:30-09:45	Kairomone A&K for adult noctuid control **Stephen Sexton**
09:45-10:00	Use of attractants in housefly baits **Dangsheng Liang**
10:00-10:15	Novel repellent compounds for managing German cockroach **Xiaojie Zhou**
10:15-10:35	**Coffee Break**
10:35-10:50	Functional study of *CYP4G19* in the German cockroach, *Blattella germanica* (L.) **Yongliang Fan**
10:50-11:05	Application of pheromones to monitoring for stored product insects **Rikiya Sasaki**
11:05-11:20	ATP detection and its role as phagostimulant in blood feeders **Isabel Ortega Insaurralde**
11:20-11:35	Development of spotted wing drosophila commercial lure and its use for management **Dong Cha**
11:35-11:50	Pheromone mating disruption development in Chinese integrated pest management: Perspectives in the last decade and prospects in next 10 years **Yinzhong Cui**
11:50-12:05	Spatial repellent, antifeedant and oviposition deterrent activity of coconut oil fatty acids and their methyl ester derivatives against biting flies **Gwang Hyun Roh**
12:05-13:30	**Lunch**
13:30-13:45	From Microscopic Characteristics of Antennal Sensilla to Enhancement of Field Attractiveness for the Management of Bean Bug, *Riptortus pedestris* **Chung Gyoo Park**
13:45-14:00	Development new commercial products for trapping insect pests based on insect pheromones and LED lights **Jianyu Deng**
14:00-14:15	Development and evaluation of food attractant for grain pest control **Maidinai Sabier**
14:15-14:30	Investigating various attract-and-kill prototypes for their potential control of *Spotted Wing Drosophila* **Juan Huang**
14:30-14:45	Efficacy of volatile infochemicals from lavenders regulating behaviour of tea green leafhopper and field application **Cheng Pan**

14:45-15:00	Production of moth pheromone precursors in *Nicotiana* spp. by *Agrobacterium*-mediated transformation **Yihan Xia**
15:00-15:15	Yeast-beetle interactions and potential insights into the control of *Carpophilus* beetles in stone fruits and almonds **Farrukh Baig**
15:15-15:30	Semiochemicals for area-wide pest management **Agenor Mafra-Neto**
15:30-15:50	**Coffee Break**
15:50-16:05	Development of natural product-based repellents and attractant-baited technologies against blood-sucking insects **Jerry (Junwei) Zhu**

Session 8
Manipulating indirect plant defences to improve pest management: can it be done?

October 12 (Sat.) Room: Creative City

Organizer	**Myron Zalucki, Michael J. Furlong, Yaobin Lu** and **Paul Cunningham**
08:30-09:00	**Keynote Lecture** Manipulating indirect plant defences to improve pest management: can it be done? **Zalucki MP**
09:00-09:15	Insect effectors in plant-insect interactions and their potential applications **Yingbo Mao**
09:15-09:30	Host plants enhance the parasitism efficiency of a solitary egg parasitoid by altering their volatile cues **Chengzhe Li**
09:30-09:45	Evolution of plant defense resistance in natural enemies of an arthropod herbivore **Xi Zhang**
09:45-10:00	Can bottom-up effects be manipulated to enhance pest control? **Peng Han**
10:00-10:15	Organic fertilizer promotes wheat aphid control: from local to landscape scale effects **Shimin Gu**
10:15-10:35	**Coffee Break**
10:35-10:50	Can prey to predator ratio be considered a criterion for successful bio-control in field? **Zhaozhi Lu**
10:50-11:05	The control of DBM with *Diadegma semiclausum* in practice in Yunnan province? **Zhenyu Li**

Session 9
Innovative insect pest management with natural products

October 12 (Sat.) Room: Creative City

Organizer	Aijun Zhang, Jian Chen, Dong Cha and Manqun Wang
11:20-11:50	**Keynote Lecture** Pyridine alkaloids in imported fire ants **Jian Chen**
11:50-12:05	Applying chemical ecology to manage insect pests of blueberries **Cesar Rodriguez-Saona**
12:05-13:30	**Lunch**
13:30-13:45	Discovery of repellents for managing spotted wing drosophila **Dong Cha**
13:45-14:00	Potential use of piperonyl butoxide in controlling Oriental fruit fly **Alvin Kah Wei Hee**
14:00-14:15	The fruit fly attractant raspberry ketone trifluoroacetate: When being the most attractive molecule isn't enough **Matthew Siderhurst**
14:15-14:30	Preparation of polymeric microspheres contain insecticide and attractant and their control effects on *Rhagoletis batava obseuriosa* adults **Jianrong Wei**
14:30-14:45	Pheromone-based attract-and-kill of cocoa pod borer **Aijun Zhang**
14:45-15:00	Particle-transport behaviors of red imported fire ants (Hymenoptera: Formicidae) in response to the repellent surfaces **Cai Wang**
15:00-15:15	The defense mechanism of the ghost ant *Tapinoma melanocephalum* against the red imported fire ant *Solenopsis invicta* **Qingxing Shi**
15:15-15:30	Cucumber and bitter melon extracts as ant repellents **Matan Shelomi**
15:30-15:50	**Coffee Break**
15:50:16:05	A defense protein MLX56 found in mulberry latex: Roles in mulberry-silkworm interaction, unique mode of function, and application to pest management **Kotaro Konno**
16:05-16:20	Correlation analysis between the shoot damages and trap catches of *Tomicus minor* Hartig in the *Pinus yunnanensis* forest **Xiangbo Kong**
16:20-16:45	Significant role of the maxillary palps in the olfactory communication of insects **Kye Chung Park**
16:45-17:00	Herbivore feeding and exogenous MeJA induced terpenoid defense in *Pinus massoniana* **Ruixu Chen**
17:00-17:15	Vanillin as a bioactive compound from resistant tomato root exudates affects *Meloidogyne incognita* infection **Tongtong Liu**
17:15-17:30	Isolation and identification of the aggregation pheromone in *Megalurothrips usitatus* (Thysanoptera: Thripidae) **Xiaowei Li**

Session 10
General chemical ecology

October 12 (Sat.) Room: Zurich

Organizer	**Junji Takabayashi, Shigeru Matsuyama, Xiaoling Sun, Koji Noge** and **Fengming Yan**
08:30-08:45	Response of gut-associated bacteria to alpha-pinene of *Ips typographus* **Jiaxing Fang**
08:45-09:00	A collaborative intrusion mechanism between pine wood nematode, pine sawyer beetle and blue stain fungi **Lilin Zhao**
09:00-09:15	Diversity of ascarosides signaling in Pristionchus nematodes **Chuanfu Dong**
09:15-09:30	Identification and field evaluation of the sex pheromone of *Orthaga achatina* (Lepidoptera: Pyralidae) **Qi Yan**
09:30-09:45	Effect of intra- and inter-specific exposure of sex pheromone on adult reproductive performance of *Helicoverpa armigera* and *H. assulta* **Guohui Yuan**
09:45-10:00	Enhancement of copulation by dim red light during scotophase in the yellow peach moth, *Conogethes punctiferalis* **Wei Xiao**
10:00-10:15	Romantic leaves: plant volatiles stimulated mating behavior by modulating vibrational communication in leafminers **Jin Ge**
10:15-10:35	**Coffee Break**
10:35-10:50	Study on pheromone binding proteins and active components of contact pheromone in *Liposcelis entomophila* **Yujie Lu**
10:50-11:05	Characterization of nine odorant binding proteins in *Diaphorina citri* **Xiaoqiang Liu**
11:05-11:20	Rice stripe virus infection regulates olfactory behavior of the small brown planthopper (SBPH) *Laodelphax striatellus* **Fang Liu**
11:20-11:35	Neural basis underlying pollinator's decoding of floral scents **Binyan Lu**
11:35-11:50	Chrysomelidae discriminates host plants by tarsal gustation **Shun Yosano**
11:50-12:05	A cyanogenic glucoside, linamarin, regulates differential oviposition on white clover by coliadine butterflies, *Colias erate* and *Eurema mandarina* **Hisashi Omura**
12:05-13:30	**Lunch**
13:30-13:45	Induced resistance of oviposition of Micromelalopha sieversi on two clones of Populus section *Aigeiros* **Zhen Zhang**
13:45-14:00	Identification of leafhopper-induced tea plant volatiles and their attraction to parasitic mymarid wasps **Baoyu Han**

14:00-14:15	Impacts of CCYV-induced plant volatiles on behaviors of vector *Bemisia tabaci* **Fengming Yan**
14:15-14:30	Root feeding larvae increase their performance by inducing leaf volatiles that attract aboveground conspecific adults **Xiao Sun**
14:30-14:45	Identification, characterization and allelochemical induced expression of *CYP321A2* in *Helicoverpa zea* **Shengyun Li**
14:45-15:00	The cosmopolitan phytopathogen *Sclerotinia sclerotiorum* detoxifies defensive isothiocyanates in a Brassicaceae host plant **Jingyuan Chen**
15:00-15:15	Complex ecological impacts of the giant willow aphid invasion in New Zealand **Andrea Clavijo-McCormick**
15:15-15:30	Increasing flavonoids enhance the AM fungal colonization in an invasive plant **Baoliang Tian**

Session 11
Prof. Kenji Mori sensei: Great legendary chemical synthesis master and the first APACE president

October 13 (Sun.) Room: Venice

Organizer	**Shigefumi Kuwahara**, **Naoki Mori** and **Junwei Zhu**
08:30-08:45	**Opening talk** Prof. Mori, President Mori and the co-Founder of APACE **Jerry Zhu**
08:45-09:30	Pheromone synthesis with my mentor, Prof. Kenji Mori **Shigefumi Kuwahara**
09:30-10:15	Teachings of Prof. Mori sensei for scientists who work for a company **Rikiya Sasaki**
10:15-10:25	**Summary** Farewell Prof. Mori **Naoki Mori**
10:25-10:45	**Coffee Break**

Session 12
Plant-plant chemical interactions

October 13 (Sun.) Room: Creative City	
Organizer	Chuihua Kong, Tran Dang Xuan and Jianqiang Wu
08:40-08:55	Root exudate analysis of buckwheat and oat in the presence of redroot pigweed **Aurélie Gfeller**
08:55-09:10	The influence of peanut/maize intercropping on jasmonates biosynthesis and secretion of root and its physiological and molecular mechanism in improving peanut iron nutrition **Nanqi Wang**
09:10-09:25	The parasite *Cuscuta australis* with a streamlined genome mediates inter-plant systemic signals **Jianqiang Wu**
09:25-09:40	Structure and origin of phenolic compounds that mediate the signaling interactions of parasitic plants with host plants **Songkui Cui**
09:40-09:55	Molecular evidence of (-)-loliolide induced the production of defensive metabolites in plants **Leilei Li**
09:55-10:10	Potential control of paddy and invasive weeds by mimilactones A,B,E and 7-ketostigmasterol isolated from rice husk **Dang Xuan Tran**
10:10-10:25	Allelochemicals: promiseful sources of natural products with ecologically functions **Bo Qin**
10:25-10:45	**Coffee Break**
10:45-11:00	Antioxidant response mechanism of freshwater microalgae species to reactive oxygen species production: a mini review **Adamu Yunusa Ugya**

Session 13
Molecular chemical ecology

October 12 (Sat.) Room: Zurich	
Organizer	**Christer Löfstedt** and **Yongping Huang**
15:50-16:20	**Keynote Lecture** Functional conservation and divergence underscore the flexibility of Lepidoptera odorant receptors **Mengbo Guo**
16:20-16:32	Odorant receptor 25 is narrowly tuned to the floral volatile eugenol and methyleugenol attracting pollinator *Eupeodes corollae* **Bing Wang**
16:32-16:44	A gustatory receptor tuned to coumarin in the cotton bollworm *Helicoverpa armigera* **Yan Chen**
16:44-16:58	The locust odorant-binding protein *Lmig* OBP1 is involved in detection of host plant odorants **Jia Li**
16:58-17:10	Functional characterization of fructose gustatory receptors in *Plutella xylostella* and *Spodoptera litura* **Xiaolong Liu**
17:10-17:12	Functional characterization of odorant receptors in the moth *Eriocrania semipurpurella* : a comparison of results obtained with the *Xenopus oocyte* and HEK cell systems **Xiaoqing Hou**
17:12-17:24	An inhibitor for mating in cotton bollworm, *Helicoverpa armigera* **Qiuyan Chen**
October 13 (Sun.) Room: Zurich	
08:30-08:50	Characterization of DHCR24 orthologs in the phytophagous insect, *Bombyx mori* **Haruna Fujimori**
08:50-09:02	Comparison of different heterologous expression systems for studies of genes involved in moth pheromone biosynthesis **Baojian Ding**
09:02-09:22	Production of insect pheromone precursor in the oil crop *Camelina sativa* **Honglei Wang**
09:22-09:34	A cytochrome P450 from mustard leaf beetles hydroxylates geraniol, a key step in iridoid biosynthesis **Nanxia Fu**
09:34-09:54	Strigolactones activate defense against the stem-boring weevil *Trichobaris mucorea* via their interactions with jasmonates and auxin **Suhua Li**
09:54-10:06	Sterol composition analysis of the two-spotted crickets, *Gryllus bimaculatus* **Shinji Nagata**
10:06-10:18	Production of (Z)-11-hexadecenal by a metabolically engineered yeast **Yuguo Jiang**
10:25-10:45	**Coffee Break**
10:45-11:15	**Keynote Lecture** Semiochemical carrier proteins in ticks and mites **Paolo Pelosi**

Poster Session

October 10 (Thu.) Room: Song Dynasty

S01-P-01	A neuropeptide inhibits feeding behavior by modulating sweet chemosensory in the brown planthopper **Di Guo**
S01-P-02	Olfactory responses of the antennae and maxillary palps to parapheromone and plant volatile compounds in the striped fruit fly, *Bactrocera scutellata* **Hyun-Woo Oh**
S01-P-03	Identification and expression profile analysis of olfactory receptor gene in *Apriona germari* (Hope) **Jiali Qian**
S01-P-04	Ultrastructural observation of the antennae of the *Zele chlorophthalmus* **Linbo Xu**
S01-P-05	Sweet sensation inhibit texture discrimination in *Drosophila* egg-laying behaviour **Shunfan Wu**
S01-P-06	Identification of Volatile Compounds from Rectal Gland and Headspace Extracts of Female *Bactrocera correcta* **Xiuge Zhang**
S01-P-07	A mechanosensitive channel modulates egg-laying in the brown planthopper *Nilaparvata lugens* and the fruit fly *Drosophila melanogaster* **Yijie Zhang**
S02-P-08	The involvement of an herbivore-induced acyl-CoA oxidase gene, *CsACX1* , in the synthesis of jasmonic acid and its expression in flower opening in tea plant (*Camellia sinensis*) **Shenglong Chen**
S02-P-09	*Bt* rice plants may protect neighboring non-*Bt* rice plants against the striped stemborer *Chilo suppressalis* **Xiaoyun Hu**
S03-P-10	Screening of chemical cues during the host searching process of weevil *Curculio chinensis* **Hualong Qiu**
S03-P-11	Tea geometrid-induced biosynthesis of polyphenol oxidase is regulated by the jasmonate pathway in tea plant **Jin Zhang**
S03-P-12	Molecular dissection of early defense signaling underlying volatile-mediated defense regulation and herbivore resistance in rice **Meng Ye**
S03-P-13	An intrinsically disordered protein regulates the resistance in rice to brown planthopper (*Nilaparvata lugens*) **Peng Kuai**
S03-P-14	The feeding preferences of *Apolygus lucorum* (Heteroptera: Miridae) by the PCR-based analysis of plant DNA **Qian Wang**
S03-P-15	Chemical mechanisms of the preferential attraction of the sugarcane stem borer, *Chilo sacchariphagus* , to the trap crop *Erianthus arundinaceus* **Vincent Jacob**

S03-P-16	The molecular cloning and characterization of *CsMYC2* , a bHLH transcription factor from tea plants (*Camellia sinensis*) **Xin Zhang**
S03-P-17	Functional characterization of herbivore resistance-related gene *OsJMJ28* in rice **Yuebai Zhang**
S04-P-18	Various bee pheromones binding affinity, exclusive chemosensillar localization, and key amino acid sites reveal the distinctive characteristics of odorant-binding protein 11 in the eastern honey bee, *Apis cerana* **Hongliang Li**
S04-P-19	Functional characterization of pheromone receptors in codling moth *Cydia pomonella* **Tian Ke**
S04-P-20	Sensilla trichodea-biased EoblPBP1 binds sex pheromones and green leaf volatiles in a geometrid moth pest *Ectropis obliqua* Prout that uses Type-II sex pheromones **Liang Sun**
S04-P-21	Functional differentiation of pheromone-binding proteins in *Hyphantria cunea* (Drury) **Longwa Zhang**
S04-P-22	Sensory neuron membrane protein 1 (SNMP1) reinforces receptivity of male *Helicoverpa armigera* (Lepidoptera: Noctuidae) to sex pheromone components **Shuai Liu**
S04-P-23	The evolution pattern of the production and processing of short chain cuticular pheromones in genus *Drosophila* **Wufan Zhang**
S05-P-24	Electroantennogram responses of *Diaphania caesalis* Walker (Lepidoptera: Pyralidae) to volatile matters elicit from *Artocarpus heterophyllus* Lam **Zheng Wang**
S06-P-25	Genotypic diversity interacts with predation risk to influence on arthropod richness, evenness and diversity in poplar plantation **Haibo Chen**
S08-P-26	The OsmiR396–OsGRF8–OsF3H-flavonoid pathway mediates resistance to the brown planthopper in rice (*Oryza sativa*) **Xiaofang Yang**
S09-P-27	Functional analysis of three olfactory protein genes in *Galeruca daurica* (Coleoptera: Chrysomelidae) by RNAi and electroantennography **Baoping Pang**
S09-P-28	Effects of jasmonic acid seed treatment on tobacco resistance to *Spodoptera litura* **Lei Wang**
S09-P-29	Study on the odorant binding proteins (OBPs) and odorant receptors (ORs) of *Bactrocera minax* **Qiong Zhou**
S09-P-30	Silicon inhibits the resistance of rice stem borer to chlorpyrifos **Rongrong Xue**
S09-P-31	The suppressing effect of leaf-radish living mulch on cabbage pests **So Nakano**
S09-P-32	JA-Ile-macrolactones induce both herbivore *Ectropis obliqua* and pathogen *Colletotrichum camelliae* resistance responses of *Camellia sinensis* **Songbo Lin**
S09-P-33	Cuticular hydrocarbon of the Japanese carpenter ant is useful in pest management on the Argentine ant (*Linepithema humile*) **Tomoya Sakita**

S10-P-34	Differential host choices of *Helicoverpa armigera* and *H. assulta* to tomato volatiles **Guohui Yuan**
S10-P-35	Rhizosphere responses to environmental conditions in *Radix pseudostellariae* under continuous monoculture regimes **Hongmiao Wu**
S10-P-36	The morphological development of antennal sensilla and corresponding expression of OBP3/7/9 after emergence in the grain aphid *Sitobion miscanthi* **Jia Fan**
S10-P-37	Development of regional attractants for *Spodoptera frugiperda* (Smith) based on sex pheromones and its application **Jianqing Dai**
S10-P-38	Detoxification of plant chemical defenses is an important virulence factor for the cosmopolitan phytopathogen *Sclerotinia sclerotiorum* **Jingyuan Chen**
S10-P-39	Electroantennographic responses of *Artona martini* Efetov (Lepidoptera: Zygaenidae) to its dorsal abdomine extracts **Junheon Kim**
S10-P-40	Host recognition of the cabbage bug, *Eurydema rugosa* (Hemiptera: Pentatomidae), and its sucking stimulant(s) from the host plant, *Brassica juncea* var. cernua (Brassicaceae) **Koji Noge**
S10-P-41	Pheromones, plant-gall allelochemicals, and division of labor in a social aphid **Matsuyama Shigeru**
S10-P-42	Two chemical defensive lines in leaf beetles: P450s are involved in the biosynthetic pathways **Nanxia Fu**
S10-P-43	Responses of nutrient elements in red clover to aluminum stress **Quan Liu**
S10-P-44	The relationship between soil nutrient elements and chemical constituents of *Apocynum venetum* L. **Quan Liu**
S10-P-45	Comparative efficacy of the entomopathogenic fungus, *Beauveria bassiana* (Bals.) Vuill. and *Metarhizium anisopliae* (Metchnikoff) Sorokin on larval mortality, enzyme inhibition of *Spodoptera litura* Fab. and their non-target activity against *Eudrilus eugeniae* Kinb **Sengodan Karthi**
S10-P-46	Direct and indirect modification of *Bemisia tabaci* feeding behavior by *Cucurbit chlorotic yellows virus* **Shaohua Lu**
S10-P-47	Effects of Volatile on the Feeding and *Mating Behaviors* of *Sitophilus zeamais* and *Sitophilus oryzae* **Shaohua Lu**
S10-P-48	Effects of salicylic acid concentration and post-treatment time on the direct and systemic defense responses in maize (*Zea mays* L.) after exogenous foliar application **Xiaoyi Wang**
S10-P-49	Microbial community structure and its temporal changes in *Panax ginseng* C.A. Maye rhizospheric soils monocultured for different years **Xuesong Zhao**
S10-P-50	No detrimental effects of Bt maize in aphid-ladybeetle systems **Yinghua Shu**

S10-P-51	Pathogenicity of the Fungus *Isaria fumosorosea* Strain (Ifu13a) against the aphid Aphis gossypii and on the predator *Harmonia axyridis* **Yinyin Ge**
S10-P-52	Effects of exogenous jasmonic acid on leaf defense response and expression profile of Bt and conventional maize seedlings **Yuanjiao Feng**
S10-P-53	Seed soaking with sodium silicate primes salt tolerance of rice seedlings without physiological cost **Cuicui Xu**
S12-P-54	Nutrient-induced shifts in fine roots architecture reflect alternate root foraging strategies in *Cunninghamia lanceolata* **Peng Wang**
S12-P-55	Behavioral, physiological and molecular responses to cadmium in the Asian corn borer, *Ostrinia furnacalis* **Hongyi Wei**
S13-P-56	Diterpenoids from the roots of *Lonicera macranthoides* **Hui Lyu**
S13-P-57	Odorant receptors for toxicants in *Ostrinia furnacalis* **Jie Yu**
S13-P-58	Research progress on insect ionotropic receptors **Jinmeng Guo**
S13-P-59	Cloning and expression of α-farnesene synthase gene from tea plant **Mengxin Wang**
S13-P-60	Identification of olfactory genes and functional analysis of GOBP2 in *Clostera restitura* **Tianzi Gu**
S13-P-61	Neuropeptides in the brain of adult male cotton bollworm and their expressions at different ages **Wei Liu**
S13-P-62	Odorant binding protein and chemosensory protein genes in *Cacopsylla chinensis* (Hemiptera: Psyllidae) **Yanan Zhang**
S13-P-63	Transcriptome analysis of sex pheromone glands in *Mythimna separate* (Walker) (Lepidoptera: Noctuidae) **Yilu Feng**
S13-P-64	Identification and Sex-biased Profiles of Candidate Olfactory Genes in the Antennal Transcriptome of the Parasitoid Wasp *Cotesia vestalis* **Yipeng Liu**
S13-P-65	Mouthparts enriched odorant binding protein AfasOBP11 plays a role in the gustatory perception of *Adelphocoris fasciaticollis* **Zibo Li**
S13-P-66	The identification, expression profile and functional analysis of chemosensory genes in legs of *Apolygus lucorum* (Hemiptera: Miridae) **Zibo Li**

Technical Session

October 13 (Sun.) Room: Creative City	
11:10-11:30	纳米孔测序技术及其最新应用进展 **毛凌峰博士（宝诚生物）**
11:30-11:45	蛋白质组学及蛋白修饰组学在植物病虫害领域的应用与研究策略 **胡香静博士（景杰生物）**
11:45-12:00	PCR仪再创新–莫纳生物国产PCR逆袭之作 **宋南（柏嘉生物）**

A-01

Back to the future: bugs, lures and toilet paper

Eric Jang

Fruit Fly Systems Applied Technologies (USDA-ARS-retired)

It is indeed and honor to be selected for the APACE lifetime achievement award by the society. Before I deliver my talk I want to thank all of you for participating in APACE activities and supporting the society over the years. As the 6th person to receive the award I follow in the shadows of 5 truly outstanding recipients (Boo, Mori, Du, Tan, Nishida) and 10 current and past presidents (and councilors) who helped shape the society is it is today.

My talk today is a bit of a retrospective on my scientific career and the eccentric thoughts, ideas and motivations that shaped it. As I look “back” at my career, I see no outstanding research discoveries but life journey from a “student” to a “leader” has been truly satisfying. I especially valued the interaction with fellow research colleagues and perhaps at times unconventional approaches to research problems. My journey did not start or stop only in the field of chemical ecology but it has been a large part of my career. For that I must acknowledge the technical support staff, post-docs and colleagues who made me look better that I was. USDA-ARS was not a perfect job but by maneuvering through the various obstacles and learning how to manage up I was able to achieve a satisfying career. The take home message is to embrace the opportunities you have in the position you occupy, identify realistic goals and objectives, take time to enjoy the benefits of being independent in thought and embrace collaborations with colleagues who can enhance your career.

A-02

Lepidopteran chemosensory gene repertoires: annotation, evolutionary and functional perspectives

Naiyong Liu[a], Shuanglin Dong[b], Wei Xu[c], Alisha Anderson[d]

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[d]*CSIRO Health & Biosecurity, Black Mountain, ACT 2601, Australia*

Lepidoptera, containing valuable economic insects, destructive agricultural and forestry pests, is the second largest order of insects and is composed of moths and butterflies. Their chemoreception is triggered through chemosensory-related gene families (OR, odorant receptor; IR, ionotropic receptor; SNMP, sensory neuron membrane protein and AOX, aldehyde oxidase). To date, genomes of over 50 lepidopteran species are available. Based on such numerous data, here we characterize these four gene families using manual curation, expression profiles, phylogeny and functional experiments. Totally 1931 IRs (1118 in 28 moths: 996 new and 813 in 24 butterflies: 755 new), 3140 ORs (1783 in 24 moths: 1193 new and 1357 in 21 butterflies: 1227 new), 156 SNMPs (84 in 28 moths: 45 new and 72 in 24 butterflies: 66 new) and 306 AOXs (139 in 13 moths: and 154 in 15 butterflies: 150 new) are identified. The phylogeny, expression profiles and gene structure allow us to classify lepidopteran IRs into three sub-families: antennal (A-IRs), divergent (D-IRs) and Lepidoptera-specific (LS-IRs) IRs; the ORs into three sub-families: odorant coreceptor (ORco), pheromone receptors (PRs) and general ORs; the SNMPs into three classes: SNMP1-3; and the AOXs into six classes: AOX1-6. Our study explores lepidopteran four chemosensory genes using a manually curated approach coupled with phylogeny, gene organization, expression profiling and functional studies. Our results have provided an extensive resource for investigating chemosensory genes of Lepidoptera, and meanwhile allow for target experiments to identify olfactory, gustatory and reproductive candidates for mating, oviposition and feeding behaviors of adults and larvae.

P-01

How do native plants simultaneously manage complicated ecological interactions?

Ian T. Baldwin

MPI for Chemical Ecology, Dept. of Molecular Ecology, Jena, Germany, 07745

Thanks to the long-term patient funding of the Max Planck Society, we have developed a fire-chasing native tobacco plant, *Nicotiana attenuata*, which grows in the Great Basin Desert, into a model for the study of plant-ecological interactions, particularly those biotic interactions that dominate the primordial agricultural niche. By training students in the lost art of natural history discovery, we have used the plant's natural history interactions to phenotype transformed and recombinant inbred lines (RILs) of this plant, at two nature preserves in the plant's native habitats, to understand the function of genes required for survival in nature. For the past two decades, the research program has used a reverse genetics approach following an 'ask the plant' paradigm to select genes for silencing experiments and field work. This talk will describe how the Department is preparing to use unbiased forward genetics wedded with unbiased metabolomics and unbiased natural history-based field biology using sentinel insects, microbes and metabolites to understand the genetics behind the management of complex ecological interactions. The over-arching take-home message of this talk is lifted from the playbook of two founders of the discipline of Chemical Ecology (Thomas Eisner and Jerrold Meinwald): the irreplaceable value of nature preserves as laboratories for the study of gene function.

P-02

Biological production of moth pheromones in plant and cell factories

Christer Löfstedt

Department of Biology, Lund University, Sweden

The need for insect pheromones for pest control is increasing, as pheromones provide a very specific and environmentally benign form of insect pest management. Although synthetic insect pheromones can be produced in large volumes and used for mating disruption of insect pests to protect crops, the high cost of organic synthesis provides an obstacle for increasing the number of target insects and applications. Microbial cell factories as well as plants have been suggested as platforms for biological production of these high-value fine chemicals. Many moth sex pheromones are blends of modified fatty acids in the form of aldehydes, alcohols and acetates. The pathways for sex pheromone biosynthesis have been determined in many moth species and many of the key genes involved in these pathways have been characterized during the last three decades. By expressing the necessary and sufficient biosynthetic genes of insect and plant origin, we have made yeast and plants produce unsaturated fatty alcohols and acetates that are common moth pheromone compounds, as well as their fatty acid precursors. As a proof of concept, we first co-expressed a Δ11 desaturase and a FAR in the Brewer's yeast *Saccharomyces cerevisiae* and produced (*Z*)-11-hexadecenol*.* In the *OLEFINE* project (OLEaginous yeast platforms for FINE chemicals, http://olefine.eu/) we develop novel technology for inexpensive biological production of pheromones from *Yarrowia lipolytica* in bioreactors. Another option is a plant factory, using genetically modified plants for production of pheromones. Using *Nicotiana benthamiana* as a platform, we produced several 14C and 16C moth sex pheromone components by transient expression of up to four genes coding for consecutive biosynthetic steps. The fatty alcohol fractions from the genetically modified plants were acetylated and mixed to successfully mimic the respective sex pheromones of the small ermine moths *Yponomeuta evonymella* and *Y. padella*. In the project *Oil Crops for the Future* (https://strategiska.se/en/research/ongoing-research/biological-production-systems-2014/project/6706) we have produced genetically modified stable lines of the oil seed plant *Camelina sativa* that produce as much as 30% of selected pheromone fatty acid precursors. The isolated target precursors were then reduced to fatty alcohols that were either used directly, or oxidized to the corresponding aldehyde or acetylated. To validate the biological activity of the seed oil-derived compounds, we formulated sex pheromone baits according to the reported optimal pheromone composition of the diamondback moth, *Plutella xylostella*, a worldwide pest on cruciferous vegetable crops. The field trapping experiments revealed that the *Camelina*-derived pheromone is as attractive as conventionally produced pheromone.

P-03

Functional integration of plant secondary metabolites across three trophic levels

Matthias Erb

University of Bern, Switzerland

Small molecular weight organic compounds are common across the galaxy and transcend all known biological interactions. Plants, in particular, have evolved a remarkable capacity to produce diverse sets of so-called specialized metabolites from a few simple, inorganic precursors. Already in 1977, Rhoades argued that plant specialized metabolites are likely multifunctional, i.e. that they serve multiple purposes. Multifunctionality may render the production of specialized metabolites more cost effective and may explain their abundance and tight spatiotemporal control in plants. Work over the last decades confirms that specialized metabolites often have a broad range of functions, from growth and development to defense. However, our understanding of how this multifunctionality affects the interactions between plants and higher trophic levels, including herbivores and their natural enemies, is limited. In my presentation, I will explore the importance of multifunctional plant metabolites in a multitrophic context by discussing our work on benzoxazinoids, the most abundant specialized metabolites in grasses such as wheat and maize. We find that benzoxazinoids act as direct defenses, within-plant defense signaling molecules, microbiome modulators and siderophores. At the same time, the western corn rootworm, a specialist maize pest and important agricultural pest, exploits benzoxazinoids as foraging cues, protective agents and micronutrient providers. Thus, the multifunctionality of plant specialized metabolites is mirrored in the adaptations of a specialist herbivore, resulting in a tightly interlocked metabolism. We are also starting to unravel how the metabolism of herbivore natural enemies such as entomopathogenic nematodes can be interlocked with the plant and the herbivore to enhance biological control. These findings have implications for our understanding of the ecology and evolution of plant specialized metabolites, and for their use in agricultural pest control.

P-04

New developments in our understanding of the use and misuse of herbivore-induced plant volatiles in insect-plant interactions

Ted Turlings

Institute of Biology, University of Neuchâtel

In response to herbivory by insects many plants release specific blends of volatiles. These herbivore-induced plant volatiles (HIPVS) are used as cues by natural enemies, such as predators and parasitoids, to locate their prey or hosts, whereas various herbivores are repelled HIPVs probably to avoid inducible plant defenses and resource competition. HIPVs are also known to serve as within and between plant signals, whereby the perception of the volatiles by neighboring plants usually primes the neighbors to prepare for an imminent attack, making them more resistant to insects. I will show that well-adapted insects have found ways to suppress the emission of HIPVs, and may even manipulate plants to emit the “wrong” signal. The latter appears to be the case for whiteflies, which triggering the release of a volatile blend that is more indicative of pathogen attack. Indeed, whitefly-induced volatiles prime pathogen defenses in neighboring plant, which goes at the cost of defenses against insects. This apparent manipulation of a plant distress signal makes the neighbors more suitable for the next generation of whiteflies. These findings highlight the specificity of HIPVs and the various messages they convey. I will give some examples of how we may eventually exploit this specificity for crop protection.

P-05

Unexpected origins of defensive compounds in animals

Naoki Mori[a], Akira Mori[b]

[a]*Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan*
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1. Oribatid mites as a major dietary source for alkaloids in poison frogs

Alkaloids in the skin glands of poison frogs serve as a chemical defense against predation, and almost all of these alkaloids appear to be sequestered from dietary arthropods. Certain alkaloid-containing ants have been considered the primary dietary source. In 2005, we found that adults of two species of oribatid mites contain dendrobatid alkaloids. Gas chromatography/mass spectrometry (GC/MS) of hexane extracts of adult *Scheloribates azumaensis* (Oribatida: Acari) revealed the presence of not only pumiliotoxin 251D, but also precoccinelline 193C and another coccinelline-type alkaloid. Oribatid mites possess oil glands that secrete a wide range of organic compounds (terpenes, aromatics, aliphatic aldehydes, and hydrocarbons). In the closely related mite group Astigmata, compounds from homologous glands also function as aggregation signals and sex pheromones. To date, it is suggested that oribatid mites are a major dietary source for alkaloids in poison frogs.

2. The chemical analysis of bufadienolides in defensive glands of the Asian Rhabdophis snakes

A Japanese snake *Rhabdophis tigrinus* has defensive glands on its neck called nuchal glands. The major chemical components of the glands are steroidal toxins known as bufadienolides (M.W., 398~434). *Rhabdophis tigrinus* sequesters the toxins from toads it consumes as prey. The nuchal glands have been reported from 17 species of snakes in Asian but chemical components of the glandular fluid have not been investigated in all species except for *R. tigrinus*. A Chinese snake *R. pentasupralabialis*, which has nucho-dosal glands, mainly eats earthworms while *R. tigrinus* eats frogs. As a result of LCMS analysis, we revealed that the former snake has some heavier bufadienolides (M.W., 448~564) than *R. tigrinus* has. Then we purified 4 bufadienolides from the glandular fluid of *R. pentasupralabialis*. Through NMR spectroscopic analysis, we identified one of them as a bufadienolide xyloside previously reported from the North American firefly *Lucidota atra*, and the others also had same planer structures (*cis*-fusion) as bufadienolides from *L. atra*. We also confirmed that the snake eats fireflies in the field. These results suggested that *R. pentasupralabialis* would sequester bufadienolides from the fireflies in the glands. It implies that the origin of bufadienolides sequestered in the glands may have shifted from toads to fireflies after the shift of main prey in the course of the evolution of *Rhabdophis* species.

P-06

Sex determination genes and sexual behavior of silkworm

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Insect courtship and mating depend on integration of olfactory, visual, and tactile cues. Compared to other insects, *Bombyx mori,* the domesticated silkworm, has relatively simple sexual behaviors as it cannot fly. Here we found that courtship and mating behaviors are regulated by sex determination cascade genes through two distinct pathways in male silkworms. Loss of *Bmdsx* gene expression significantly reduced the peripheral perception of the major pheromone component bombykol by the product of the *BmOR1* gene and completely blocked the courtship in males. Interestingly, mating behavior was separately regulated by another sex determination gene, *Bmfru.* Loss of *Bmfru* completely blocked mating, but males displayed normal courtship behavior. Lack of *Bmfru* expression significantly reduced the perception of minor pheromone component bombykal due to the down regulation of *BmOR3* expression. The product of *BmOR3* plays a key in ending mating behavior. Our results suggest that the *Bmdsx-BmOR1*-bombykol and *Bmfru-BmOR3*-bombykal cascades are the two primary pathways that regulate olfactory-based sexual behavior. These cascades may provide potential targets for lepidopteran pest control.

P-07

Something old, something new: caterpillar movement and feeding behaviour on whole plants-traversing a treacherous landscape

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The survival and reproductive success of plant feeding insects is directly related to feeding and foraging behavior; moving and selecting feeding sites; and consequently, central to understanding their population dynamics. Plants defend themselves against insects by producing chemicals that adversely influence insect growth. Mechanical damage to plant cells and chemicals in the oral secretions of insect herbivores create so called inducible defenses; a cascade of biochemical changes within plants resulting in the production of local and systemic toxins, alkaloids, anti-feedants, and volatile chemicals. Progress has been made in our understanding of the molecular mechanisms of induction by plants, but the literature is unclear about the ecological consequences on insects, partly due to a naïve experimental approach. Studies imply that induced chemicals drive insect movement away from local sites of induction and from systemically-induced whole plants. In cropping systems, herbivore feeding has a direct impact on the productivity, quality and value of the crop. Any increased movement within or between plants caused by induced chemicals will significantly affect patterns of herbivore damage. As herbivorous insects cause billions of dollars of damage to agriculture every year, an understanding of the relationship between insect foraging movement and induced chemical defenses in plants is vital to the development and protection of crop plants. Plant protection needs to be based on research founded on an understanding of the mechanistic interaction of insects and plants at appropriate spatio-temporal scales. But determining the mechanisms is not straightforward. I summarise some “old” experiments on neonate behavior of monarch on milkweeds in relation to latex and cardenolides and then highlight our more recent (new) work on *Helicoverpa* and induced plant defences using *Arabidopsis* as a model system. The challenge to translate mechanistic understanding into ecological consequences remains.

S01-01

Field evaluation of a new attract-and-kill trap for mated female Queensland fruit fly

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Queensland fruit fly (Qfly, *Bactrocera tryoni*) is considered the number one insect pest for Australian horticulture. A mass trapping system for female flies using ‘attract-and-kill’ traps is one of the envisaged strategies to be used as part of an integrated pest management (IPM) program for Qfly. However, the effectiveness of commercially available attract-and-kill female Qfly traps is still unclear, particularly with regards to the different reproductive stages of the female fruit fly population these traps attract. Over the last three years, Agriculture Victoria Research has developed a new attract-and-kill trap to specifically target mated female Qfly. We present an overview of the chemical ecology behind the development of the synthetic lure in this trap, which incorporates a blend of fruit esters and fungal volatiles in slow-release sachets placed inside fruit mimicking *Ladd* traps. In 2019 field trials conducted within different fruit orchards, our new trap captured significantly more mated and virgin females than commercially available protein (*Biotrap*) and synthetic fruit odour (*Fruition*) traps.

S01-02

Scents from the wild: the vinegar fly *Drosophila suzukii* prefers volatiles from wild than cultivated blueberries

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Highbush blueberry (*Vaccinium corymbosum* L.) is a crop native to the northeast USA that has been domesticated for about 100 years. Native to Southeast Asia, the spotted wing drosophila, *Drosophila suzukii* (Matsumura), was first detected in the USA in 2008 and has since become a major pest of highbush blueberries in the USA. Here, our objectives were to: 1) compare the attraction of *D. suzukii* adults to volatiles from wild and cultivated highbush blueberry fruits; 2) analyze the volatile profiles emitted from wild and cultivated highbush blueberry fruits; 3) identify the antenally-active compounds using gas chromatography-electroantennogram detection (GC-EAD); and, 4) determine the attraction of *D. suzukii* flies to EAD-active compounds. Fruits from wild and cultivated blueberries, growing in close proximity, were collected from June through August of 2017 and 2018 from three locations in the New Jersey Pinelands National Reserve. In choice bioassays, *D. suzukii* flies were more attracted to volatiles from wild than cultivated blueberry fruits. Wild blueberry fruits emitted higher amounts of volatiles than cultivated blueberry fruits. Nine EAD-active compounds were identified from wild blueberries; however, there was a stronger preference for four of these volatiles. Although both**,** the 4- and 9-component blends, were attractive to *D. suzukii* compared to blank controls, the 4-component blend was more attractive in dual-choice tests. Future studies will determine the attractiveness of this blend to *D. suzukii* under field conditions. Our results show that breeding for agronomic traits has lowered volatile emissions in blueberry fruit, which decreased attraction to *D. suzukii* flies.

S01-03

An improved understanding on male fruit fly-phytochemical lure interactions benefitting fruit fly control

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Males of certain tephritid fruit flies from the genera of Bactrocera and Zeugodacus actively forage for semiochemicals or their synthetic analogues that consist primarily phenylbutanoids (e.g., raspberry ketone) and phenylpropanoids (e.g., methyl eugenol). Fruit fly-phytochemical lure interactions are unique and species-specific phenomena. Whilst newly emerged male fruit flies do not respond to lures, their response instead increased concomitant with attainment of sexual maturity. Information on lure dose-response and rate of age-related lure response, which varies with lure and fruit fly species, are important parameters of consideration in implementing a male annihilation programme (MAT). Lure feeding by males also invariably enhances male mating performance, except for *B. cacuminata*, by increased male sexual signalling and/or increased attractiveness of sexual signals. Hence, sterile males such as that of *B. dorsalis* are now fed with methyl eugenol before releases to improve mating competitiveness against the feral males in an area-wide sterile insect technique (SIT) programme. However, recent detailed studies involving other *Bactrocera* and *Zeugodacus* species revealed a more intricate and diverse fruit fly-lure interactions that may provide insightful consideration for improving MAT and SIT programmes against other pestiferous fruit flies. These interesting examples will be presented and discussed in my talk.

S01-04

Functional characterization of olfactory receptors in Dacini fruit flies (Diptera: Tephritidae) that respond to semiochemicals

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Dacini fruit flies, including destructive pest species, are strongly affected by semiochemicals in their reproductive behaviors. Various compounds, including aromatic and aliphatic volatiles, have been identified as components in the male rectal glands, which is considered to be a secretory organ of male sex pheromones. Furthermore, volatiles derived from host fruits play a crucial role in the search for oviposition sites by gravid females. Although multiple semiochemicals associated with the life cycles of Dacini fruit flies have been identified, chemosensory mechanisms by which the perception occurs have not been fully elucidated. Therefore, we conducted RNA sequencing analysis of the chemosensory organs of the three related pest species—the Oriental fruit fly, *Bactrocera dorsalis*, the solanaceous fruit fly, *B. latifrons*, and the melon fruit fly, *Zeugodacus cucurbitae*—to identify the genes coding for chemosensory receptors. We analyzed phylogenetic relationships of olfactory receptors (ORs) among the three species. Furthermore, we functionally analyzed ORs co-expressed with the obligatory co-receptor ORCO in *Xenopus* oocytes to identify their ligands. We characterized functional properties of OR74a homologs in the three Dacini species to aliphatic components in the male rectal glands. We also found that OR13a and OR82a homologs responded robustly to host plant volatiles. The volatiles elicited responses of ORs were subsequently subjected to behavioral bioassays. Certain plant volatiles had a significant effect on the landing behavior of mated females. These results suggest that the ORs characterized in the present study are involved in the perception of plant volatiles that affect host-finding behavior of mated females.

S01-05

Identification of the odorant receptors responsible for methyl eugenol perception in the oriental fruit fly, *Bactrocera dorsalis*

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The oriental fruit fly, *Bactrocera dorsalis* (Hendel), is one of the most devastating pests causing substantial economic damage to the fresh vegetables and fruits worldwide. The most effective way to control the fruit fly is luring and killing. The most effective commercial component of attractant is methyl eugenol (ME), but the molecular mechanism of the olfactory perception remains unknown. Here, we therefore attempted to identify the odorant receptors (ORs) responsible for ME in *Bactrocera dorsalis*. We annotated the 63 OR-like genes of the *Bactrocera dorsalis* based on its genome information. Furthermore, we investigated their temporal and spatial expression profiles. In addition, we determined their expression profiles of the male flies exposed to 5% ME for several time gradients to screen out 15 candidate OR-like genes responsible for ME perception in terms of the down-regulated expression. In order to further confirm the binding capability of the candidate ORs with ME, the live calcium imaging using HEK cell expression system as well as and voltage clamp recording in *Xenopus* oocytes are performing. Besides, genome editing tool such as CRISPR/Cas9 is going to be employed to knock out the essential ORs to measure the olfaction guided behaviors in vivo. We expect to identify odorant receptors responsible for the ME perception in this notorious fly. Our results will not only reveal the molecular basis of ME perception in *B. dorsalis*, but also lay a solid foundation for the development of novel effective attractant targeting key ORs in this fly.

S01-06

Proteome-transcriptome analysis of maxillary palp and antenna of male oriental fruit fly following strong attraction to methyl eugenol

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The Oriental fruit fly, *Bactrocera dorsalis* (Hendel) is one of the world's most destructive insect pests of fruits throughout the tropical and subtropical regions. Multiple tactics have been developed by using methyl eugenol (ME) as a potent male attractant for this species, leading to its successful use in area-wide fruit fly monitoring and control programmes. Whilst it is generally recognized that the antenna is the olfactory organ primarily responsible for the male flies' detection of potent attractants such as ME over long distances, little is known of the involvement of the maxillary palp in maneuvering males towards ME at short range. Using a complementary proteomics followed by transciptomics approach, we aimed to evaluate for the protein and transcriptome changes in maxillary palp and antenna following the unique strong attraction of *B. dorsalis* males to ME. These changes determine how the maxillary palp complement the antenna in successful male detection and attraction to ME. Initially, a number of OBPs at the proteome level plus other OBPs, ORs, IRs and GR at the transcriptome level were detected from flies which were not exposed to ME. However, following the strong male attraction to ME, we discovered several OBPs that were regulated at the proteome and transcriptome level. The involvement of those different OBPs in the maxillary palp and antenna suggests the complementary functions of both organs that are intricate leading to successful detection and attraction of male flies to ME.

S01-07

Cross-species comparison of fruit fly olfactory sensitivity to host fruits as a way of exploring new attractive blends

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La Réunion Island houses nine fruit fly species with partial host-range overlapping that are impacting fruit and vegetable production. It includes *Bactrocera dorsalis*, *Bactrocera zonata*, *Ceratitis capitata*, *Ceratitis quilicii*, *Ceratitis catoirii*, *Neoceratitis cyanescens*, and *Zeugodacus cucurbitae*. We intend to identify new attractants for these species by exploring the kairomones of host fruits that attract gravid females. First, we explored the volatilomes of 28 different fruit species and estimated the genericity of hundreds of volatile compounds among the preferred hosts of the main fruit fly species. Secondly, we compared the olfactory sensitivity of seven fruit fly species to chemical compounds released by strawberry-guava. Dual-probe antennal recordings of electric potentials were used to assess the olfactory response of the whole antenna. We found kairomones that are detected by neuronal pathways conserved among species. Such pattern would be expected for fundamental semiochemicals submitted to purifying selection. Other Kairomones were detected by species-specific pathways. Such pattern might emerge from positive selection and suggests specific semiochemical. The affinity of the insects to these chemicals remains to be elucidated. Anyway, distinguishing these two categories of kairomones should be an asset in designing chemical blends that could induce generic or specific attraction of fruit flies.

S01-08

Monitoring individual fruit fly responses to attractants using radio frequency identification

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Tephritid fruit flies respond to a number of semiochemical cues including volatiles from host plants, food (protein) odors, and compounds related to mating (pheromones and parapheromones). Olfactory responses are fundamental to detection and control of pest tephritids, and vary with age, physiological state, and environmental conditions. In order to study behavioral responses to olfactory cues it is often important to be able to identify individual insects and record information about their activity over time. To this end, insects are usually marked and then followed by direct observation or video. Shortcomings of these techniques include the limited number of individuals that can be monitored, limited experiment duration, and requirements for observation under artificial conditions. It is now possible to collect insect behavioral data by use of radio-frequency identification (RFID) technology. RFID has been used to study eusocial insects, bees and ants, by attachment of an RFID tag to individual insects, which is then read when the marked insect passes close to a reader. In order to study the olfactory responses of oriental fruit flies, *Bactrocera dorsalis*, and melon flies, *Zeugodacus cucurbitae*, we developed methods to RFID tag flies and automated reader stations (reading stations record proximal flies and release attractant compounds). These methods have the potential to provide large behavioral data sets while addressing experimental variables such as age, diurnal patterns, environmental conditions, physiological state, multiple attractants, etc. Our application of RFID to tephritids allows analysis of behavior with a degree of detail not obtainable via other observation techniques.

S01-09

Olfactory learning and memory in the polyphagous frugivore, *Bactrocera tryoni*

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Learning has been demonstrated in a number of tephritid species, including *Bactrocera tryoni*, but the ecological value of it has never been investigated. In this study we present two ecologically relevant questions to do with memory and learning (1) is memory and learning modified or influenced by the quality of the host plant for oviposition and larval survival; and (2) does memory and learning help *B. tryoni* locate a host fruit in a complex landscape. No-choice olfactometer assays were conducted to determine how prior oviposition experience on nine different fruits of high to low quality affected the learning ability and memory duration of female *B. tryoni*. Field cages with varying densities of either good or poor quality hosts were used to determine whether prior oviposition experience enhanced host location. Olfactometer assays showed that memory duration was correlated with fruit quality. Females displayed the longest memory when experienced on high quality fruits and shortest memory on low quality fruits. In field cage experiments the host location behaviour of *B. tryoni* was influenced by prior oviposition experience, whereby experience of a particular host increased the selection of that host despite its abundance. For example, in a field cage that contained significantly more blueberry (poor host) than guava (good host), prior experience on guava resulted in more flies selecting and accepting guava than did naïve flies. However, the results also highlight that learning can be a disadvantage, if prior experience on a poor host leads to flies repeatedly using that host over a host more suitable for offspring development.

S01-10

Olfactory cues of predators influence vital life processes of *Bactrocera tryoni*

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Predators can impose substantial selection on prey species and, in turn, prey species commonly make use of cues emitted by their enemies to aid in detecting and assessing predation risk. However, responses to cues emitted by enemies can also have adverse effects on prey fitness through “non-consumptive effects” on behavior and physiology. Although, non-consumptive effects of predator olfactory cues have been quite well studied in some vertebrate and aquatic systems, they are less understood in terrestrial insect systems. Using the interaction between the Queensland fruit fly, *Bactrocera tryoni*, and its potential predators, we demonstrate that olfactory cues from predators influence diverse fitness-related behavior. Flies were subjected to headspace volatiles from 4 potential predators with different abundance and diurnal activity and the effects on mobility, foraging, oviposition and mating were assessed. In mobility assays, flies increased or reduced movement depending on which predator volatiles they encountered. Further, flies significantly reduced foraging, oviposition and mating behavior in the presence of predator volatiles. Our results suggest that olfactory cues from predators not only convey crucial information about potential danger, but also have far-reaching effects on fitness-related behavior.

S01-11

Identification and field evaluation of male-produced sex pheromone of *Neoceratitis asiatica* (Becker)

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Chinese wolfberry (*Lycium barbarum*), an edible and medicinal plant with high economic value, has been widely planted in Northwestern China for many years. Having rich nutrients, like polysaccharides and amino acids, wolfberry fruits are highly vulnerable to diseases and pest insects. *Neoceratitis asiatica* Becker is a major pest of wolfberry, especially in organic wolfberry orchard. Male adults of *N. asiatica* were found to produce sex pheromones to attract females. Gas chromatography coupled to electroantennographic detection (GC-EAD) and gas chromatography-mass spectrometry (GC-MS) techniques were used to identify the sex pheromone components. Two EAD-active compounds were identified as N, I. Field trapping experiments were conducted using both fruit fly traps and sticky card traps baited with single (N, I) or mixture (NI) sex pheromone components in Qinghai organic wolfberry orchards. The results indicated that NI mixture was more attractive than either single component, N, I. Sticky card trap captured significantly more flies than fruit fly trap. The high attractiveness of the male-produced sex pheromones suggests that they may be useful for mass trapping of *N. asiatica*.

S01-12

Gut microbiota affects development and olfactory behavior in *Drosophila melanogaster*

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It has been shown that gut microbes are very important for the behavior and development of *Drosophila*, as the beneficial microbes are involved in the identification of suitable feeding and oviposition places. However, in what way these associated gut microbes influence the fitness-related behaviors of *Drosophila melanogaster* remains unclear. Here we show that *D. melanogaster* exhibits different behavioral preferences towards gut microbes. Both adults and larvae were attracted by the headspace of *Saccharomyces cerevisiae* and *Lactobacillus plantarum*, but were repelled by *Acetobacter malorum* in behavioral assays, indicating an olfactory mechanism involved in these preference behaviors. While the attraction to yeast was governed by olfactory sensory neurons expressing the odorant co-receptor Orco, the observed behaviors towards the other microbes still remained in flies lacking this co-receptor. By experimentally manipulating the microbiota of the flies, we found that flies did not strive for a diverse microbiome by e.g. increasing their preference towards gut microbes that they had not experienced previously. Instead, in some cases the flies even increased preference for the microbes they were reared on. Furthermore, exposing *Drosophila* larvae to all three microbes promoted *Drosophila*'s development while only exposure to *S. cerevisiae* and *A. malorum* resulted in the development of larger ovaries and in increased egg numbers the flies laid in an oviposition assay. Thus our study provides a better understanding of how gut microbes affect insect behavior and development, and offers an ecological rationale for preferences of flies for different microbes in their natural environment.

S01-13

Identification of odorant binding proteins which binding with methyl eugenol and their function research in *Bactrocera dorsalis*

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Odorant binding proteins (OBPs) play an important role in insect olfactory perception. The oriental fruit fly, *Bactrocera dorsalis*, is one of the most destructive fruit-eating pests, causing enormous economic losses to the fruit and vegetable industry worldwide. Methyl eugenol (ME) is a powerful attractant for mature males of *B. dorsalis*, and has been widely used for detecting, luring and eradicating *B. dorsalis* populations worldwide. However, the molecular mechanism underlying the olfactory perception of ME remains largely unknown. In our study, we expanded the repository of *B. dorsalis* OBPs to 49. Phylogenetic analysis of OBPs with other species revealed that these proteins grouped into four subfamilies. Furthermore, we determined the expression profiles in six body parts and five internal tissues. Then we focused on the identification of the OBPs which plays an indispensable role in the perception of ME in *B. dorsalis*. We screened 10 candidate OBPs based on the triple screening method including expression pattern analysis, phylogenetic analysis, simulating molecular docking. The results of SDS-Page and Western Blot indicate 6 OBPs of heterologous expression were successfully. Then, three of them showed higher affinity with ME through ligand-binding assays. After that, we will knock out the key *OBPs* with CRISPR/Cas9 technology and locate them with Fluorescence in situ hybridization. Above all, our result enriched the knowledges of OBPs of *B. dorsalis* and it will reaceal some of the molecular mechanism about olfactory reception of ME in *B. dorsalis.*

S02-01

Effects of crop nutrition on anti-herbivore resistance

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Crop nutrition plays a key role in growth and development. However, how nutrition affects crop anti-herbivore resistance is ambiguous. Nitrogen (N) represents one of the most important limiting nutrient elements required for growth and reproduction in both plants and herbivorous insects. Although silicon (Si) is not considered an essential element of plants, the ability of Si to significantly enhance crop resistance to both biotic and abiotic stresses as a “beneficial element” has been well demonstrated. Jasmonates (JAs) are lipid-derived plant hormones that play an essential role in plant development, as well as defense responses against insect herbivores. We examined the effects of different levels of N and Si on rice resistance against insect herbivores. Higher N levels significantly reduced rice resistance, while Si improve rice resistance against both chewing and sucking insect pests. Si not only served as a physical barrier, but also enhanced inducibility of chemical defense of rice plants. Deficiency in silicon transporter Lsi1 compromises inducibility of anti-herbivore defense in rice plants. Exogenous application of methyl jasmonate increased Si accumulation in rice plants. There existed a strong interaction between JA and Si in rice defense. Si also adjusted N availability in rice plants. Meanwhile, JA signaling mediates large-scale systemic changes in N uptake and allocation in rice plants. Our study suggests that appropriate manipulation of plant nitration can enhance crop anti-herbivore resistance and minimize the use of synthesized chemical pesticides.

S02-02

***Diabrotica virgifera virgifera* females can sequester multiple plant toxins to protect their eggs against predators**

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Various herbivorous insects have been shown to sequester defensive secondary metabolites from their host plant and use them against their natural enemies. The known examples of sequestration involve one specific type of chemical defense and this is well documented for insect larvae and adults, it is still rarely shown that metabolites can be transferred to eggs and to our knowledge there are no examples of insects sequestering multiple types of defense metabolites. We studied sequestration by *Diabrotica virgifera virgifera* beetles and the possible transfer to eggs. The adult stage feeds on various host plants, including maize, cucumber and bean, containing defensive benzoxazinoids, cucurbitacins, and cyanogenic glucosides, respectively. Chemical analyses revealed that *D. v. virgifera* beetles sequester and transfer benzoxazinoids and cucurbitacins to their eggs, but not cyanogenic glucosides. To test whether the two sequestered toxins protect eggs against predators, we fed *D. v. virgifera* beetles with toxin-free or toxin-containing plants, and offered their eggs to the rove beetle *Atheta coriaria* and the minute pirate bug *Orius laevigatus*. In choice experiments, both predators consumed more toxin-free eggs than toxin-containing eggs. Moreover, survival assays confirmed the toxic effects of benzoxazinoid-containing eggs on the predators, but, surprisingly, cucurbitacins had no apparent effect. Our results reveal a unique ability of *D. d. virgifera* to use multiple plant defensive chemicals against higher trophic levels, which may in part explain the extraordinary success of this invasive pest.

S02-03

Plant volatiles as mate finding cues for insects

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Plant volatiles are not only used by herbivorous insects, but also by the natural enemies of the herbivores to find food. There is also increasing evidence that plant volatiles, in combination with species specific pheromones, help these insects to find mating partners. Indeed, flowers, fruits and leaves often serve as rendezvous sites for mate-seeking insects. Moreover, plant volatiles may stimulate the release of sex pheromones and can render insects more receptive to potential mates. We speculate here that the distinct properties of typical plant- and insect-produced volatiles and the differential odor plumes they form may contribute to an efficient synergistic use of these cues to locate plants that offer access to food as well as mates.

S02-04

Volatiles from un-infested rice plants enhance the spread of the major rice pest, brown planthopper *Nilaparvata lugens* Stål

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Infestation by herbivorous insect pests can change plant volatile profiles leading to the attraction of natural enemies and modifying the behaviour of the pests. In this current study, eight bioactive volatiles, methyl salicylate, methyl benzoate, 2-nonanone, linalool, (*E*)-4,8-dimethyl-1,3,7-nonatriene (DMNT), veratrole, β-ionone and (*E*,*E*)-4,8,12-trimethyl-1,3,7,11-tridecatetraene (TMTT) were identified by GC-EAG from the susceptible rice variety TN1 infested by the major rice pest the brown planthopper *Nilaparvata lugens,* Stål (BPH). We determined the quantitative differences in the production of these bioactive volatiles between BPH susceptible and resistant rice varieties. There was no clear linear correlation in the volatile production with the levels of rice pest resistance against BPH. The total amount of emitted volatiles was significantly higher from susceptible varieties than those from resistant varieties. The expression of volatile biosynthesis genes was much higher in the susceptible rice variety TN1 plants than in resistant varieties, and extremely upregulated upon BPH-infestation. In behavioural experiments, we found that the un-infested rice volatiles (UIRVs) were more attractive to BPHs in single choice bioassays and more than those from the infested rice plants (IRVs) in dual choice bioassays. Surprisingly, the attractiveness of UIRVs was significantly reduced by addition of the blend that mimics the natural composition of these compounds in the IRV of the variety TN1. Furthermore, the 1:1 molar mixture of eight EGA active compounds identified from IRVs repelled BPHs. These results suggest that UIRVs could initially serve as attractive signals to rice pests for crop protection in the push-pull strategy. Then the pest infestation changes the rice volatile profile and makes UIRVs less attractive, which pushes more insect pests to un-infested plants nearby, resulting in further spread of the pest infestation in rice field. We hypothesise that such indirect defence of plant volatiles against insect pests can be explored further to manipulate the behaviours of insect pests as well as natural enemies and predators but not as a direct defence mechanism.

S02-05

Chemical responses in plant-insect interaction of plant gall

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As the important elements of the world, plants and insects use chemicals to influence each other during their survival and reproduction. The chemical interaction of plant *Amygdalus persica* f. *rubro-plena* with their feeding insect peach aphid have been investigated. According to field observation, aphids were harmful seriously to the leaves of *A. persica* f. *rubro-plena* to form gall. More than 80% of the branches of the plants have been infected by aphids in some area of Liaoning Province.

Interestingly, these aphid galls showed green or red.The galls in the shade area were mostly green, while they were mostly red in the sunny areas. Furthermore, the UV-B and UV-C radiation in the red gall areas were significantly higher than that in the green gall areas. By comparing the morphological and molecular information of the aphids in green and red galls, it was found that the aphids in the two tissues were the same. So, we inferred that the red pigments on the galls of *A. persica* f. *rubro-plena* was related to UV-B and UV-C radiation. Compared with normal leaves by HPLC and UPLC-MS/MS analyses, the contents of chlorogenic acid and rutin were increased in green and red gall tissues, and the anthocyanins were higher in red gall tissues. C3G and C3R were identified to be the anthocyanins in red gall tissues by chemical separation and NMR spectra analyses. Further UPLC-MS/MS analysis showed that the contents of C3G and C3R in green gall increased significantly after 3 hours of UV-B and UV-C radiation (simulated field radiation). UV-B and UV-C radiation showed that the mortality rate of peach aphids in red galls was significantly lower than that in green galls. The anthocyanin C3G and C3R were applied on the surface of normal peach leaves and then irradiated by UV-B and UV-C. It was found that C3G and C3R had protective effects to the peach aphids against UV-C radiation, indicating that C3G and C3R in red gall tissues provided protective role for peach aphids against UV radiation. Moreover, the bioactivity test showed that the phenolic compounds chlorogenic acid and rutin inhibited the growth of the phytophagous insect *Helicoverpa armigera*, but had no significant toxicity to the growth of the peach aphids, suggesting that these phenolic compounds were the defensive substances of the *A. persica* f. *rubro-plena*. It was possible that the specialized insects peach aphids have shown adaptability to these phenolic compounds.

In summary, the morphology and structure of leaves were changed after aphid feeding. Plants were synthesized anthocyanins after aphid feeding and UV radiation. These anthocyanins provided the defensive function for insects against UV radiation, indicating that insects used plant chemical defense system.

S02-06

Understanding the dynamics of wheat chemical and physical defense mechanisms against aphids

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Young wheat plants are continuously exposed to insect herbivorous attack. To maintain their fitness, plants have evolved different defense mechanisms, including the biosynthesis of toxic compounds and/or trichome formation that provides physical barriers. It is unclear whether both of these mechanisms are equally critical in providing an efficient defense for wheat seedlings against the bird cherry-oat (*Rhopalosiphum padi*) aphid—an economically costly pest in cereal production. In our research, we compared the transcriptomic, metabolomic, chemical, and physical defenses of three selected wheat genotypes, two tetraploid wheat genotypes, domesticated durum ‘Svevo’ and wild emmer ‘Zavitan,’ and one hexaploid bread wheat, ‘Chinese Spring.’ The full transcriptomic analysis revealed a major difference between the three genotypes, while the clustering of significantly different genes suggested a higher similarity between the two domesticated than the wild wheat. Measurement the levels of toxic compounds, benzoxazinoid, at the three time-points revealed high abundance levels in the two domesticated genotypes, while the levels were very low in the wild emmer wheat. In contrast to the benzoxazinoid levels, the trichome density was dramatically higher in the wild emmer than in the domesticated wheat. Evaluation of aphid reproduction indicated that the domesticated bread wheat is more resistant than the tetraploid genotypes. Overall, the results suggested that although wheat seedlings possess both chemical and physical defense mechanisms, the chemical defense plays a more significant defensive role than the physical barriers.

S02-07

Ecological and biochemical mechanisms that determine the preference of *Nilaparvata lugens* for Bt over nonBt rice plants

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Introducing insect-resistant genetically engineered plants into an agroecological system will undoubtedly influence the interactions with and among insect species that are closely associated with the plants. Field surveys indicated that *Bt* rice harbours considerably fewer brown planthoppers (BPHs) than non-*Bt* rice even though planthoppers are not sensitive to the *Bt* Cry proteins. The mechanisms underlying this phenomenon remain unknown. Here we studied the interspecific interactions among the striped rice stem borer (SSB), which is the target pest, the brown planthopper (BPH), as well as its egg parasitoid, *Anagrus nilaparvatae.* In laboratory and field-cage experiments, BPH showed no feeding preference for undamaged *Bt* or non-*Bt* plants, but it exhibited a strong preference for SSB-damaged plants whether *Bt* or non-*Bt*. Under open field conditions, BPH were more abundant on SSB-damaged non-*Bt* rice than on neighbouring *Bt* rice, which were not or less infested by SSB. GC-MS analyses showed that SSB-damage induces the release of rice plant volatiles that are known to be attractive to planthoppers. Moreover, metabolome analyses revealed SSB-damage plants had higher amino acid contents and reduced sterol contents, which should benefit planthopper development. Furthermore, we found that the parasitoid, avoids the odor of rice plants that are infested by SSB. BPH females laid considerably more eggs on SSB-infested than on insect-free plants. The importance of HIPVs for this preference was confirmed by testing synthetic blends of volatiles identified from rice plants infested by BPH and/or SSB. In greenhouse and field cage experiments, parasitism rates of BPH eggs were up to 80% lower on plants that were co-infested by SSB, confirming the adaptiveness of the BPH oviposition strategy. These results imply that Lepidoptera-resistant Bt rice is less attractive to BPH due to reduced caterpillar damage relative to non-Bt rice, suggesting that Bt rice can also provide ecological resistance to non-target planthoppers.

S02-08

Root herbivores require intact carbon dioxide and sugar perception for optimal foraging

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Belowground herbivore insects are capable of perceiving and integrating different olfactory, gustatory, and tactile cues to locate their host plant and optimize their foraging decisions in complex soil environments. However, the molecular basis of chemical perception in root herbivores is poorly understood. In this study, we identified potential odor and gustatory receptors of *Diabrotica virgifera virgifera*, the western corn rootworm, silenced their expression through RNA interference and conducted behavioral experiments to determine the importance of these receptor candidates for host location and foraging. Our results uncover two genes, the putative carbon dioxide group 2 receptor (*DvvGr2*) and the putative gustatory sugar-receptor 43a (*DvvGr43a*), as important mediators of western corn rootworm foraging. *DvvGr2*-silenced larvae did not behaviorally respond to carbon dioxide. By consequence, their capacity to locate and move towards host plants from a distance was reduced. However, they were still able to perceive host plants through other volatile cues, supporting earlier findings that the larvae can use volatiles other than CO_2 for host location. *DvvGr43a*-silenced larvae did not respond to sugars as phagostimulants. By consequence, they had a reduced capacity to recognize maize roots as a food source and to discriminate between nutritious crown roots and less nutritious primary roots, thus demonstrating the importance of sugar perception for *D. v. virgifera* foraging success. Taken together, our study uncovers that the capacity to detect different root volatile- and non-volatile metabolites is important for host location and foraging of a specialist root herbivore. Modulating olfactory and gustatory perception through environmental RNAi is a promising approach to understand how essential plant metabolites that cannot be manipulated *in planta* determine foraging decisions by belowground herbivores and plant-herbivore interactions.

S02-09

Feeding preferences and taste responses to plant substances in two species of *Helicoverpa* caterpillars

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The cotton bollworm *Helicoverpa armigera* (Hübner) (Lepidoptera: Noctuidae) and the oriental tobacco budworm *Helicoverpa assulta* (Guenée) are closely related species. *H. armigera* is a polyphagous species, while *H. assulta* is an oligophagous species mainly feeding on tobacco and pepper fruits in fields. In the present study, we investigated the behavioral feeding preferences and electrophysiological responses of caterpillars of the two Helicoverpa species to different compounds originated from host plants, non-host plants and the common plant, in an aim to explore the clues of species diversification of *Helicoverpa* species. Firstly, we compared the feeding preference bahaviors and gustatory responses of caterpillars to mixtures of sucrose, a phagostimulant and sinigrin, a deterrent. It shows that sucrose could induce feeding whereas sinigrin could inhibit feeding behaviors of caterpillars of the two species. Sucrose and sinigrin could inhibit each other by caterpillars' feeding and electrophysiological responses. Secondly, we tested the feeding preference behaviors and taste responses to tomatine, the secondly substance of *H. armigera*'s host plant, the capsicine, the secondly substance of H. assulta's host plant, and the nicotine, the secondly substance of common host plant. In general, it show caterpillars of each species prefer to accept compounds from host plant, while exhibit aversive feeding behaviors for non-host plants. These results show plant second compounds may play important role in the host recognition and species diversification of the two Helicoverpa species.

S02-10

Detoxification of brassicaceae glucosinolates in multi-trophic interactions

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In Brassicaceae plants, glucosinolates and their hydrolytic enzymes, the myrosinases, form the characteristic two-component chemical defense system against herbivores often called the “mustard oil bomb”. Glucosinolates and myrosinases are stored in separate compartments to avoid self-intoxication. Chewing by herbivore ruptures this compartmentalization, and glucosinolates are hydrolyzed by myrosinases to produce toxic isothiocyanates (ITCs). In the crucifer-specialized herbivore *Plutella xylostella* (diamondback moth, Lepidoptera: Plutellidae), glucosinolate sulfatases (GSS) appear to function as a counter-adaptation to glucosinolates, desulfating these defenses to form harmless desulfo-glucosinolates, which cannot be hydrolyzed to ITCs. To test this hypothesis, we used plant-mediated RNAi to manipulate GSS function *in vivo*. The successful silencing of *gss* in *P. xylostella* larvae significantly lowered GSS activity and concomitantly elevated the concentrations of toxic ITCs in larval tissues, leading to dramatic negative effects on fitness. Thus, desulfation was proved as an effective and critical countermeasure against the mustard oil bomb. Nevertheless, in the next trophic level, a natural predator of *P. xylostella*, the lacewing *Chrysoperla carnea*, efficiently degraded the glucosinolate-derived ITCs present in *gss*-silenced larvae via a general conjugation pathway. Therefore in this case the toxic effects of plant glucosinolate hydrolysis will not be transferred on to higher trophic levels.

S02-11

Aphid-borne viral spread is enhanced by virus-induced accumulation of plant reactive oxygen species

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Most known plant viruses are spread from plant to plant by insect vectors. There is strong evidence that nonpersistently transmitted viruses manipulate the release of plant volatiles to attract insect vectors, thereby promoting virus spread. The mechanisms whereby aphid settling and feeding is altered on plants infected with these viruses, however, are unclear. Here we employed loss-of-function mutations in cucumber mosaic virus (CMV) and one of its host plants, tobacco (*Nicotiana tabacum*), to elucidate such mechanisms. We show that, relative to a CMVΔ2b strain with a deletion of the viral suppressor of RNAi 2b protein in CMV, plants infected with wild-type CMV produce higher concentrations of the reactive oxygen species (ROS) H_2O_2 in plant tissues. Aphids on wild-type CMV-infected plants engage in shorter probes, less phloem feeding, and exhibit other changes, as detected by electrical penetration graphing technology, relative to CMVΔ2b-infected plants. Therefore, the frequency of virus acquisition and the virus load per aphid were greater on CMV-infected plants than on CMVΔ2b-infected plants. Aphids also moved away from initial feeding sites more frequently on wild-type CMV infected versus CMVΔ2b-infected plants. The role of H_2O_2 in eliciting these effects on aphids was corroborated using healthy plants infused with H_2O_2. Finally, H_2O_2 levels were not elevated, and aphid behavior was unchanged, on CMV-infected RbohD-silenced tobacco plants, which are deficient in the induction of ROS production. These results suggest that CMV uses its viral suppressor of RNAi protein to increase plant ROS levels, thereby enhancing its acquisition and transmission by vector insects.

S02-12

What omnivores don’t eat: nonconsumptive ecological effects of phytophagy by *Macrolophus pygmaeus*

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Omnivorous predators can induce plant defences when feeding on plants, affecting the performance of herbivores. We showed previously that the omnivorous predator *Macrolophus pygmaeus* induces direct defences in sweet pepper plants, which negatively affects the performance and host plant choice of several herbivores. Furthermore, the omnivore can also affect plant phenology and reproduction. Here, we studied the effects of plant responses induced by the omnivorous predator *Macrolophus pygmaeus* on other natural enemies that share the same prey. We found that plant feeding by the omnivorous predator induced the production of plant volatiles, which attracted a specialist predator (predatory mite) even when its prey was absent, showing that the plant response to omnivore feeding may interfere with the searching behaviour of this important natural enemy. Thus, plant responses induced by plant feeding by the omnivorous predator affect interactions among omnivores, plants, herbivores and natural enemies.

S02-13

Anabolism of homoterpenes involved in indirect defense of *Gossipium hirsutum*

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Homoterpenes, such as (*E*)-4, 8-dimethylnona-1, 3, 7-triene (DMNT) and (*E,E*)-4, 8, 12-trimethyl-1, 3, 7, 11-tridecatetraene (TMTT), play an essential role in plant indirect defense by attracting herbivores’ natural enemies. For our work, we focused on the function and biosynthesis of homoterpenes in cotton. Firstly, the influence of DMNT and TMTT on behavioral preference of parasitic wasps in laboratory was clarified by EAG and Y-tube assay. And then candidate *CYP*s involved in homotepenes biosynthesis were filtered from genomic and transcriptome data of cotton. Functions of candidate *CYPs* were identified by using heterologous expression in yeast, enzymatic assay, GC-MS, qPCR, transgenic technology and virus-induced gene silencing techniques. *GhTPSs* and *GhCYPs* involved in homoterpenes metabolic pathway were co-expressed in *Saccharomyces cerevisiae* via employing yeast expression vector with two multiple cloning sites and tobacco plants via using multiplegene assembly vector system, and DMNT was de novo synthesized successfully. Moreover, transgenic tobacco plants releasing DMNT constitutively showed a statistically higher ability to attract parasitic wasps of *Helicoverpa armigera*, which laid a foundation to develop homoterpene overemitting crop cultivars to efficiently regulate the behavioral preference of parasitic wasps in IPM strategy.

S02-14

ER-body system in plant is involved in production of volatile compounds to suppress feeding motivation of insect: a model study using *Arabidopsis thaliana* and *Phormia regina*

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ER bodies derived from the endoplasmic reticulum and are distributed in epidermal cells of Brassicaceae seedlings. ER bodies accumulate b-glucoisdase (PYK10) that catalyzes glucosinolates to produce toxic compounds. Thus, the ER-body system has been proposed to function in defense. However, how this system protects seedlings from feeding by insects is unclear. To examine it, we established an experimental system with the blowfly, *Phormia regina*, in which the flies perceive simultaneously the sweet taste of sucrose and the odors produced from *Arabidopsis thaliana* homogenates. We found that the homogenate odors have a negative effect on their sucrose feeding motivation, which was evaluated using the proboscis extension reflex (PER). The PER threshold sucrose concentration was twice as high as that in the absence of the homogenates. On the other hand, the PER threshold in the presence of the homogenates from glucosinolate-deficient mutant (qKO) was the same as that in the absence of the homogenates. These results suggest that upon cell damage, the ER body system produces the volatile toxic compounds from glucosinolates, which induces avoidance behavior of the flies.

S03-01

A ligand-receptor pair for plant recognition of orally secreted elicitor peptides

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Inducible defense responses in plants are mediated by recognition of herbivore-associated molecular patterns (HAMPs), but specific mechanisms for HAMP perception have remained elusive. To identify a putative receptor for HAMPs, we utilized inceptin peptides: a set of ATP-synthase derived elicitors of plant defense found in Lepidopteran oral secretions. Recognition of inceptin is limited to certain legume species; therefore, we hypothesized that a legume-specific receptor mediates recognition. Using both QTL mapping and GWA as forward genetic approaches leveraging diverse germplasm of cowpea (*Vigna unguiculata*), we mapped inceptin-induced response variation to a single genetic locus. A leucine-rich repeat family receptor at this locus functioned as an Inceptin Receptor (INR) when expressed as a transgene in the non-legume species *Nicotiana benthamiana,* and was sufficient to confer peptide-inducible binding, signaling, and defense outputs. Stable transgenic lines expressing INR exhibited resistance to larvae of the generalist herbivore beet armyworm (*Spodoptera exigua*). The discovery of INR conceptually links cell surface immune recognition to perception of chewing herbivory, and provides a novel tool for studying the ecological consequences of a specific herbivore perception event. We will discuss INR and inceptin response variation within and between legume species as evidence for a molecular arms race at the level of immune recognition, as well as the development of genetic resources to link HAMP recognition to herbivore-induced responses in nature.

S03-02

The systemin receptor SYR1 enhances resistance of tomato against herbivorous insects

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Plant peptides play important roles regulating growth, development and interaction with other organisms. Discovered nearly thirty years ago as the first plant peptide hormone, systemin was shown to be critical for systemic wound response and anti-herbivore defense in tomato, yet its receptor remained mysterious. Here we report the discovery of the genuine systemin receptor. Starting with the observation that the wild tomato *S. pennellii*, in contrast to the cultivated tomato *S. lycopersicum*, lacks sensitivity to systemin, we mapped the trait responsible for systemin responsiveness by using a collection of introgression lines between these two species. We cloned two closely related leucine-rich repeat receptor like kinases (LRR-RLKs) that defined sensitivity to systemin. Heterologous expression of these receptors, named Systemin Receptor 1 (SYR1) and Systemin Receptor 2 (SYR2), confers systemin responsiveness to *Nicotiana benthamiana* and *Arabidopsis thaliana*, two plants otherwise blind to systemin. SYR1 exhibits specific, high-affinity binding for systemin whereas SYR2 acts as a low-affinity receptor. We further show that SYR1 mediated systemin signaling, although not decisive for local and systemic wound responses, is important for defense against herbivorous insects.

S03-03

Integration of herbivore-induced plant volatiles into plant defense and resistance

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Plants emit specific herbivore-induced plant volatiles (HIPVs) upon herbivore attack. HIPVs can prime the defenses and resistance of intact plant tissues to subsequent herbivore attack. However, whether plants are able to integrate multiple HIPV cues, and how HIPVs are integrated into the early plant defense signaling are unclear. Here, we found that maize plants can integrate two herbivore-induced volatile priming cues the aromatic volatile indole and the green leaf volatile (Z)-3-hexenyl acetate (HAC), with complementary information content. Dual exposure of these two volatiles results in synergistic priming effects on plant defenses and resistance. Indole exposure primes the activation of early signaling components OsMPK3 and OsMPK6, the expression of *OsWRKY70* and jasmonate-biosynthesis genes of rice plants. Using transgenic plants defective in early signaling, we found that OsMPK3 is required, and that OsMPK6 and OsWRKY70 contribute to indole-induced defense priming. We are currently investigating the molecular basis of HAC-induced defense priming. Taken together, multiple volatile cues can be integrated by plants and may prime plant resistance by regulating early defense signaling components.

S03-04

Getting tuned: understanding specificity in plant volatile signaling

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Plant leaves emit large amounts of volatile blends. When attacked by insects, the composition of these blends changes markedly. These changes not only alter the behavior of insects interacting with the plant but also affect the metabolism of the emitter itself and of those plants growing in close vicinity to the emitter. Our research focuses on a group of plant volatiles earliest emitted upon herbivory, called “green leaf volatiles” (GLVs). We uncovered enzymes present in plants and insects profoundly affecting multiple ecological interactions by converting the highly abundant GLV *Z*-3-hexenal into *E*-2-hexenal. These two compounds, as well as their derivatives, have distinct effects on insect herbivore and predator behavior as well as on plant metabolism. We show that the presence of a salivary hexenal isomerase in the tobacco hornworm *Manduca sexta* can be both beneficial and detrimental for the insect. We have already generated mutant hornworms and we are currently busy with generating mutant plants with impaired hexenal isomerase activity. With these mutants in hand we will not only be able to assess the importance of hexenal isomerization in a tri-trophic ecological interaction but also to gain insight in to the primary function of this enzyme for plants and insects.

S03-05

The oriental armyworm (*Mythimna separata*) feeding induces local and systemic defense responses within and between maize leaves

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Attack from insect herbivores poses a major threat to maize, and as other plant species studied, maize has evolved sophisticated systems to defense against herbivores. However, the herbivory-elicited within-leaf and leaf-to-leaf systemic signalling in maize remains largely unexplored. We studied the response of maize to mechanical wounding (W) and simulated *Mythimna separata* (a specialist insect) herbivory by applying its oral secretions (OS) to wounds. Locally, OS elicited larger and longer-lasting changes in the maize transcriptome, proteome, metabolome and phytohormones compared with W. Specifically, many genes, proteins and metabolites were uniquely induced or repressed by OS. Systemically, both OS and W treatment elicited increased levels of jasmonic acid (JA), JA-Ile (JA-isoleucine conjugate) and benzoxazinoids (Bxs) in specific systemic regions within a leaf. Importantly, increased contents of Bxs were detected in a systemic leaf, and consistently, this leaf exhibited increased defence against *M. separata*. Increased JA/JA-Ile and altered transcriptome, including Bx biosynthesis genes, were detected in systemic leaves after wounding or simulated herbivory treatments, although only simulated herbivory induced increase of the contents of Bxs systemically. Promoter and co-expression analysis revealed that transcription factors *bHLH57* and *WRKY34* may regulate Bx biosynthesis genes in systemic leaves. Moreover, leaf ablation experiment indicated that the systemic signal rapidly exited the local leaves within 30 min after elicitation. This study provides new insight into the temporal and spatial regulation of defence responses of maize against lepidopteran insects.

S03-06

Chemical cues linked to risk: plants and insect herbivores respond to chemical cues from entomopathogenic nematodes

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Chemical cues play important roles in mediating interactions among organisms at different trophic levels. Insect herbivores, for example, frequently use plant odors to locate suitable host plants and herbivore natural enemies, including predators and parasitoids, are often attracted to chemical cues associated with their prey. Here, we explored the ecological significance of chemical cues produced by herbivore natural enemies for plant protection against herbivores. We investigated whether chemical cues from beneficial entomopathogenic nematodes (EPNs), which are important natural enemies in agroecosystems, influence plant defense responses or herbivore behavior. We recently reported that potato plants exposed to live EPNs or their chemical cues had enhanced systemic resistance against foliar-feeding Colorado potato beetles and that female beetles avoided EPN cues. Building on this work, our current findings indicate that exposure to chemical cues from EPNs also enhanced systemic defenses in cucumber plants and that some root-feeding insects detect and avoid EPN chemical cues.

S03-07

Insights from the JA signaling cascade and down-stream defense responses into herbivore perception through AMF networks in the *Nicotiana attenuata* system

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Arbuscular mycorrhizal fungi (AMF) establish symbiotic associations with a majority of terrestrial plants to form underground common mycorrhizal networks (CMNs) that connect neighboring plants. Since *Nicotiana attenuata* plants do not respond to herbivory-elicited volatiles from neighbors, we used this ecological model system to evaluate if CMNs function in inter-plant transmission of herbivory-elicited responses. A mesocosm system was designed to establish and remove CMNs linking *N. attenuata* plants to examine the herbivory-elicited metabolic and hormone responses in CMNs-connected "receiver" plants after the elicitation of "donor" plants by wounding (W) treated with *Manduca sexta* larval oral secretions (OS). AMF colonization increased constitutive jasmonate (JA and JA-Ile) levels in *N. attenuata* roots*,* but did not affect well-characterized JAs-regulated defensive metabolites in systemic leaves. Interestingly, larger JAs bursts and higher levels of several amino acids and particular sectors of hydroxygeranyllinalool diterpene glycoside metabolism were elevated in the leaves of W+OS-elicited "receivers" with CMN connections with "donors" that had been W+OS-elicited 6 h previously. These results demonstrate that AMF colonization alone does not enhance systemic defense responses, but that sectors of systemic responses in leaves can be primed by CMNs, suggesting that CMNs can transmit and even filter defense signaling among connected plants.

S03-08

Expressing *OsMAPKb* increases rice resistance to BPH but accelerate rice senescence

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Mitogen-activated protein kinases (MAPKs) play a pivotal role in many plant physiological processes such as cell division and differentiation, plant growth, development and senescence as well as plant responses to abiotic and biotic stresses. Although the role of MAPKs in plant-pathogens interactions has been well documented, their roles in plant-herbivores interactions are largely unexplored. Here, we identified a MAPK gene from rice (*Oryza sativa*), *OsMAPKb*, whose expression was induced by infestation of gravid female adults of a destructive rice pest, brown planthopper (BPH, *Nilaparvata lugens*), but not by BPH nymphs. Overexpression of *OsMAPKb* (oeMAPKb) increased accumulation of gravid BPH female-induced salicylic acid (SA), jasmonic acid (JA), jasmonoyl-isoleucine (JA-Ile) and abscisic acid (ABA) in rice plants, and thereby enhanced the resistance of rice plants to BPH adults and eggs. Exogenous application of ABA and methyl jasmonate (MeJA) on rice decreased the hatching rate of BPH eggs and delayed their developmental rate. Interestingly, when exposed to high densities of gravid BPH females, oeMAPKb plants wilted earlier than wild-type plants, which could be attributed to the hyperaccumulation of SA, JA, JA-Ile and ABA in oeMAPKb plants. Moreover, when released into a field, oeMAPKb plants displayed resistance to both BPH and white-backed planthopper (*Sogatella furcifera*), another destructive pest of rice, but produced lower yield than wild type plants. Taken together, our findings suggest that OsMPKb functions as a positive regulator of rice resistance to planthoppers and rice senescence partialy at least by regulating ABA, JA and SA signaling.

S03-09

Systemic stomatal closure induced by herbivores is dependent on jasmonic acid-mediated synthesis of H_2O_2 in guard cells

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Wounding or insect herbivory specifically induces rapid down-regulation of plant systemic photosynthesis, characterized by rapid response of stomatal aperture to herbivory-induced systemic signals. To understand the molecular and physiological mechanisms of herbivores-induced jasmonic acid (JA) defense signals in regulating stomatal aperture in systemic plant leaves, wild-type tomato CM and *suppressor of prosystemin-mediated responses8* mutant (*spr8*) were subjected to simulated-herbivory treatment of local tomato leaflets by wounding + water (W+W) and wounding + oral secretion (W+OS). Changes in stomatal aperture and photosynthetic gas exchange in the short-term (≤3h) of local and systemic tomato leaflets (uninjured, vascular connection) were examined. Wounding or herbivory rapidly led to induced expression of JA synthesis genes *LOXD*, *AOS*, *AOC* and *OPR3* in local leaves, and the accumulation of JA and down-regulation of photosynthesis in whole plants. Both local W+W and W+OS treatments induced systemic stomatal closure, while the responses were compromised in the JA-deficient mutant *spr8*. Defense responses (proteinase inhibitors) and stomatal closure were similarly induced in CM and *spr8* scions in response to graft-transmissible signals from elicited CM stocks, but these were compromised in the scions with *spr8* as a stock. Further experiments showed that JA signal was generated locally and transmitted to the system to integrate the stress signal into ROS in the leaf guard cells of the systemic to trigger downstream signal transduction events and induce systemic stomatal closure. Taken together, we conclude that the systemic stomatal closure induced by wounding or herbivory in tomato is regulated by the locally generated JA signal. JA may regulate herbivore-induced stomatal closure by triggering ROS bursts in guard cells in systemic leaves. This finding highlights the complexity and role of JA signaling in regulating systemic defense and carbon assimilation pathways in response to herbivorous attacks.

S03-10

Solar UV-B radiation and ethylene play a key role in modulating effective defenses against herbivore insects in field-grown soybean

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Solar UV-B radiation has been reported to enhance plant defenses against herbivore insects in many species. However, the mechanism and traits involved in the UV-B mediated increment of plant resistance are largely unknown in crops species, such as soybean. Here we determined in undamaged and damaged leaves by *Anticarsia gemmatalis* larvae and in pods by stink bugs of two soybean cultivars (cv.) grown under attenuated or full solar UV-B radiation changes in jasmonates, ethylene, salicylic acid, trypsin protease inhibitor activity, flavonoids and mRNA expression of genes related with defenses. Ethylene emission induced by herbivory was synergistically increased in plants grown under solar UV-B radiation and was positively correlated with malonyl genistin concentration, TPI activity and expression of IFS2 and the defensive protein PR2, while was negatively correlated with leaf consumption and stink bug damage. The precursor of ethylene ACC applied exogenously to soybean was enough to strongly induce leaf isoflavonoids. Our results showed that in field-grown soybean isoflavonoids were regulated by both herbivory and solar UV-B inducible ET, while flavonols were regulated by solar UV-B radiation and not by herbivory or ET. Our study suggests that although ET can modulate UV-B-mediated priming of inducible plant defenses, some plant defenses, such as isoflavonoids are regulated by ET alone.

S04-01

A novel lineage of pheromone receptors for sex communication in moths

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Sex pheromone receptors (PRs) are key players in chemical communication between mating partners in insects. In Lepidoptera, male PRs tuned to female-emitted type I pheromones (which make up the vast majority of pheromone compounds identified in this highly diversified insect order) form a dedicated subfamily of odorant receptors (ORs). Here, using a combination of heterologous expression and *in vivo* genome editing methods, we bring functional evidence that at least one moth PR does not belong to this subfamily but to a distantly related OR lineage. This PR, identified in the cotton leafworm *Spodoptera littoralis*, is over-expressed in male antennae and is specifically tuned to the major sex pheromone component emitted by females. Mining genomic data in related species, we identified ORs that grouped together with the newly identified PR in a defined phylogenetic clade. Their functional studies revealed that they were also tuned to sex pheromone components, suggesting two independent apparitions of PRs tuned to type I pheromones in Lepidoptera, opening up a new path for studying the evolution of moth pheromone communication.

S04-02

CRISPR/Cas9 mediated gene knockout reveals different contribution of three PBP genes in female sex pheromone perception in *Spodoptera litura*

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Three pheromone binding proteins (PBPs) commonly exist in the sensilla lymph of noctuid moth antennae, but their relative contribution in perception of the sex pheromone is rarely verified *in vivo*. Here we reveled the different contributions of three *Spodoptera litura PBPs* (*SlitPBP1, 2* and *3*) by using CRISPR/Cas9 system. First, by co-injection of Cas9 mRNA/sgRNA into newly laid eggs, high rate of target mutagenesis was induced (51.5%, 46.8% and 39.1% for *SlitPBP1, 2* and *3*, respectively) determined by restriction enzyme assay. Then, the homozygous PBP knockout lines were purified by an in-crossing strategy. Finally, electrophysiological (EAG recording) and behavioral analyses were performed, using homozygous knockout male moths. Results showed that PBP knockout males decreased EAG response by a similar extent to the three pheromone components (Z9,E11-14:Ac, Z9,E12-14:Ac and Z9-14:Ac), around 60%, 40% and 20% for *SlitPBP1*, *2* and *3* knockout males, respectively, indicating that three PBPs are non-selective among pheromone components but different in contribution to the sex pheromone perception. Consistently, behavioral assays with the major component (Z9,E11-14:Ac) showed that *SlitPBP1* knockout males responded in much lower percentages than *SlitPBP2* knockout males in terms of orientation to the pheromone, and close range behaviors such as hairpencil display and mating attempt. Taken together, our study provides direct functional evidence for the roles of three *SlitPBP*s, as well as their relative contribution (*SlitPBP1*> *SlitPBP2*> *SlitPBP3*) and non-selectivity among sex pheromone components. This would be helpful for deep understanding the mechanism of sex pheromone perception, and for developing PBP-targeted pest control techniques.

S04-03

An odorant receptor mediates pheromone to regulate locust density

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Sensation to pheromones are important for animal to behave properly with partners. Most studies on molecular mechanisms of reception to sexual pheromones. The molecular mechanisms of olfaction underneath aggregation behavior which is universal in animals are still mysterious. Here we demonstrate an insect odorant receptor expressed on neurons in trichoid sensillum tunes to aggregation pheromones with locust (*Locusta migratoria*). An odorant receptor, named as *Lmig*OR3 is identified in locust antenna, and is demonstrated to be expressed in olfactory sensilla which distribute quite widely on antenna by *in situ* hybridization experiment. *Lmig*OR3 tuned broadly to 18 odorants including HP and DP which are locust body volatiles, in aT1 neuron of transgenic Drosophila antennal trichoid sensilla in single unit electrophysiological experiment. DP can attract larval locust behavioral response at proper concentrations, but repel at high concentrations. Consequently, the results of experiments with RNAi of *LmigOR3* showed that locusts which are depressed *LmigOR3* significantly decrease the responses (numbers of spikes per unit) of olfaction receptor neuron to DP, but significantly increase their preference index of behavior to DP, compared to wild types. Taken together, *Lmig*OR3 is a pheromone receptor which mediates DP, a component of aggregation pheromone to regulate locust density.

S04-04

Genome-wide identification and functional study of chemosensory genes in three notorious rice planthoppers

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Three rice planthoppers (The brown planthopper (BPH), *Nilaparvata lugens*, the small brown planthopper (SBPH), *Laodelphax striatellus* and the whitebacked planthopper (WBPH) *Sogatella furcifera*) are notorious pests causing a huge rice loss every year. They not only damage rice plant by sap-sucking but also transmitting various plant viruses. Chemoreception play an indispensable role in locating and selecting rice plant, which have been identified three decades ago. But its molecular mechanism is rarely unknown.

In this study, based on the WBPH, SBPH and BPH transcriptome and genome data, we first annotated a large numbger of genes encoding for several families of chemosensory genes, We identified141 ORs (odorant receptors), 28 GRs (gustatory receptors) and 24 IRs (ionotropic receptors) in BPH; 135 ORs, 18 GRs and 16 IRs in WBPH; and 132 ORs, 13 GRs and 23 IRs in SBPH. Except for chemosensory receptors, we further discovered the presence of 12, 12, and 16 OBPs (odorant binding proteins) in WBPH, BPH, and SBPH, respectively, including two novel OBPs. Phylogenetic analysis indicated that most of these OBPs have homologous genes, and one group (SfurOBP11, NlugOBP8, and LstrOBP2) show a slower evolution rate and are more conserved. Furthermore, *in vitro* binding studies demonstrated that the three OBPs have similar binding affinities for some rice plant volatiles. Finally, RNA interference successfully inhibited the RNA expression of the three OBP and odorant co-receptor (Orco) genes, and *in vivo* behavioral tests showed that the OBP- and Orco-deficient rice planthoppers were partly anosmic and lost some of their ability to locate rice plants.

Taken together, these findings will be helpful for determining the potential physiological functions of chemosensory genes of rice planthoppers, which in turn may help to discover new targets for broad specrum behavioral antagonists for use as control strategies.

S04-05

Physicochemical basis and comparison of two type II sex pheromone components binding with pheromone-binding protein 2 from tea geometrid, *Ectropis obliqua*

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Lepidopteran geometrid moth can produce complex Type II sex pheromone components to attract males and trigger mating behavior. Although several sex pheromone components have been identified, it remains unclear whether their physicochemical roles in sex pheromone sensing are the same. Therefore, we utilized tea geometrid (*Ectropis obliqua*) as an example model to investigate and compare the physicochemical basis of two key Type II sex pheromone components, cis-6,7-epoxy-(3Z,9Z)-3,9-octadecadiene (Z3Z9-6,7-epo-18:Hy) and (Z,Z,Z)-3,6,9- octadecatriene (Z3Z6Z9-18:Hy), interacting with pheromone-binding protein 2 (*Eobl*PBP2) from *E. obliqua*. Multispectral, thermodynamic, docking, and site-directed mutagenesis indicated that the major sex pheromone component Z3Z9-6,7-epo-18:Hy is more susceptible to pH-tuned than the minor component Z3Z6Z9-18:Hy, whereas Z3Z6Z9-18:Hy seems to be more susceptible to temperature and amino acid mutations than Z3Z9-6,7-epo-18:Hy. Our study suggests that different components of Type II sex pheromone play different binding characters under specific conditions in the physicochemical behavior. This deeply supplements the theoretical knowledge of Type II pheromones involved in the recognition and discrimination in the Lepidopteran sex pheromones family.

S04-06

Identification and chemoreception of sex pheromone in *Athetis lepigone*

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Two sex pheromones were detected by GC-EAD analysis in the extracts of the female sex pheromone gland of *Athetis lepigone*, (Z)-7-dodecenyl acetate (Z7-12:Ac) and (Z)-9-tetradecenyl acetate (Z9-14:Ac) in a ratio of 1:5 by mass spectral analysis of natural pheromone components and dimethyl disulphide adducts. Pheromone receptors (PRs) of male adult insects are generally thought to function in the recognition of female sex pheromones, and are also important molecular targets for the development of behavioral inhibitors and insecticides. Then, we successfully expressed and functionally analyzed four AlepPRs of *A. lepigone* in *Xenopus* oocytes using the two-electrode voltage-clamp method. The results demonstrated that AlepOR3 responded exclusively to the sex pheromone compound of *A. lepigone*, Z7-12:Ac ($EC_{50} = 8.830 \times 10^{-6}$ M), while AlepOR4 responded to all five compounds [(Z7-12:Ac, (Z)-8-dodecenyl acetate (Z8-12:Ac), Z9-14:Ac, (Z,E)-9,11-tetradecadienyl acetate (Z9,E11-14:Ac), and (Z,E)-9,12-tetradecadienyl acetate (Z9,E12-14:Ac)] and had a higher response to Z9-14:Ac ($EC_{50} = 2.243 \times 10^{-5}$ M) than to Z7-12:Ac. However, AlepOR6 displayed a significantly higher response to a non-pheromone of *A. lepigone*, Z9,E12-14:Ac ($EC_{50} = 7.145 \times 10^{-6}$ M), than to the other four compounds. AlepOR5 displayed no responses to any of the pheromone compounds of *A. lepigone*, but responded exclusively to (Z)-11-hexadecenyl acetate (Z11-16:Ac) ($EC_{50} = 7.870 \times 10^{-6}$ M), a sex pheromone compound of other Noctuidae species. These findings can help explore the molecular mechanisms of sex pheromone recognition in *A. lepigone* and other moths.

S04-07

Olfactory coding of sex pheromone blends in Heliothine moth species

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Heliothine species include some of the World's most devastating pest species, such as *Heliothis virescens* and *Helicoverpa zea* in the New World and *Helicoverpa armigera* in the Old World. The sex pheromone communications of these agricultural pest species have been investigated from pheromone molecules, pheromone receptors (PRs), to brains and behaviors in detail. In this presentation, I will summarize recent progresses in identification of the PRs tuned to principal sex pheromone components including Z11-16:Ald, Z9-16:Ald, Z9-14:Ald, and related alcohols and acetates in Heliothine species. Focusing on two sympatric *Helicoverpa* species, *H. armigera* and *H. assulta* sharing Z11-16:Ald and Z9-16:Ald as pheromone components but in reversed ratios, 97:3 and 7:93, respectively, I will report how we assign different PRs to OSNs and types of sensilla responding to the pheromone components and the related compounds. We find that the PR orthologs in the two species do not necessarily have the same selectivity, and their species-specific changes in the tuning selectivity in male moths could be achieved with just a few amino acid mutations. We conclude that evolution of the olfactory coding mechanisms for pheromones of the two species satisfies the need of specific-species pheromone detection, which shed new light onto the reproductive isolation between these species.

S04-08

Putative neural network within a *S. basiconoica* for nestmate and non-nestmate CHC discrimination in the Japanese carpenter ant: the ultrastructure and mathematical simulation

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Ants are known to use a colony-specific blend of cuticular hydrocarbons (CHCs) as a pheromone to discriminate between nestmates and non-nestmates, and the CHCs were sensed by the basiconic type of sensilla (*S. basiconica*). To investigate the functional design of S. basiconica, we observed its ultrastructure in the Japanese carpenter ant, *Camponotus japonicus*, using a serial block-face scanning electron microscopy (SBF-SEM), conventional and ultra-high voltage electron microscopies (C-TEM and UHV-EM), and super-resolution microscopy (SRM) combined with immunohistostaining. Our new findings were as follows; Based on SBF-SEM images, 3D model of the ultrastructure of *S. basiconica*, was constructed. It revealed that more than 100 unbranched dendritic processes of olfactory receptor neurons (ORNs) had characteristic “beaded structures”and formed a twisted bundle. C-TEM and UHV-EM images showed that the cell membranes of the dendritic processes were closely adjacent in the interdigitated profiles at “beads”. Immunohistostaining proved that *C. japonicus* Innexin 3 (CjapInx3), i.e., the invertebrate gap junction (GJ) protein, were localized inside of the sensillum. It showed a characteristic twin-peak-distribution similar to the distribution of “beads”. These results suggest that the ORNs in a S. basiconica form an electrical network via GJs between dendritic processes at the “beads”. Mathematical simulations supported that such an ORN network can modify olfactory inputs consisting of multiple odor components.

S04-09

Identification and function researches of Dendrolimus specific pheromone receptor genes

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Dendrolimus punctatus Walker is a serious pest affecting conifers in southern China. Chemosensory genes represent potential molecular targets for development of alternative pest control strategies. We analyzed the transcriptomes of *D. punctatus* collected at different developmental stages organs. A total of 171 putative chemosensory genes were identified. Expression analysis indicated that the antennae possess the largest number of highly expressed olfactory genes; olfactory gene expression patterns in the eggs, larvae, and head were similar to one another, with each having moderate numbers of highly expressed olfactory genes; Fat body, ovary, midgut, and testis tissues also had similar olfactory gene expression patterns, including few highly expressed olfactory genes. Particularly, we identified no pheromone receptors in *D. punctatus*. To further identify the PRs, we generated transcriptome data from male and female adult *D. punctatus* specimens at four mating stages: eclosion, calling, copulation, and post-coitum. Levels of OBPs, CSPs, and ORs were closely correlated with mating behavior. Comparison with ORs from other *Dendrolimus* and Lepidoptera species led to the discovery of a group of ORs specific to *Dendrolimus*. Further function researches indicate that these ORs specific to *Dendrolimus* were pheromone receptors of this insect. This work promote research into the mechanisms underlying insect olfactory recognition.

S04-10

Comparison of chemosensory receptor genes in the antennae transcriptome of *Sirex noctilio* and *S. nitobei* (Hymenoptera: Siricidae)

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Sirex noctilio Fabricius is a worldwide quarantine pest of forestry, mainly harms conifers, especially *Pinus* species. Meanwhile, *Sirex nitobei* Matsumura is a closely related species of *S. noctilio*, which is native to China. Olfaction and gustation play a vital role in insect survival. However, the molecular mechanism of chemoperception in the two woodwasps are still unknown. In the present study, we performed a thorough comparative analysis of 62 chemosensory receptors in *S. noctilio* and 69 in *S. nitobei* by transcriptome sequencing and molecular approaches, including 41 odorant receptors (ORs), 13 ionotropic receptors (IRs), 8 gustatory receptors (GRs) in *S. noctilio* and 43 ORs, 16 IRs and 10 GRs in *S. nitobei*. The sex- and tissue-specific expression profiles of these genes were investigated by reverse transcription PCR (RT-PCR) and quantitative real-time PCR (qRT-PCR). The results suggested that 36 ORs, 7 IRs, 3GRs were enriched in the antennae of *S. noctilio*. Among them, 19 ORs were female-biased, whereas 4 ORs (*SnocOR6*, *SnocOR15*, *SnocOR18*, and *SnocOR30*) were significantly male-biased, implying that they may sense pheromones. Meanwhile, 34 ORs, 7 IRs, 3GRs were highly expressed in *S. nitobei* antennae. Among these antennae-enriched genes, 22 ORs were female-biased, whereas, *SnitOR2*, *SnitOR18* and *SnitOR30* were significantly male-biased. These results provide an important basis for revealing the chemoreception molecular mechanism in the two closely related species, as well as a new idea for pest control from the perspective of Anti-chemical ecology.

S04-11

Identification and functional study of the pheromone receptors in *Apolygus lucorum*

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The green mirid bug (GMB), *Apolygus lucorum* is an important agricultural pest in China. The mechanism of olfactory recognition in the GMB is a hot issue in neurology and chemical ecology, and the functions of pheromone receptors attract more attentions because of their special importance. Previous studies have demonstrated the presence of intraspecific sex pheromones in Mirada. And the component and biological activity of the pheromones has also been clearly studied. However, few studies have been focused on the molecular and neural mechanisms of pheromone perceiving in the GMB so far. In our recent study, we identified and systematically studied the sex pheromone receptors of GMB. We sequenced the antennal transcriptoms of three species including GMB, *Adelphocoris lineolatus* and *Adelphocoris suturalis*. Four candidate pheromone receptor genes of GMB were identified by comparative transcriptome and expression pattern analysis. The full-length sequences of four candidate pheromone receptor genes were cloned, and all candidate pheromone receptor genes were expressed in *Xenopus* oocyte expression system. The responses of these receptors to sex pheromone components were recorded by two-electrode voltage clamp. We proved that these four receptors were pheromone receptors and could be activated by different sex pheromone components of GMB. This study will provide a theoretical basis on which we can screen new behavioral disturbance agents that are more effective than sex pheromones at molecular level.

S05-01

Info-chemical flows among plants, flies and microbial communities of larval growth and oviposition environments

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Chemical cues have been widely used for flies for their host and host associate environment location. Some of flowers are capable of using their deceptive pollination strategy to mimic the pollinating flies' courtship pheromones to enhance the pollination. In this presentation, I will report several case studies describing how these flies use various classes of chemical cues either associated with their hosts or host plants for locating food sources and oviposition sites. How animal pollinated plants use a variety of mechanisms to attract pollinators and induce behaviors resulting in the transfer of pollen between the flowers. In addition, how some of these chemical cues can be used for developing novel pest management tools. Fly species included in this report are pollinating flies, predacious flies, public health concerned flies and flies that attack livestock animals and human beings.

S05-02

Neighbours matter: community effects on plant-volatile emissions

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Plants are well known to affect the volatile emissions of adjacent plants; however, this phenomenon has been rarely recorded on non-crop species under natural conditions where multiple environmental variables can also impact volatile emissions. Here, we report the results of a field study exploring the volatile organic compound (VOC) emissions of an invasive plant species (heather, *Calluna vulgaris*) in the Central Plateau of the North Island of New Zealand, where it naturally occurs in combination one of two native species, Monoao and Mānuka (*Dracophyllum subulatum* and *Leptospermum scoparium*), or another invasive (Scotch broom, *Cystius scoparius*). We collected headspace samples from heather in vicinity with con- and hetero-specifics, alongside environmental and soil data from the collection sites. Our results show that heather changes its volatile profile according to its competitors, significantly reducing its VOC emissions when paired with another invasive species (Scotch broom), which is well known to affect soil nutrient availability. In agreement with this observation, for the majority of the identified compounds, differences in VOC emissions were associated with changes in soil nutrients. Other factors such as temperature and herbivory had a minor, although significant, effect in the emission of a few compounds such as the homoterpene (*E*)-DMNT and the green leaf volatile hexyl-acetate. In this study, the soil water content did not have a significant impact on VOC emission. These results suggest that, under field conditions, invasive plants change their volatile emissions in response to the identity of their competitors and their associated environmental changes.

S05-03

A practical technique for EAG recording from lamellated antenna of scarab beetle

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Host-plant volatiles play a key role in finding mate and suitable host plants of phytophagous scarab beetles. Hence it is immensely important to collect and identify these volatiles. The gas chromatography coupled with electroantennographic detection (GC-EAD) technique has been used as a rapid and convenient tool for the identification of physiologically active components from plants. Here, we describe a practical method for electrophysiologically recording from lamellated antenna of scarab beetles. This method enables direct electroantennogram (EAG) recordings from antennal club without damage to the antenna in a similar manner to the conventional cut-tip EAG recording technique for clavate antenna. The headspace volatiles from walnut (*Juglans regia* L.) trees were collected with a Poropak-Q trap at dusk and then analyzed with GC-EAD. Those volatile compounds that elicited electrophysiological responses on the antennae of a scarab beetle, *Metabolus flavescens* Brenske (Coleoptera: Scarabeidae: Melolonthinae) were determined by means of gas chromatography-mass spectrometry (GC-MS). The lamella directly connected to the recording electrode was held apart from the other two lamellae on the antenna with a minuten pin and a disposable syringe needle. In order to improve electrical contact, a surfactant, Tween® 80, was used to lower the surface tension of Beadle–Ephrussi Ringer solution. This study demonstrated that addition of 0.05% Tween® 80 to the Beadle–Ephrussi Ringer solution suppressed baseline noise and assured significantly greater EAG response in general. Due to its simplicity and efficiency, this method may also be useful for studying the electrophysiology of other insect species having club-like antennae.

S05-04

Volatile production by banana plants infected with *Fusarium oxysporum* f.sp. *cubense*

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Panama disease or Fusarium wilt is the most devastating disease of bananas of modern times, caused by the soil-borne fungus *Fusarium oxysporum* f.sp. *cubense* (Foc). Four races of Foc are recognised, based upon the cultivars which they impact: Race 1 is virulent on Gros Michel and Lady Finger cultivars, while Race 4 is virulent on Cavendish, as well as the cultivars susceptible to race 1 and 2. Race 4 is further subdivided into Tropical Race 4 (TR4) and Subtropical Race 4 (STR4); STR4 only infects Cavendish and Race 1 and 2 susceptibles under abiotic stress. Work from the 1990s demonstrated that, when grown on rice, Race 4 isolates produce distinctive odours, which are not produced by isolates of Race 1. The work described here investigated whether volatiles produced by banana plants inoculated with Foc could be used to identify infected plants, before the onset of disease symptoms. Banana plants were inoculated in the glasshouse with Foc (Race 1 (VCG 0124) and 4 (VCG 0120) in Lady Finger, and Race 4 in Cavendish), and plants allowed to develop. After six weeks, while the plants were still pre-symptomatic, volatiles were sampled by SPME and analysed by GC-MS. The odours of plants were significantly different between cultivars. In Lady Fingers, plants infected with STR4 were significantly different to both control plants, and those infected with Race 1, this appeared to be due to increases in levels of a variety of monoterpenes. In Cavendish plants, there was no difference in the odours of plants infected with the two Fusarium races. Once the plants expressed symptoms, these differences between STR4 plants and controls was no longer in evidence, perhaps due to damage by the fungus to the vascular tissue inhibiting spread through the plants. At the end of the trial, the corm of the plant was destructively sampled, and volatiles analysed. Plants affected with STR4 were, again, significantly different to the other treatments. These results are promising for the early detection of Foc in bananas, assisting in the management and control of this extremely destructive disease.

S05-05

Provisioning pheromone: parents regulate larval begging by the pheromone in a burying beetle

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Parental feeding is an important behavior forming the basis of family life. Since the optimal feeding amount is different between parents and offspring, it is estimated that there is an evolutionary conflict of interests between them. In previous studies, it has been considered that the interaction between offspring begging and parental feeding response determines the feeding amount. However, superfluous begging can inhibit larval growth, it is no wonder that parents develop some mechanisms regulating larval begging. In this study, we discovered that parents of the burying beetle *Nicrophorus quadripunctatus* regulate the larval begging by volatile pheromone, which we termed “provisioning pheromone”. The larvae of this species synchronously show begging behavior just before parental feeding. We compared the chemical profiles of the hexane extracts of provisioning females (the individuals that approach larvae to feed and are begged by larvae) and non-provisioning females (the individuals not begged by larvae) by using gas chromatograph-mass spectrometry. As a result, an aromatic compound, 2-phenoxyethanol, was detected specifically in the extract of provisioning females, and this compound elicits larval begging. Furthermore, our behavioral experiment showed that the larval growth and survival rate were decreased if the larvae were continued to force to beg by 2-phenoxyethanol, demonstrating that superfluous begging is costly for offspring for the first time in insects. This study suggests that a parental provisioning signal can reduce the conflict over feeding between parents and offspring.

S05-06

Regulation of aphid population and distribution on host plants by tending ants: benefits to mutualistic insects with a sacrifice of host plants

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In aphid-ant mutualism, ants consume honeydew produced by aphids that gain protection from ants in return. Little is known, however, about whether/how ants regulate aphid population, and its potential influence on the organisms involved in this system. Here, we examined dynamic population and distribution of cotton aphid (*Aphis gossypii*) on cotton (*Gossypium* spp.) plants, and the impact on growth of host plants, in the presence of tending red imported fire ants (*Solenopsis invicta*) in an enemy-free system. The results showed a faster aphid colony growth under the coexistence of ants compared to that without ants. After being tended by ants for several days, aphids aggregated on stem and petiole of cotton plants, with shorter distances to ant nests compared to those from most of other cotton parts, suggesting that the regulation of aphid distribution on host plants may assist ants in saving time and energy cost during foraging. No ant was observed transporting aphids mechanically, implying that chemical, visual, or tactile cues probably play major roles in this regulation. More alate aphids reproduced in mutualistic colonies indicated that the faster aphid population growth was unlikely due to limited flight dispersal. Ant-tending inflicted a cost on cotton growth, with reduced growths of leaf area and plant height compared to those in ant-free controls. This study reveals a regulation of aphid population and distribution on host plants by their tending ants, which may benefit both mutualistic insects but harm host plants.

S05-07

Aposematic signal and antipredator defense in locusts

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Many aggregating animal species utilize aposematic signals to advertise their toxicity to predators. However, the functional coordination and biosynthesis of aposematic signals and toxins are poorly understood. Here, we reveal that phenylacetonitrile (PAN), a phenylalanine-derived volatile, acts as an aposematic olfactory signal and as a precursor compound of hypertoxic HCN, to facilitate the antipredator defense response of gregarious locusts. We find a novel gene encoding a cytochrome P450, *CYP305M2*, which is able to catalyze a rate limiting step of the biosynthesis of PAN from phenylalanine. The expression levels of *CYP305M2* directly respond to the changes in locust population density. The elevation of PAN levels through supplementation with synthetic PAN increases the resistance of locusts to bird predation. By contrast, the knockdown of *CYP305M2* through RNA interference increases the vulnerability of gregarious locusts to predation. When locusts are suddenly disturbed, PAN is rapidly converted to HCN. Our results indicate that locusts have developed a novel defense mechanism wherein an aposematic compound is converted to a hypertoxic cyanide in response to predation by natural enemies.

S05-08

Detection of chemical signals from host and non-host organisms in insects

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The chemical signals in ecosystems are complex and dynamic, in which each species of insects needs to detect important chemical signals and discriminate them from various background chemical noise. To achieve this, insects have developed highly sensitive and selective chemosensory system. In both contact chemoreception and olfactory perception, many insects appear to have a common architecture of agonist-antagonist sensory system. A contact chemosensillum often contains a combination of an agonist sensory neuron for host-specific compound and an antagonist sensory neuron for nonhost-specific bitter taste compound. Similarly, our electrophysiological studies on various phytophagous insects have indicated that each species has a species-specific set of highly specialized olfactory sensory neurons (OSNs), in which some OSNs are specialized for detecting host-specific volatile compounds and some others are specialized for detecting nonhost-specific volatile compounds. In this system, it is suggested that a combinational sensory input from both host-specific and nonhost-specific OSNs enhances the discrimination between host and nonhost plants, and this kind of multi-species chemosensory information flow is common in ecosystems. Our electrophysiological and behavioral studies have also demonstrated that the specialization of chemosignal perception and species-specific chemosensory information flow is also present in the tritrophic system among parasitoids, their host insects, and plant hosts.

S05-09

Mechanism of methyl eugenol perception in *Bactrocera dorsalis*: a molecular approach

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The oriental fruit fly, *Bactrocera dorsalis*, is one of the most destructive pests, causing enormous economic losses to the fruit and vegetable industry worldwide. Methyl eugenol (ME) is a powerful attractant for mature males of *B. dorsalis*, and has been widely used for detecting, luring and eradicating *B. dorsalis* populations. However, the molecular mechanism underlying the olfactory perception of ME remains unknown. In insect, the first two steps of olfactory perception are odorant-binding proteins (OBPs) bind with odors and then transport to odorant receptors (ORs). Here, to better understand the mechanism of *Bactrocera dorsalis* responsible for methyl eugenol (ME), we therefore use multiple molecular methods to screen out key genes responsible for ME. As for OBPs, microscale thermophoresis (MST) is applied to conform the binding capability. Meanwhile, the live calcium imaging using HEK cell expression system as well as and voltage clamp recording in *Xenopus* oocytes are performing to identify the binding capability of candidate ORs. Finally, genome editing tool CRISPR/Cas9 is going to be employed to knock out the essential genes to measure the olfaction guided behaviors in vivo. We expect to identify key genes responsible for the ME perception in this notorious fly. Our results will not only conduct several technology platforms to confirm key genes responsible for specific odorants, but also lay a solid foundation for the development of novel effective attractant targeting key genes in this oriental fruit fly.

S05-10

A phylogenomics approach to characterizing sensory neuron membrane proteins (SNMPs) in Lepidoptera

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Sensory neuron membrane proteins (SNMPs) play a critical role in the insect olfactory system but there is a deficit of functional studies beyond *Drosophila*. Here, we use a combination of available genome sequences, manual curation, genome and transcriptome data, phylogenetics, expression profiling and gene knockdown to investigate SNMP superfamily in various insect species with a focus on Lepidoptera. We curated 81 genes from 35 insect species and identified a novel lepidopteran SNMP gene family, SNMP3. Phylogenetic analysis shows that lepidopteran SNMP3, but not the previously annotated lepidopteran SNMP2, is the true homologue of the dipteran SNMP2. Digital expression, microarray and qPCR analyses show that the lepidopteran SNMP1 is specifically expressed in adult antennae. SNMP2 is widely expressed in multiple tissues while SNMP3 is specifically expressed in the larval midgut. Microarray analysis suggests SNMP3 may be involved in the silkworm immunity response to virus and bacterial infections. We functionally characterized SNMP1 in the silkworm using RNA interference (RNAi) and behavioral assays. Our results suggested that *Bombyx mori* SNMP1 is a functional orthologue of the *Drosophila melanogaster* SNMP1 and plays a critical role in pheromone detection. Split-ubiquitin yeast hybridization study shows that BmorSNMP1 has a protein-protein interaction with the pheromone receptor (BmorOR1), and the co-receptor (BmorOrco). Concluding, we propose a novel molecular model in which BmorOrco, BmorSNMP1 and BmorOR1 form a heteromer in the detection of the silkworm sex pheromone bombykol.

S05-11

Transcriptome analysis of priming defense between and within *Brassica nigra*

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Priming of plant defenses is an induced mechanism that prepares the plant for faster and stronger response against upcoming biotic stresses. *Pieris brassicae* eggs deposition on leaf can induce priming on *Brassica nigra*. Meanwhile, primed plants by eggs can activate adjacent plant's priming process via volatile chemicals. It is probable two different priming processes might exist on this system, one is intra-plant priming, while another is inter-plant priming. This unique combination of intra- and inter-plant priming makes the system of *Pieris brassicae* and *Brassica nigra* very interesting to test further ecological and molecular questions regarding priming of plant defenses. It is unclear whether these two priming processes use similar downstream molecular pathway to activate the plant defense or not. Since the details of these two priming pathways are highly unstudied, we aim to elucidate the potential mechanism regulating these two priming processes.

RNA-seq is used to construct the transcriptome of different experiment groups and different time points. By comparing transcriptomes, potential genes responsible for the different priming processes are isolated and grouped. It is shown that these two priming processes share common genes while preserve relative unique expression profiles. For example, eggs deposition activates SA pathway and related bacterial infection induced genes. While neighboring plant volatiles can activate JA pathway to defense against the upcoming caterpillar attack. Additional data such as volatolomics, metabolomics and phytohormones are also used to integrate information from different -omics levels to elucidate potential functional modules underneath different priming effects.

S05-12

Responses of *Tribolium castaneum* to infested wheat and aggregation pheromone

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The red flour beetle, *Tribolium castaneum* (Herbst) (Coleoptera: Tenebrionidae), is a worldwide pest of stored grains. Using 'Y'-tube olfactometry we studied the response of *T. castaneum* to odours from simulated wheat infestations containing conspecifics, and infestations containing the lesser grain borer, *Rhyzopertha dominica* (Fabricius) (Coleoptera: Bostrichidae), and the grain weevil *Sitophilus granarius* (Linnaeus) (Coleoptera: Curculionidae). *T. castaneum* larvae were significantly attracted to odours from all three test species. *T. castaneum* adults were attracted to grains infested by *R. dominica* and flour infested by *T. castaneum* but repelled from grains infested by *S. granarius*. Further behavioural analysis showed *T. castaneum* were significantly attracted to their aggregation pheromones, dimethyldecanal (DMD), but not to a mixture of dominicalure 1 and 2 which are aggregation pheromone of *R. dominica*. Female *T. castaneum* adults were attracted to approximately 50-fold less DMD than larvae and 100-fold less than male adults, suggesting they are more sensitive to DMD. This study improves our understanding of *T. castaneum* behaviours to infested grain volatile compounds and pheromones, and may help develop new control methods for grain pest species.

S06-01

Host selection in bark beetle *Ips typographus*: understanding anti-attractants like NHV and their possible use for mitigation in the Anthropocene

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“Stand behind the science” is relevant for curbing of green-house gases emissions mandated by climate science, but we still need to handle the consequences of such gases emitted and will be so for some time: Mitigation

We try to address three questions of relevance for both basic and applied science to protect Northern forests.

A. How does potential anti-attractants function so strongly and specifically? What is their role in the host-selection sequence?

B. Can we find new anti-attractants from non-host or resistant hosts?

C. How strong are effects biological and their cost effectiveness, in long and short term?

Anti-attractants from non-host trees or habitats (non-host volatiles, NHV) are strongly active and has specific receptors been since long demonstrated, as has unsuitable host signals such as verbenone. Similarly, a resistance indicator 1,8-cineol, interfering with a pheromone component detection, is established. Several non-volatile phenolics compounds are also possible resistant indicators and anti-feedant semiochemicals at end of host selection sequence.

Trace host compound 4-thujanol, an oxygenated host monoterpene associated with resistant (younger) trees, has field activity and several such compounds are under behavioural testing.

Data from 32 experiments on *Ips typographus* and *Dendroctonus ponderosae*, were tested for an overall effect of anti-attractant semiochemicals, i.e. if treatments reduced the number of attacks on standing trees on stand scale. This meta-analysis showed a substantial overall effect size -0.96.

However, for large scales of space and time, management of forests towards increased tree species diversity is suggested.

S06-02

Bacterial volatile ammonia regulates the consumption sequence of D-pinitol and D-glucose in a fungus associated with an invasive bark beetle

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Interactions among microbial symbionts have multiple roles in the maintenance of insect–microbe symbiosis. However, signals mediating microbial interactions have been scarcely studied. In the classical model system of bark beetles and fungal associates, fungi increase the fitness of insects. However, not all interactions are mutualistic, some of these fungal symbionts compete for sugars with beetle larvae. How this antagonistic effect is alleviated is unknown, and recent research suggests potential roles of bacterial symbionts. Red turpentine beetle (RTB), Dendroctonus valens LeConte, is an invasive pest in China, and it leads to wide spread, catastrophic mortality to Chinese pines. In the symbiotic system formed by RTB, fungi and bacteria, volatiles from predominant bacteria regulate the consumption sequence of carbon sources D-pinitol and D-glucose in the fungal symbiont Leptographium procerum, and appear to alleviate the antagonistic effect from the fungus against RTB larvae. However, active components of these volatiles are unknown. We detected 67 volatiles by Gas Chromatography-Mass Spectrometer (GC-MS). Seven of them were identified as candidate chemicals mediating bacteria-fungus interactions, among which ammonia made L. procerum consume its secondary carbon source D-pinitol instead of its preferred carbohydrate D-glucose. In conclusion, ammonia regulated the consumption sequence of these two carbon sources in the fungal symbiont.

S06-03

Facile and efficient syntheses of (11Z, 13Z)-hexadecadienal and its derivatives key sex pheromone and attractant components of notodonfidae

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Sex pheromones offer an environmentally-friendly alternative to control insect populations via mating disruption or other strategies in integrated pest management. Notodontidae (Lepidoptera, Noctuoidea) is a family of moths with approximately 3800 known species. Some Notodontids cause noticeable defoliation of their hosts, which causes serious ecological and economic losses. The (*Z*,*Z*)-dienes and conjugated en-yne moieties are common in sex pheromone and attractant components for many Notodontide insect pests. Based on a C10 + C3 + C3 strategy, facile and efficient syntheses of (11Z,13Z)-hexadecadienal (**1**), alcohol (**2**), corresponding acetate (**3**), and (Z)-13-hexadecen-11-ynal (**4**), which are key sex pheromone and attractant components of Notodontidae, were achieved from commercially available starting material 10-bromo-1-decanol. The key steps were accomplished by the alkylation of lithium alkyne under a low temperature, a cis-Wittig olefination of the aldehyde with propylidentriphenylphosphorane, and hydroboration-protonolysis of alkyne. This synthetic route provided (11*Z*,13*Z*)-hexadecadienal (**1**) in a 23.0% total yield via an eight-step sequence, alcohol (**2**) in a 21.9% total yield, acetate (**3**) in a 21.4% total yield, and (*Z*)-13-hexadecen-11-ynal (**4**) in a 34.7% total yield. This simple, convenient, and efficient synthetic route will be greatly helpful for the further practical testing and the use of pheromones as benign environmental tools for the pest control of Notodontidae.

S06-04

Phylogeographical analysis of *Dendrolimus punctatu*s based on the whole mitochondrial DNA and ITS markers

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In southern China, the masson pine caterpillar, *Dendrolimus punctatus*, has caused serious damage to the forest tree, Pinus massoniana (Lamb.). Here, whole mitochondrial DNA and internal transcribed spacer 1 were employed to analyze *D.punctatus* evolution and to understand the process underlying its current phylogenetic pattern. The populations in the *D. punctatus* distribution range were categorized into four subgroups (K=4): central and eastern China (CEC), southwestern China (SWC), Yibin and Baise (YBBS), and Luoding in Guangdong (GD), with a high levels of haplotypes diversity (ITS1-Hd: 0.849) and nucleotide diversity (ITS1-Pi: 0.0075) berween them. The overall genetic differentiation coefficient (F_{ST}: 0.535) and gene flow (N_m: 0.220) indicate very high genetic differentiation and little gene flow between the subgroups. However, there was some gene flow between populations in the CEC subgroup, suggesting that more individuals migrated between populations in this subgroup. The Mantel test showed that geographic distance had an important influence on the genetic distance (r=0.3633, P<0.001) and genetic differentiation (r=0.4388, P<0.001) of different geographic populations. The neutrality tests, Bayesian skyline plot, and haplotype network showed that the D. punctatus populations experienced a population expansion around 100,000 years ago. The divergence times of YBBS, SWC, GD, and CEC were 0.347, 0.236, 0.200, and 0.110 million years, respectively, The SWC, CEC, and GD branches may have evolved from the YBBS branch via migration along the Yangtze River. The population genetic structure of *D*. *punctatus* was closely related to the geographic distance among populations, the weak flight capacity, and eco-environment conditions.

S06-05

Mating behavior and attractiveness of male cuticle extracts based on electroantennogram and behavioral assay in *Sirex noctilio* Fabricius

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Sirex noctilio was a major forest invasive pest worldwide and has caused tremendous damages. After a careful observation of mating behavior and rhythm of S. noctilio, four types of male cuticle extracts were collected. Electroantennogram (EAG) and behavioral responses of both sexes to these extracts were investigated. According to sex ratio of 1:3 (female to male), wasps were put into the cages and then the number of mating couples was recorded throughout the day. Male cuticles were extracted by hexane (HPLC), and then EAG and olfactory responses of both sexes to the extracts were determined. The extracts were as follow, sample 1 (separately reared in plastic cage), sample 2 (males gathering without female), sample 3 (males attracted females, but no mating occurred), and sample 4 (after mating). The results showed that the mating process can be divided into five phases: searching, attracting, seizing, copulating and ending. The highest mating frequency occurred at 9:00-11:00 in a day. Both males and females had the highest selection to the sample 3 and sample 4. Male extracts could elicit much stronger EAG response from female wasps antennae than from male wasps antennae. Behavior test showed that only sample 3 was attractive to females, sample 1-4 were attractive to males, but with no significant difference. Males released pheromone which can attract both male and female wasps. We could hypothesis that males could release aggregative pheromone to attract males in the canopy after emergence, also could release likely sex pheromone to attract females once they were much closer to females.

S06-06

Functional analyses of chemosensory proteins in the apple buprestid beetle *Agrilus mali*

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The apple buprestid beetle, *Agrilus mali* Masumura, is the most destructive insect pest in wild apple forests (i.e., rare germplasm resources) in Xinjiang. There is an urgent need to develop new monitoring and management strategies for this pest. We identified 63 olfactory genes from the antennal transcriptome of *A. mali*, and they included 11 odorant-binding proteins (OBPs), eight chemosensory proteins (CSPs), 17 odorant receptors (ORs), nine gustatory receptors (GRs), 17 ionotropic receptors (IRs), and one sensory neuron membrane proteins (SNMPs). We cloned four CSPs (i.e., AmalCSP1, AmalCSP4, AmalCSP5 and AmalCSP8), and analyzed their tissue expression patterns and binding profiles. AmalCSP1 was abundantly expressed in antennae of males, and in abdomens and wings of females. AmalCSP4 and AmalCSP5 exhibited higher transcript levels in antennae and abdomens than in other tissues. High expression of AmalCSP8 was found in antennae of both sexes of *A. mali*. AmalCSP5 showed good binding ability with 13 odor ligands, but it did not bind with alkanes and nitriles. AmalCSP5 showed strong binding affinities to dodecanol and dodecanal， as well as C5 to C10 compounds. AmalCSP8 only bound effectively with eight ligands, and exhibited relatively strong binding capacity with (*Z*)-α-ocimene, α-pinene and limonene. AmalCSP1 and AmalCSP4 could bind poorly with all the 40 test plant volatiles, but they might be important in perception of sex pheromones in *A. mali.* Our results have significant implications for clarifying chemical communication in buprestid beetles, and provide a basis for developing effective management tools for *A. mali* using attractants and repellents.

S06-07

Molecular and functional characterization of candidate sex pheromone receptors in *Dendrolimus punctatus* Walker

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Odorant receptors (ORs) are key proteins in insect olfactory recognition, mediate the specific combination of odor molecules and olfactory neurons. Pheromone receptors (PRs) are special ORs from males that can discriminate the sex pheromone emitted by females. In this study, we cloned six candidate pheromone receptors (*Dpun*OR 20/45/46/51/54/58) and Orco of antennae from *Dendrolimus punctatus* Walker (Lepidoptera: Lasiocampidae). Each of the six genes was expressed with an Orco gene in xenopus oocyte. By two-electrode voltage-clamp recordings, we investigated that *Dpun*OR45 was tuned to three main pheromone components, *Z*5, *E*7-12:OH; *Z*5, *E*7-12:OAc; *Z*5, *E*7-12:OPr and the second major pheromone component from *Denlimus houi*, *E*5, *Z*7-12:OAc. *Dpun*OR46 specially tuned to the third major pheromone component, *Z*5, *E*7-12:OPr. While *Dpun*OR20/51/54/58 had not shown any response to the sex pheromone components tested in this study. On the phylogenetic tree, PRs are usually conserved and clustered together. However, PRs from *Dendrolimus* located another branch in the phylogenetic tree. Motifs analysis showed difference between *Dendrolimus* PRs and other insects PRs from lepidoptera. *D. punctatus* is the pine caterpillar moth for southern china forests, make bad influence for the growth and development of trees. Our study of the sex pheromone percept mechanisms of *D. punctatus* may provide clues for the new control strategies.

S06-08

Two trace volatiles released from living adult of *Aromia bungii* Faldermann (Coleoptera: Cerambycidae) as minor component of pheromone

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Insect behavior is often influenced by chemical signals, and identification of volatiles released from insect body might explain their behavior. *Aromia bungii* Faldermann is a main wood borer of many broad-leaved trees, especially peach in China. Solid phase microextraction (SPME) with DVB/CAR/PDMS was employed to extract the volatile compounds released from living adult of *A. bungii*. Extracts were analysised by gas chromatography-mass spectrometry (GC-MS) and synthesized compounds. Results showed that (*R*)-(+)-citronellal was only detected from female body, and *trans*-2,*cis*-6-Nonadienal was only released from male body[1]. The Y-tube olfactory bioassay showed that (*R*)-(+)-citronellal was attractive to the male *A. bungii*[2], and *trans*-2,*cis*-6-nonadienal was proved an effective attractant of *A. bungii* in the field by other scientists[3]. More field tests are carried out by our lab in 2019.

S06-09

Chemical ecological mechanism of conexistence among three *Tomicus* species

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Bark beetle is one of the important forest pests, which not only seriously affect the growth of pine trees, but also cause a great threat to the ecological environment. Three sympatric bark beetle, *Tomicus minor*, *T. yunnanensis*, and *T. brevipilosus* infested *Pinus yunnanensis* in southwest of China, which have caused tremendous loss to forestry production and ecological environment. we studied the intraspecific and interspecific relationships and their chemical and ecological mechanisms of three *Tomicus* species, which compete and coexist in the same host during the shoot-feeding and trunk-breeding phase, based on behavior ecology, chemical ecology and molecular ecology, and the key genes involved in the regulation of the synthesis of chemical pheromones related to the coexistence and competition of the *Tomicus* species were analysed in the transcriptome level.The species were significantly attracted by their own species and the same sex, and this attraction behavior was inhibited by exposure to additional beetles or to the hindgut extracts of beetles which had shown interaction. Contents of (-)-*trans*-verbenol in female and male *T. minor* and *T. yunnanensis* hindguts increased from 0.19, 0.09, 0.22, and 0.05 ng/individual respectively to 16.74 – 292.71 ng/individual following interaction with additional beetles. Mean concentration of verbenone detected in the hindguts of female/male individuals of *T. minor* and *T. yunnanensis* under natural conditions were 0.16, 0.06, 0.03, and 0.05 ng/individual, respectively, but these correspondingly increased to 5.90, 2.43, 0.06, and 0.19 ng/individual after exposure to additional insects. In *T. yunnanensis*, the amounts of detectable (-)-*trans*-verbenol and verbenone extracted from hindguts were lower than those from *T. minor*. The levels of cis-verbenol and (-)-*trans*-verbenol most attractive to walking *T. yunnanensis* and *T. minor* were 0.1 and 1.0 ng/µl, respectively. The addition of verbenone to cis-verbenol or (-)-*trans*-verbenol reduced the attraction responses.The transcriptomes analysis of the intestines and fat bodies of *T. minor* and *T. yunnanensis* within and between intraspecific and interspecific interactions for 24 and 48 h were analyzed using the Illumina sequencing. The genes involved in the regulation of pheromone biosynthesis were discovered: *CYP306A1*, *CYP302A1*, *CYP314A1*, *CYP18A1*, *CYP307A*.

S07-01

A to Z: the journey from synthesis to global commercialization of semiochemicals

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Insect semiochemicals are necessary tools used in pest management strategies. These compounds have been proven useful for monitoring, disrupting mating, mass trapping, and attract and kill strategies. Ideation to commercialization involves the assistance and participation of a multifaceted team of collaborators, including scientists, financers, chemical manufacturers, formulators, distributors, regulators, and consumers. In our in-depth discussion of the steps leading to the commercialization of semiochemicals, we will showcase the complex route of ingredient manufacturing, along with pitfalls in chemical synthesis, raw material sourcing, and technical quality requirements. We will also discuss external factors that influence commercial activity, including global business and regulatory opportunities and constraints and how they facilitate and sometimes hinder semiochemical product development.

S07-02

Rescue® dual bait technology for common household ants

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There are many types of ant bait stations in both commercial and consumer markets for various common household ants. They typically include an attractant (e.g., food-based proteins, carbohydrates, or lipids), a carrier, and an active insecticide ingredient. Baits work by taking advantage of ant biology and behavior such as social grooming and trophallaxis. Once the bait is discovered, the foraging ants collect the bait and transport it back to the colony. At the same time, they will communicate the location and quality of the baits to other foragers in the colony via trail pheromone. In a short period, many more workers follow the foraging trail, quickly arriving at the bait source, and transfer the bait back to the nest for sharing with other members of the colony. Worker ants (foragers, nurses and guards) eat sugar-based foods in liquid form for energy; ant larvae eat proteins in semi-liquid or solid forms for growth; whereas queens need to have both proteinaceous foods for reproduction and some sugar for energy.

Current ant bait stations on the markets, regardless of their AIs, are loaded with either a thick paste/solid block (with a mixed sugar/protein matrix) or a sugar liquid/gel formulation in single compartment. The sugar alone formulation (liquid or gel) lacks the protein contents necessary for larval grow and queen's reproduction, whereas the mixed sugar/protein matrix needs tedious work from workers to extract the needed sugar for workers and the needed protein for larvae and queens. The food extraction or separation process by foraging workers will significantly slow down the transfer and distribution/re-distribution of a lethal dose of insecticide to all caste members of the nest. This will reduce the killing efficacy of the target ant colony since some foraging workers might be killed by the toxic AI during the food extraction/separation process before being able to share the foods with their colony members. Thus, a new and smart bait matrix/station system is surely needed to overcome these drawbacks.

In 2018, Sterling International, Inc. launched our first ever Rescue® Ant Bait Station product (AI: 5.4% borax) [1-2] based on our patented Dual-Bait Technology [3] in the U.S. consumer market. This bait station has multiple separated compartments, one with protein bait and the other(s) with sugar gel, which could meet all the variable nutritional demands of an ant colony throughout the season. The presence of all potential nutrients in separated forms in the bait station should increase the likelihood that foraging ants will find what they need. Such a bait station design would not only significantly increase ant foraging activities and the overall nutrient acquisition efficacy, but more importantly will increase and maximize the transfer and distribution of a lethal dose of insecticide with delayed toxicity to all members of the colony, especially to larvae and queen(s) through the protein bait intake. This bait station will work effectively on all the common household ant species regardless of their colony development stages.

S07-03

Identification of the sex pheromone of the spherical mealybug *Nipaecoccus viridis*

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The spherical mealybug *Nipaecoccus viridis* is a major worldwide pest of citrus. The sex pheromone of the *N. viridis* females was identified by using automated Sequential SPME/GC–MS analysis. The mealybug releases γ–necrodyl isobutyrate and γ–necrodol in a circadian rhythm. Pheromone components were synthesized by rearrangement of *trans*–α–necrodol isolated from Spanish lavender essential oil, *Lavandula luisieri*. Males of spherical mealybugs were attracted in flight bioassays to baits of γ–necrodyl isobutyrate alone but not to baits of γ–necrodol or unbaited controls. A 1:1 mixture of γ–necrodyl isobutyrate and γ–necrodol was no more attractive than γ–necrodyl isobutyrate alone.

S07-04

Kairomone A&K for adult noctuid control

Stephen Sexton

Nanjing Xinan Biological Technology Company

Noctuids are major pests of vegetables, cereals and fibre crops in China and most parts of the world where agriculture is practiced. The principal noctuid pests in China include *Helicoverpa armigera, Helicoverpa assulta, Spodoptera litura, Spodoptera exigua* and *Mythimna separata.* Early in 2019, *Spodoptera frugiperda* was reported in Yunnan. It has rapidly spread north and now threatens the major corn growing regions of north east China. Noctuid moths are highly mobile and are capable of flying hundreds of kilometres in a night. This behavior generally makes them unsuitable as candidates for control by pheromone mating disruption. The same behavior makes them hungry for sources of energy, particularly nectar and they are drawn to volatiles that signal energy sources. This and their mobility makes them vulnerable to the 'attract and kill' control approach. Targeting adult female moths can be a powerful strategy with many advantages. It reduces insecticide use and labour for application to 1-2% of that required for conventional cover sprays, allows flexibility in choice of insecticides, simplifying resistance management strategies. The approach minimizes harm to beneficial insects. Rapid treatment of large areas using drones or spray planes is possible and equally simple affordable technologies for treatment of smallholdings. Effectiveness of an A&K formulation is largely dependent on having the right attractant blend. Details of work on *Helicoverpa armigera* in cotton and grain legumes in China, South Africa and Australia is presented and preliminary studies which point to a powerful kairomone attractant for adult female *Spodoptera frugiperda*.

S07-05

Use of attractants in housefly baits

Dangsheng Liang, Ana Story

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Bait has been widely used for control of house flies, *Musca domestica* (Muscadae, Diptera). The most widely used attractant for house fly bait is (Z)-9-tricosene. It became an industry standard soon after a report of its discovery in *Science* magazine in 1971. Meanwhile the research community has questioned its functions and effectiveness over the years. We have conducted a re-evaluation of (Z)-9-tricosene as an attractant for house flies and concluded that it is not attractive over a distance. Since then, we have started a search for the long distance attractants for house flies. We will report some preliminary results on the discovery and use of long distance attractants in house fly baits.

S07-06

Novel repellent compounds for managing German cockroach

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German cockroach, Blattella germanica (L.), is an important pest of homes, restaurants, and commercial food processing facilities worldwide. They are also a major public health concern in hospitals, kitchens, and food manufacturing plants. Control of cockroach populations is primarily dependent on continued applications of residual insecticides, and stomach poisons for several decades. However, these conventional insecticides are responsible for environmental pollution, causing toxicity to humans and animals, and leading to the pests developing resistance. Thus, concerns regarding such adverse effects have increased the need for the development of novel alternative cockroach control technologies.

In this presentation, I will share our results including the EAG activity of male and female antennae to 9 repellent candidates against adult German cockroaches, which include coconut fatty acids, DEET, Catnip oil, caprylic acid (C8), capric acid (C10), lauric acid (C12), and the methyl esters of the last 3 fatty acids (C8-Me, C10-Me, C12-Me). We found that catnip oil, caprylic and capric acids induced the most EAG responses among tested compounds. DEET did not elicit significant EAG responses, similar to the controls (air and hexane). Further behavioral tests including the filter paper test, 2-shelter choice test, and 3-box harborage choice test were conducted to investigate the repellent effectiveness and longevity on adult female German cockroach. Our preliminary results indicate that natural product repellents may provide effective control against cockroaches, which can be used in a “push and pull” strategy for managing their infestation.

S07-07

Functional study of *CYP4G19* in the German cockroach, *Blattella germanica* (L.)

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Cuticular penetration plays a significant role as a mechanism of insecticide resistance, but the underlying molecular mechanism remains unknown. In *Blattella germanica*, the cytochrome P450 gene, *CYP4G19*, is over-expressed in a cypermethrin-resistant strain. We investigated whether *CYP4G19* is involved in the biosynthesis of hydrocarbons and further contributes to cuticular penetration resistance in *B. germanica*. Compared to the susceptible strain, the cypermethrin-resistant cockroaches showed lower cuticular permeability with Eosin Y staining. Removal of epicuticular lipids with a hexane wash intensified the cuticular permeability and decreased the resistance index of the resistant strain. *CYP4G19* was mainly expressed in the abdominal integument and was up-regulated by desiccation stress or a short exposure of cypermethrin. Over-expression of *CYP4G19* in the resistant strain was positively correlated with a higher level of cuticular hydrocarbons (CHCs). RNAi-mediated knockdown of *CYP4G19* significantly decreased its expression and caused a reduction in CHCs. Meanwhile, *CYP4G19* suppression resulted in altered lipid layer, enhanced cuticle permeability, compromised insecticide tolerance and lower mating rate. Our findings confirm that *CYP4G19* is involved in HC derived contact pheromone production and contributes to hydrocarbon-based penetration resistance in *B. germanica*. This study highlights the important role of lipid-based penetration resistance and may improve our strategy in the management of the *B. germanica*.

S07-08

Application of pheromones to monitoring for stored product insects

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Stored product insects feed on dry material of plant and animal origin and mainly come into two orders, Coleoptera (beetles) and Lepidoptera (moths). They infest seeds (cereal grain, beans, oilseeds, nuts), dried fruit, herbs and spices, dried fish and meat. They have global distributions through trade of thousands of years and become cosmopolitan species.

Stored product insects mainly bring two types of damage to materials and products: loss by their infestation and contamination by insect bodies and waste products. The former damage used to be major and sole once but the latter has a big impact for the society nowadays. Pest management is conducted to reduce such direct and indirect damage. Systems for pest management are constructed on the basis of IPM (Integrated Pest Management). IPM is a concept to make varied activities for pest management more environment-friendly. IPM focuses on monitoring in order to grasp a situation of a site.

There are many tools for monitoring. Pheromone traps have been generally used for stored product insects. Pheromones are chemicals and insects communicate among individuals of the same species with them in the natural world. As a result, pheromone traps are easy to monitor specific species, the target. Fundamental idea related to usage of pheromones is nature-derived.

I introduce situation of pheromone utilization for pest management of stored product insects in the symposium.

S07-09

ATP detection and its role as phagostimulant in blood feeders

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Once a blood-sucking insect reaches the host skin, it bites and tastes the blood. Gustatory evaluation of chemicals of the blood occurs in contact chemoreceptors situated in the pharynx. Most blood-sucking insects are highly sensitive to adenosine triphosphate (ATP), triggering gorging responses. Here, we characterized the ATP receptor through pharmacological experiments and traced the pharyngeal chemoreceptors to the brain to uncover central regions where gustatory information is processed in the kissing bug *R. prolixus*. The ingested volume and pumping parameters of the pharyngeal muscles were significantly reduced or enhanced when insects were fed with known mammals' purinoceptor antagonists or agonists, respectively. We traced the pharynx neurons by means of anterograde backfills to the brain. Stained pharyngeal neuronal tracks innervated the tritocerebrum through the labral nerves. Untangling the ATP detection mechanism will provide with novel targets in the search of tools addressed to diminish interactions between disease-vector insects and humans.

S07-10

Development of spotted wing drosophila commercial lure and its use for management

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The spotted wing drosophila (SWD), introduced from Asia, is now a serious pest of numerous soft fruits throughout North America and Europe. Efforts continue to improve monitoring and control methods. A four-component lure comprised of ethanol, acetic acid, acetoin, and methionol was developed and marketed by several companies for trapping SWD. In this talk, I describe the multidisciplinary processes used to isolate, identify and develop that lure, and provide specifications for its use as a trap lure. The on-going projects on the development of specific and improved lure will be also discussed.

S07-11

Pheromone mating disruption development in Chinese integrated pest management: perspectives in the last decade and prospects in next 10 years

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MD was developed greatly in the last decades in China though we had rarely any commercial mating disruption activities ten years ago; But if we go through the MD situation a little bit more, we will find out there are problems on many aspect, and this will decide the future development of MD in integrated pest management in China, we will take this chance to present you our views.

S07-12

Spatial repellent, antifeedant and oviposition deterrent activity of coconut oil fatty acids and their methyl ester derivatives against biting flies

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Stable flies are one of the most detrimental arthropod pests to livestock. With changing climates and agronomic practices, they expand their roles as pests and disease vectors as well. The present study reports new results concerning the spatial repellency, antifeedant and oviposition deterrent activity of a bio-based product, coconut fatty acid and their methyl ester derivatives of free fatty acids of $C_{8:0}$, $C_{10:0}$ and $C_{12:0}$ to stable flies. Only the $C_{8:0}$ acid, $C_{8:0}$- and $C_{10:0}$ methyl esters elicited significant antennal responses. Laboratory single cage olfactometer bioassays revealed that coconut fatty acid and $C_{8:0}$ methyl ester displayed active spatial repellency. All three methyl esters showed strong antifeedant and toxicity activity and their strengths were dose-dependent. The coconut fatty acid formulation showed strong oviposition deterrent activity against stable fly. The coconut fatty acid and their three medium chain fatty acid methyl esters were demonstrated to have strong blood-feeding deterrence and toxic activity against stable fly adults. These findings are important in the development of more powerful stable fly control formulations.

S07-13

From microscopic characteristics of antennal sensilla to enhancement of field attractiveness for the management of bean bug, *Riptortus pedestris*

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The bean bug, *Riptortus pedestris* (Hemiptera: Alydidae) is a major pest of soybeans and some tree fruits in north-east Asian countries. The bug passes three generations per year, and enters reproductive diapause during winter. Antenna of *R. pedestris* consists of four segments; scape, pedicel, basiflagellum, and distiflagellum. Scanning electron microscopic study revealed that the antenna sensilla (s.) could be classified into four major types (trichodea, basiconica, chaetica, and coeloconica), which could be further classified into subtypes based on their size, tip shape, presence of socket and surface structure. Among them, two subtypes of s. trichoid, all three subtypes of s. basiconica, all four subtypes of s. chaetica and all two subtypes of s. coeloconica had numerous nano-scale pores throughout the cuticular surface, suggesting their olfactory function. Among the four antennal segments, the distiflagellum possessed highest number of sensilla. Trichoid sensilla were most abundant, followed by s. basiconica, s. chaetica, and s. coeloconica. The male adults of bean bug release aggregation pheromones (AP) to attract conspecific nymphs and both sexes of adults; (*E*)-2-hexeny (*Z*)-3-hexenoate (E2HZ3H), (*E*)-2-hexenyl (*E*)-2-hexenoate (E2HE2H), tetradecyl isobutyrate (TI), and octadecyl isobutyrate (OI). Electroantennography (EAG) and field studies revealed that only the distiflagellum responded to the AP. There were no significant differences in the amounts of AP secretion by mating, body weight, and time in a day. Higher amount of AP was detected from older males than younger ones. Field tests on the composition ratio of the three components (E2HZ3H:E2HE2H:TI) said that traps baited with mixture of 20:20:10 or 16.7:16.7:16.7 (in mg per lure) attracted more number of adults than the mixture of 7:36:7 (but, not significantly). Water-pan trap baited with pheromone + food (dried soybean, dried peanut, water) attracted significantly more number of females and males than those with pheromone only or control trap. Among the three components of the AP, only the E2HZ3H attracted the egg parasitoid of bean bug, *Ooencyrtus nezarae* (Hymenoptera: Encyrtidae). Treatment of E2HZ3H lures in the soybean field increased the parasitism by *O. nezarae*, but did not increase the parasitism by *Gryon japonicum* (Hymenoptera: Scelionidae) in two years' field study.

S07-14

Development new commercial products for trapping insect pests based on insect pheromones and LED lights

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The use of pheromones for pest monitoring and for a tool as accurately timing insecticide sprays has become a cornerstone feature of many prominent IPM programs. In addition, applications of pheromone-based technologies for direct pest control such as mass trapping and attract-and-kill have shown promise in specific instances. LEDs (light-emitting diodes) are also used for the mass trapping and monitoring of phototactic insects. The diamondback moth, *Plutella xylostella*, is a worldwide crucial pest of Cruciferous vegetables with higher fecundity and severe insecticide resistance. In order to enhance the trapping efficiency of *Plutella xylostella*, we have investigated the synergism between sex pheromone- baited lures for *Plutella xylostella* and different wavelength LED lights in the field trapping test based on a series of specific wavelengths in the indoor screening test. In the field test, UV (390-410nm) LEDs attracted significantly more moths than any other single LEDs or sex pheromone alone. UV (390-410nm) LEDs equipped with sex pheromone- baited lures performed best in capturing diamondback moth, with a mean catch up to 95.7 per day per trap, over four times the number of sex pheromone alone. This study provides a reference for the combined application of LED lights and sex pheromones to achieve efficient trapping of *Plutella xylostella*. The combination of olfactory and night-visible visual cues significantly enhanced trap effectiveness for this nighttime-active insect species. These results provide promise for improved some pest insect detection and suppression in mass trapping programs.

S07-15

Development and evaluation of food attractant for grain pest control

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Oryzaephilus surinamensis (Linnaeus) is a common, worldwide pest of grain and grain products as well as chocolate, drugs, and tobacco. In China, for a long using grain fumigant such as PH_3 is main method to control population of *O. surinamensis*, which cause pest forming high resistance to chemicals. So it is imporant to develop new and ecological methods to control the grain pest such as pest food attractant. In this study, the allure activity of 38 kinds of foods were tested to *O. surinamensis* under laboratory conditions and six kinds of foods were screened out with good allure effect. Base on the six foods, using latin square design several formulas with better allure activity were developed and the No.17 of formula was verified under the warehouses conditions. Subsequently, volatiles of No. 17 were colloected and analyzed by gas chromatography-mass spectrometry (GC-MS), more than twenty chemicals in volatiles were found.

S07-16

Investigating various attract-and-kill prototypes for their potential control of *Spotted Wing Drosophila*

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Various attract-and-kill prototypes (MSU prototype, prototype A and B) were investigated for their effectiveness of controlling spotted wing drosophila in cherry orchards in MI, USA. All of three prototypes consisted of a device treated with deltamethrin and a food based bait. MSU prototype (AK pouch) was deployed at 500/ac in 0.5 ac plots, along with two controls: one plot with no pouch and the other containing 500 untreated pouches with the bait. Interestingly, the plot with untreated pouches had at least 2 times more males and females SWD than the plot with no pouch or with AK pouch, indicating that the baits might draw flies from neighboring area into the testing plots. The prototype A was deployed at 0, 20, or 40 per plot (plot size: approximately 0.7 ac). Numbers of SWD captured in control plot were similar to those in plots containing attract-and-kill devices. Prototype B was deployed at 0, 70, and 210/ac in one-acre plots. Plots containing 210 prototype B had the lowest number of SWD among all the treatments. Therefore, attract-and-kill prototype B may have a potential to suppress SWD population.

S07-17

Efficacy of volatile infochemicals from lavenders regulating behaviour of tea green leafhopper and field application

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Volatile Infochemicals, which has been seen as an important medium between plants and insects, play a certain role in regulating the behavior of phytophagous insects. Push-pull control strategies have been proven effective in the control of agricultural pests. Most of the studies on integrated control of tea plants focused on the development of attractants for tea green leafhopper, while the reports on repellents were less. We determined the feasibility of using the *Lavendula pinna*t as the push component in a push-pull strategy to control or reduce damage of tea green leafhopper. Using headspace dynamic adsorption method via a custom-made aeration system, volatiles of lavender was collected, which was firstly analyzed combined with gas chromatography mass spectrometry (GC-MS), and added to rubber carrier to form push element. Push-pull strategy, which combines screened repellents with existing attractants, was applied among tea gardens. The results showed that: Volatiles of lavender significantly repelled the tea green leafhoppers; 28 volatile compounds were detected in lavender. The olefins (53.23%) were the most abundant. Benzene,1-methoxy-4-methyl-2-(1-methylethyl)-(38.41%) was the largest single component. Nine-component, seven-component and thymol 1 had significant repellent effect, thymol 1 had the best repellent effect, while thymol and benzene, 1-methoxy-4-methyl-2-(1-methylethyl)- were a good repellent. The application of push-pull strategy may prove to be effective in the control of tea green leafhoppers through the manipulation of differences in the attractiveness of tea plants. In summary, information from this study will be used to guide to establish push-pull chemical ecological control system in tea garden.

S07-18

Production of moth pheromone precursors in *Nicotiana* spp. by *Agrobacterium*-mediated transformation

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Pheromones are environmentally friendly alternatives to traditional pesticides for pest control. *Nicotiana benthamiana* and *N. tabacum* are potential green biomass production platforms of moth sex pheromones. Using these two *Nicotiana* species as plant factories we expressed biosynthetic genes of plant and insect origin in leaf tissue. Moth sex pheromone precursors (*E*)-11-tetradecenoic acid, (*Z*)-11-tetradecenoic acid and (*Z*)-11-hexadecenoic acid, were produced by introducing the acyl-ACP thioesterases *CpuFatB1* from *Cuphea pulcherrima* or *CpaFatB2* from *C. palustris* and the fatty acyl desaturases *AveΔ11* from *Argyrotaenia velutinana*, *CpaE11* from *Choristoneura parallela* or *AtrΔ11* from *Amyelois transitella*, under the control of CaMV-35S promoter. Among all the *Nicotiana* spp. transformants for the production of pheromone precursors, the best *N. benthamiana* transformed lines in the T0, T1 and T2 generations respectively, produced (*Z*)-11-hexadecenoic acid at 4.8%, 10.1% and 13.6% (weight%) of total fatty acids in leaves. Production of (*Z*/*E*)-11-tetradecenoic acid in *N. tabacum* was found to be lower. Therefore, in this study, the (*Z*)-11-hexadecenoic acid production lines from *N. benthamiana* were selected for further propagation to obtain homozygous lines. Our study demonstrates the feasibility of stable transformation of *N. benthamiana* for production of moth pheromone precursors in vegetative tissue.

S07-19

Yeast-beetle interactions and potential insights into the control of *Carpophilus* beetles in stone fruits and almonds

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Carpophilus beetles are considered a key pest of fruits and nuts in Australia. Adult beetles cause direct damage through feeding, and indirect damage as vectors of fungal diseases. Our study isolated several species of yeast from the gut of wild collected adults of *C. hemipterus* (which prefers rotting fruit), *C. davidsoni* (which prefers ripe fruit on trees), and a new emerging pest in almonds (*C. nr dimidiatus*). In fruit attacking species, *Carpophilus* beetles are closely associated with two yeast species, *Pichia kluyveri* and *Hanseniaspora guilliermondii*. In attraction (olfactory traps) and oviposition (egg counts) assays for stone fruit species, adult *C. davidsoni* and *C. hemipterus* beetles had significantly stronger preferences for fruit substrates inoculated with *H. guilliermondii*, compared to *P. kluyveri* and sterile substrate, whilst *P. kluyveri* inoculated media was significantly better for larval survival. GC-MS analyses showed significant quantitative differences in volatile emissions between the two yeasts, indicating that yeast odours may play an important role on *Carpophilus* beetles behaviour. Another yeast (*Wickerhamomyces rabaulensis),* isolated from *C. nr dimidiatus (almond-attacking species)* and exhibiting a different headspace profile from that of *H. guilliermondii,* trapped significantly higher numbers of beetles than the latter during field trials in almond orchards.

Understanding the ecology of yeast-insect interactions may provide a significant insight into potential attractants that could be used for trapping and monitoring *Carpophilus* beetles in different orchard crops.

S07-20

Semiochemicals for area-wide pest management

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Insect pest control techniques based on behaviormodifying chemicals (semiochemicals) have long been promoted as promising alternatives to broadspectrum pesticides. They have better safety and environmental profiles, present reduced risks to beneficial insects, and are typically more specific in their range of susceptible species than conventional chemical pesticides. However, semiochemical active ingredients are typically more difficult and expensive to produce than traditional pesticides, and due to their volatile nature, often require more exacting formulation work to achieve the field life necessary to deliver effective suppression of a pest population. For this reason, semiochemical-based pest control strategies to date have been restricted to highvalue specialty crops, and deemed unfeasible for largerscale growing operations. This discussion will focus on ISCA Technologies' expansion of the utility of semiochemical technologies from specialty crops, into a heretofore untapped semiochemical market: management of insect pests of large-scale row crops (corn, cotton, soybean, etc.). In recent years, ISCA has developed a number of products to improve the performance, ease of use, and commercial viability of semiochemicalbased strategies. An example of products resulting from these efforts are Noctovi, an attractandkill product for Noctuid moths, and SPLAT FAW, a mating disruption technology for fall armyworm (*Spodoptera frugiperda*) which have been field-tested in cotton, soy, pulses, and corn, both conventional and transgenic.

S07-21

Development of natural product-based repellents and attractant-baited technologies against blood-sucking insectsDevelopment of natural product-based repellents and attractant-baited technologies against blood-sucking insects

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Hematophagous arthropods are capable of transmitting human and animal pathogens worldwide. Vector-borne diseases account for 17% of all infectious diseases resulting in 700,000 human deaths annually. Repellents are a primary tool for reducing the impact of biting arthropods on humans and animals. N,N-Diethyl-meta-toluamide (DEET), the most effective and long-lasting repellent currently available commercially, has long been considered the gold standard in insect repellents, but with reported human health issues, particularly for infants and pregnant women.

Natural products including plant essential oils have been used for their insecticidal and repellent properties for at least two millennia in ancient China, Egypt, and India. However, nearly all plant-based repellents derived from plant essential oils have limited residual activity, primarily due to their high volatility. Although, the residual activity of a few plant-based essential oils can be extended up to 8 hours by the addition of a fixative such as vanillin. DEET (>25%) provides up to 10 hours of protection against mosquitoes. There is considerable interest in developing plant-based repellents with greater efficacy and extended residual activity due to increasing regulations and growing negative public perceptions against synthetic repellents and insecticides like DEET.

Natural product-based repellent compounds have been widely used against blood sucking insects in veterinary and public health fields. However, one of the biggest shortcomings of those repellent compounds are short-lived in their effectiveness. Therefore, it is necessary to discover and explore more resources/compounds of plant origins with extended longevity. In this presentation, I will share some recent developments of several natural product-based repellent compounds isentfied from various plant essential oils or food grade substances, which some can provide repellency lasting up to 2 weeks against several types of blood-sucking insects, including biting flies, ticks, mosquitoes, and bed bugs. Some of these compounds' derivatives also act as strong bio pesticide that inhibit pest larval growth and deters female oviposition. In one case, the strength of repellency from these natural repellent products is even stronger than the golden standard, universal insect repellent, DEET (N,N-Diethyl-3-methyl-benzamide).

S08-01

Manipulating indirect plant defences to improve pest management: can it be done?

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Research on insect-plant interactions has highlighted the intricacies of constitutive and induced plant defences. Of particular interest has been the relationship of natural enemies (especially parasitic hymenoptera) to herbivore induced changes to plants, particularly their responses to herbivore induced plant volatiles (HIPVs). In recent decades this has been a fertile area for research, with elegant experiments showing that HIPVs are important to attracting natural enemies to plants. We critically appraise the application of work on HIPVs in plant-insect-natural enemy interactions. The promise of applications to improved pest management has not been forthcoming. We attribute this to failure to include the multifaceted aspects of natural enemy-prey interactions – attraction, location, subjugation and experience. Attraction in an olfactometer by naïve parasitoids has not been translated to methodologically sound field-based estimates of higher parasitism rates. Few, if any, experiments at realistic scales have shown that the chemicals involved in the interaction can lead to improved pest management outcomes. We highlight what needs to be done to better understand the information that HIPVs convey, how this is utilised by parasitoids and how a greater understanding of these interactions might lead to new strategies so that this knowledge can be effectively deployed for improved pest management. In particular consideration will need to be given to the whole crop production system from the ground (soil and fertilisers) to the ecology of natural enemies at landscape scales.

The Abstract is based on: Furlong, M.J., Ang, G.C.K., Rehan Silva, R., Zalucki, M.P. 2018. Bringing Ecology Back: How Can the Chemistry of Indirect Plant Defenses Against Herbivory Be Manipulated to Improve Pest Management? *Frontiers in Plant Science* 9:1436. doi: 10.3389/fpls.2018.01436

S08-02

Insect effectors in plant-insect interactions and their potential applications

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Jasmonates (JAs) are the major defense phytohormone involved in transducing external signals (such as wounding) to activate defense reactions. To adapt to their host plant, insects have evolved effectors to conquer with plant defense. Most known insect effectors are isolated from sucking insects and very few other than GOX from chewing insects have been reported. Moreover, the target protein of insect effector in host plant remains unknown. Here, we isolated two effectors (HARP1, HAS1) from cotton bollworm (*Helicoverpa armigera*), a chewing insect widely existing in nature that severely affects crop productivity. HARP1 directly interacted with JASMONATE-ZIM-domain (JAZ) repressors to prevent the COI1-mediated JAZ degradation, thus blocking JA signaling transduction. HAS1 can interact with bHLH homologous transcription factors (TFs), including MYC3 and MYC4 in Arabidopsis and GhPGF in cotton. The protein-protein interactions inhibit the bHLH TFs to activate downstream defense genes. When plants were attacked by cotton bollworm larvae, the wounding damages quickly induced the JA-Ile accumulation in plant and triggered the JA signaling cascades. Meanwhile, the cotton bollworm larvae secrete effectors including HARP1 and HAS1. The insect effectors can migrate into plant cells and act as heterogenous regulators dually inhibiting defense signaling pathway in different layers. We generated transgenic plants (*35S:dsHARP1*) expressing dsRNA related to HARP1. When cotton bollworm larvae fed on *35S:dsHARP1*, the HARP1 accumulation in OS were largely reduced and the transgenic plants exhibit enhanced resistance to cotton bollworm. This indicated that genes encoding insect effectors can be used as the target for RNAi based plant protection technology. On the other hand, insect effectors are able to migrate from outside to inside of the plant cells, they can be potentially developed into a system to deliver active molecules.

S08-03

Host plants enhance the parasitism efficiency of a solitary egg parasitoid by altering their volatile cues

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When attacked by herbivores, plants synthesize and release herbivore-induced plant volatiles (HIPVs) to attract parasitoids and predators of herbivores. However, we face scarcity of information regarding plant volatiles affecting subsequent conspecific parasitoids' behavior when herbivores were parasitized by parasitoids. In this study, we recorded that rice plants infested with gravid females of brown planthopper (BPH) *Nilaparvata lugens* for 24 h followed by 24 h parasitism of the egg parasitoid *Anagrus nilaparvatae* (BPH infestation+parasitoid) decreased the attractiveness of their volatiles to subsequent conspecific parasitoids compared to rice plants infested with gravid BPH females alone (BPH infestation). Chemical analysis revealed that 4 volatile compounds, linalool, MeSA, α-zingiberene and an unknown, emitted from rice plants received "BPH infestation + parasitoid" were significantly higher than those emitted from plants received BPH infestation. By bioassays in the laboratory and field, we observed that one of the increased 4 chemicals, α-zingiberene had a repellent effect on the parasitoid. These results suggest that host plants have developed such a mechanism by which plants could help parasitoids to find appropriate hosts by fine-tuning their volatiles.

S08-04

Evolution of plant defense resistance in natural enemies of an arthropod herbivore

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Specialized herbivores have evolved the ability to tolerate, detoxify or sequester plant defense metabolites. Sequestering insects can use plant toxins to protect themselves from natural enemies. Whether natural enemies can in turn adapt to sequestered toxins remains poorly understood. WCR larvae sequester maize plant benzoxazinoids (BXs) and use them against entomopathogenic nematodes (EPNs). To evaluate the potential of EPNs to adapt to benzoxazinoid-dependent WCR defenses, we collected 25 strains of *Heterorhabditis* EPNs that are either sympatric or allopatric to the western corn rootworm (WCR). We then evaluated EPN infectivity towards BX-containing and BX-deficient rootworms. To understand the underlying mechanisms, we tested BX repellence and BX toxicity and conducted a real-time evolution experiment with BX susceptible nematodes. We found a strong positive correlation between the co-occurrence history and the resistance of nematodes to BXs. The EPNs collected from WCR occurring regions are more infective towards BXs containing larvae than the nematodes that were collected in areas where WCR do not occur. Higher nematode infectivity correlates with lower responsiveness to BX repellent effects and increased survivor upon BX exposure *in vitro*. Nematodes that were otherwise susceptible to BXs became more infective towards BX containing WCR larva when reared in WCR larvae for 5 consecutive rearing cycles. Thus, plant toxic secondary metabolites can drive the rapid adaptations of plant toxin resistance in herbivore natural enemies. Our study expands the biochemical co-evolutionary arms race between plants and herbivores to the third trophic level and provides a novel target for the improvement of biocontrol agents.

S08-05

Can bottom-up effects be manipulated to enhance pest control?

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Multitrophic interactions and specifically plant-mediated bottom-up effects have received increasing interest in recent years. Using the tomato leaf miner, *Tuta absoluta* Meyrick (Lepidoptera: Gelechiidae), as the focal pest in our tomato-pest-natural enemy testing system, a series of experiments manipulating nitrogen and/or water inputs to tomato have clearly shown the role of bottom-up effects in controlling the pest. Such findings may have broader importance since we found the bottom-up effects were consistent on different tomato cultivars even though they responded differently to nitrogen and/or water inputs. Reduced nitrogen supply lowers pest performance while not disrupting the predation and/or parasitism pressure by its natural enemies, suggesting the compatibility of bottom-up effects and top-down forces in integrated pest management. In addition, plant nutrient supply alters the magnitude of indirect interactions between the insect pests that share a host plant and a predator (*i.e.* a so-called four-species “diamond” food web). We highlight a holistic approach, from community dynamics, insect development and behavior, to foliar chemistry, for disentangling the indirect interactions in a simple food web. The take-home messages are: (i) bottom-up effects have the potential to be manipulated to enhance pest control; and (ii) more large-scale field experiments are encouraged in future to fully test these exciting findings.

S08-06

Organic fertilizer promotes wheat aphid control: from local to landscape scale effects

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Excess mineral fertilizer input results in little extra yield but aggravates herbivory, adversely affecting environmental health and ecosystem services. Organic soil fertilizer is a promising way to resolve these problems but potential mechanisms and effects on pest control services on a landscape-scale have rarely been studied. Here, field-scale experiments over a large spatial scale comparing different fertilizer regimes were conducted in Shandong province, Northern China. Soil fertilizer type and nutrient content, wheat plant metabolism, cereal aphids density and parasitism rate were quantified. We found that a maize straw amendment, as one typical organic fertilizer management approach, had significantly reduced cereal aphid abundance and benefited parasitism rate. A similar maize straw amendment but with added mineral fertilizer had relatively higher pest abundance and lower parasitism rates. On a landscape scale, simulations indicated if most crops were treated with maize straw amendment organic fertilizers with only a small number of conventional fertilizers treated fields, biological pest control function could be optimized. Plant free amino acid types and contents, but not plant defense compounds, most likely account for the variation of aphid abundance and biological control efficiency. Plant straw amendment may promote bottom-up effects that resist herbivory. Thus, organic soil fertilizer-dominated landscapes drive plant nutrient diversity to herbivores that could be a key aspect to supply pest control services on a larger spatial scale.

S08-07

Can prey to predator ratio be considered a criterion for successful bio-control in field?

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Spraying insecticides to suppress pests while keeping a comparatively higher density of predators in a field is a challenging problem. Manipulating natural enemies via conservation methods, inoculation or semiochemicals to achieve such control will require reliable assessment tools. Different ratios of cotton aphid (*Aphis gossypii)* to predators were tested to understand which ratio of prey to predator can be a threshold of successful bio-control of aphid in cotton at the seedling stage. We used a cage based experimental system, a dataset containing 20 years of long-term monitoring of cotton aphid and predators in open fields, and corresponding simulation models as a reference. Experiments showed the bio-control of cotton aphids by natural enemies under the ratio of 500:1 (prey to predator) can be successful, and population of aphid will decline to 50% at least in 10 days in both field and caged experiment. The ratio of prey to predator significantly correlated with the increase rate of aphid population growth, and with the control efficiency. Our study suggests that a ratio of 500:1 (prey to predator) is a good criterion for successful bio-control in cotton aphid in cotton seedling. How to achieve better natural enemy numbers in crop fields is discussed.

S08-08

The control of DBM with *Diadegma semiclausum* in practice in Yunnan province?

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We compared five different sex pheromones formulations for DBM and found one of them more effective at attracting the moth. Using this sex pheromone to monitor the field population of moth, we found the highest population of DBM was in the south-Yunnan and the lowest was in the northeast-Yunnan. Population of middle-Yunnan and southwest-Yunan were intermediate. The most likley reason for the different population levels might be the climate. We investigated the natural enemies of DBM in Yunnan and found that there were at least 8 main parasitic wasps of *Plutella xylostella* in Yunnan Province: *Trichogramma sp.*, *Cotesia plutellae* (Kurdjumov), *Meloboris sp.*, *Macromalon orientale* Kerrich, *Phaeogenes sp.*, *Pimpla sp.*, *Pteromalus sp*. and *Diadegma semiclausum* Hellen. *Diadegma semiclausum* is the dominant species and our objective was to develop practical ways of increasing natural mortality by this parasitoid. We tested the toxicity of 10 insecticides to *D. semiclausum*; 97% Badan, 5% beta-cypermethrin, 10% bromofenil, 5% fluorofenac and 2.5% polybactericide were highly toxic to this natural enemy (mortality >80%); 5% indoxicarb, 5% fluridylurea and 10% tebufenozide were slightly toxic (mortality 30-79%). After treatment with diafenthiuron and Bt, the mortality of parasitoids was considered negligible at less than 30%. The killing rate of 2% abmectin was the lowest, only 3.3%. We optimized the technology for mass production in the lab and established the technical regulations of indoor batch breeding. At the same time, the field application technology of *D. semiclausum* was formulated. Effective management of diamondback moth can be achieved through artificial supplementary release of wasps and natural field propagation, combined with culture control, cultivation systems and physical control (especially the use of sex pheromone).

S09-01

Pyridine alkaloids in imported fire ants

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Venomous imported fire ants cause significant medical problems. Alkaloids are an important component of imported fire ant venom. Piperidine and piperideine alkaloids have been identified in fire ant venom. In this study, we studied the venom alkaloids of the red imported fire ant, Solenopsis invicta Buren, the black imported fire ant, *Solenopsis richteri* Forel, and the hybrid, *S. invicta* × *S. richteri*. Pyridine alkaloids were detected the first time in fire ants using solid-phase microextraction (SPME) coupled with gas chromatography–mass spectrometry (SPME-GC-MS). The thermal desorption process was manipulated to facilitate the isolation and identification of pyridine alkaloids that were co-eluted with piperidine or piperideine alkaloids in GC. After SPME extraction of ant venom, we conducted a series of consecutive GC-MS injections, each with a partial desorption. Hidden pyridine alkaloid peaks were revealed after the overlapping piperidine or piperidiene alkaloid peaks had been desorbed. Using this approach, ten 2-methyl-6-alkyl (or alkenyl) pyridines (1-10) were found the first time in the venom of imported fire ants. Structures of three pyridine alkaloids were confirmed by synthesis, including 2-methyl-6-undecylpyridine (1), 2-methyl-6-tridecylpyridine (7), and 2-methyl-6-pentadecylpyridine (10). We also developed a silica gel column chromatography method to separate the pyridine alkaloids from other alkaloids. Using column chromatography and GC-MS with single ion monitoring at 107 m/z, five pyridine alkaloids were quantified for both workers and female alates of *S. invicta* and *S. richteri*.

S09-02

Applying chemical ecology to manage insect pests of blueberries

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The Oriental beetle (OB), *Anomala orientalis* (Waterhouse), and the spotted wing drosophila (SWD), *Drosophila suzukii* (Matsumura), are two invasive pests of highbush blueberries in the USA. OB damages the root system, while SWD attacks fruit. Current management practices for these pests are driven by chemical control; however, this strategy is not sustainable and its reliance increases environmental, human, and market concerns. To mitigate this, for the past decade, we have been testing behavioral control as an alternative strategy to manage OB and SWD populations in blueberries in New Jersey (USA). To this end, we have evaluated the feasibility of sprayable attract-and-kill OB and SWD SPLAT (Specialized Pheromone & Lure Application Technology; ISCA Technologies, Inc.) formulations to manage these pests under laboratory and field conditions. These formulations are composed of an attractive semiochemical and a small dose of an insecticide; in case of SWD SPLAT, it also contains a phagostimulant. In laboratory studies, OB and SWD SPLAT formulations increased adult OB and SWD mortality, respectively. In field trials, OB SPLAT reduced OB captures in pheromone-baited traps by >95%, as a measure of trap shutdown; the probability of OB females mating was also reduced under the OB SPLAT treatment. SWD SPLAT application to blueberry plots reduced SWD fruit infestation by 2-8 times compared with untreated plots. Our results demonstrate the possibility of implementing behavior-based (i.e., attract-and-kill) technologies to manage OB and SWD populations in blueberries, that can be used under conventional and organic farming. Factors potentially limiting grower adoption will be discussed.

S09-03

Discovery of repellents for managing spotted wing drosophila

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The spotted wing drosophila (SWD), introduced from Asia, is now a serious pest of numerous soft fruits throughout North America and Europe. Unlike other fruit flies, SWD lays eggs into marketable fruit. Significant damage, increased pesticide use, and increased economic losses have occurred due to SWD. We are developing a management tactic based on manipulation of SWD behavior with repellents and attractants to reduce SWD infestation. In this talk, we will describe the on-going work on isolating and identifying SWD repellents.

S09-04

Potential use of piperonyl butoxide in controlling oriental fruit fly

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The Oriental fruit fly, *Bactrocera dorsalis* (Hendel), is the world's most destructive and invasive fruit pest. Significant progress has been achieved in managing this pest - ranging from use of new and narrow spectrum insecticides in both protein bait-sprays and male trappings to releases of sterile male flies. In male trappings, insecticide-laced baits containing the potent male lure, methyl eugenol (ME), continues to be a popular choice of growers. Thus, to reduce the reliance on synthetic insecticide use, it is imperative that an effective alternative be found. We have previously demonstrated that the strong attraction of *B. dorsalis* males to and compulsive feeding on ME has been attributed to the production of ME-metabolites that act as sex pheromone components. This significantly increases male mating competitiveness. Taking cognizance of the ability to biotransform ingested ME that is catalyzed by mixed function oxidases, we further demonstrate that the use of a common insecticide synergist, piperonyl butoxide (PBO) that is also an oxidase inhibitor, can exert mortality effects when consumed together with ME by male flies. The efficacy of PBO, via determining median lethal dose (LD_{50}) against male Oriental fruit fly in laboratory evaluations, and field trappings will be further discussed in the presentation.

S09-05

The fruit fly attractant raspberry ketone trifluoroacetate: when being the most attractive molecule isn't enough

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Raspberry ketone trifluoroacetate (RKTA) is a novel fluorinated analog of the widely used fruit fly lure cuelure (CL), which is used to attractant the agriculturally important melon fly, *Zeugodacus cucurbitae*, and Queensland fruit fly, *Bactrocera tryoni*, along with other tephritid fruit flies. Both *Z. cucurbitae* and *B. tryoni* have responded more strongly to RKTA than to CL in laboratory bioassays, outdoor screen cage testing, and in short-term field tests conducted in Hawaii and Australia, respectively. However, despite the strong behavioral activity of RKTA, this molecule has not been deployed in monitoring and control programs due to the instability of the trifluoroacetate functional group which readily hydrolyses to raspberry ketone and trifluoroacetic acid under typical field conditions. In an attempt to alleviate the hydrolysis issues associated with RKTA use in field conditions, a number of release devises and compound matrices have been tested including, waxes, plastics, nanoparticle coatings, and the use of desiccants. Successes and roadblocks in this research will be discussed. This research illustrates that sometimes finding a potent insect attractant does not directly lead to improved pest detection and control.

S09-06

Preparation of polymeric microspheres contain insecticide and attractant and their control effects on *Rhagoletis batava obseuriosa* adults

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【Objective】 Sea buckthorn, *Hippophae rhamnoides*, is a widely distributed tree species that contributes to soil and water conservation. Its fruits, seeds and leaves are also raw materials for many health products. *Rhagoletis batava obseuriosa* Kol. (RBO) is a major fruit fly pest that attacks sea buckthorn berries. Since attractant or pesticide alone have limitations on control of RBO adults, the microsphere techniques were used to embed pesticides and attractants into microspheres in order to attract and kill the RBO adults, and prolong their effectiveness period in the field.

【Method】 Gelatin and polylactic acid were used as the wall materials of microspheres, and ammonium carbonate and spinosad (or abamectin) were used as the core materials. Microspheres were prepared by the solvent evaporation method. The influence of different ammonium carbonate contents encapsulated in the microspheres on the physical and chemical properties of the microspheres were evaluated firstly, then the attractiveness and lethal effect of the microspheres on the RBO adults were studied by bioassay. The microspheres were also sprayed in the field by the drone to test their control of the RBO adults.

【Result】 The microspheres prepared by the different ammonium carbonate contents were uniformly spherical and porous, and could continuously release the attractants and insecticides. The mean particle diameter was 55-78 µm. Microspheres attracted significantly more RBO to sticky traps than the control, indicating that the prepared microspheres had attract and kill ability to the RBO adults. There were significant differences between the four kinds of ammonium carbonate content microspheres and the control in the attractive and the lethal experiments, and were $P< 0.05$ respectively. The field experiment of the drone spraying demonstrated that all four microspheres reduced the population densities of the RBO and the damage rates of the seabuckthorn fruits.

【Conclusion】The ammonium carbonate and Spinosad (or abamectin) were successfully encapsulated into the microspheres, and both embedded compounds had continuous release effect. The prepared microspheres had the attractive and lethal effect on RBO adults, and could be used for the control of RBO and other *Rhagoletis* species.

S09-07

Pheromone-based attract-and-kill of cocoa pod borer

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As an alternative tool to chemical control, sex pheromone-based attract-and-kill strategy (CPB sex-pheromone as attractant and Delta trap without sticky liner sprayed with cypermethrin solution as killing station) was evaluated in Malaysia cocoa plantation. In order to more economically produce CPB sex pheromone, synthetic pathway has been modified. With impure sex pheromone (100 µg and 33.3 µg CPB-pheromone loading per station, respectively), attract-and-kill strategy showed high efficiency at reducing male flight activity ($p < 0.05$) in attract-and-kill plots comparing with standard CPB chemical management plots. The percentage of CPB-infested pods was significantly ($p = 0.021$) reduced with lower pheromone loading (33.3 µg) comparing with chemical management plots. Our result demonstrated that this sex pheromone-based attract-and-kill strategy is far superior to and more feasible than the currently applied conventional synthetic pesticide management.

S09-08

Particle-transport behaviors of red imported fire ants (Hymenoptera: Formicidae) in response to the repellent surfaces

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Our previous studies showed that the red imported fire ants, *Solenopsis invicta* Buren (Hymenoptera: Formicidae), relocated soil particles on the substance treated with essential balm (a repellent against fire ants) during foraging. We hypothesized that ants placed particles onto the unfavorable surfaces to facilitate food transport. In the present study, we conducted laboratory experiments to investigate the particle-relocation behavior of *S. invicta* in response to the viscose surface, or surface treated with essential balm or liquid paraffin, when the real food (sausage) or false food (acrylic plates) was provided. Interestingly, *S. invicta* workers transported a large amount of soil particles onto the three types of treated surfaces regardless of food availability, whereas few particles were relocated onto control (untreated) surfaces. On viscose surface or surface treated with liquid paraffin, ants transported significantly more particles (measured by weight) when the real food was provided compared with non-food conditions. Our study showed that unfavorable surfaces triggered particle-relocation behavior by ants. Interestingly, food is not the key factor to cause the transport of soil particles, though presence of food items may increase particle relocation.

S09-09

The defense mechanism of the ghost ant *Tapinoma melanocephalum* against the red imported fire ant *Solenopsis invicta*

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The ghost ant, *Tapinoma melanocephalum* (Fabricius), a dominant native ant species in South China, can successfully compete with the red imported fire ants, *Solenopsis invicta* Buren, at the community level. When confronting with fire ants, ghost ant workers usually spray and/or smear a viscous secretion to the fire ants to avoid being attacked. So far, the mechanism of how this defensive secretion works is not well understood. Here, we identified the defensive components of ghost ant workers' pygidial gland secretion by GC-MS. And pygidial gland secretion was assayed for its contact toxicity, fumigation and repellency to fire ant workers and its effect on the walking speed of fire ants was also evaluated.

These experiments revealed that six isomers of iridodials were detected as major chemical components in the pygidial gland secretion. Pygidial gland secretion had contact toxicity, repellency to fire ant workers, but its volatiles had no fumigation effect on fire ants. The walking speed for ants that had been placed together with 10 or 20 ghost ants was 4.67 ± 0.88 and 3.31 ± 0.59 mm/s respectively, significantly slower than ants in the control (7.16 ± 0.67 mm/s). The sticky defensive secretion of ghost ants physically slow down the movement of fire ants. These results suggested that pygidial gland secretion of ghost ants may function both chemically and physically in defense against their competing ant species.

S09-10

Cucumber and bitter melon extracts as ant repellents

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Cucumber peel is listed in the informal literature as a natural ant repellent for those seeking botanical alternatives to artificial compounds. While certain compounds in cucumber can repel roaches, and some attract herbivorous cucumber beetles, no data existed on cucumbers and ants. Is there truth to the myth? Furthermore, some sources claim that “bitter” cucumber has a more potent effect. Could these be references not to true cucumber, *Cucumis sativus,* but to the related Cucurbitaceous plant, *Momordica charantia*, or bitter melon? We tested the effects of extracts of peels of these two fruits in various polar and nonpolar solvents on several species of ants. We found that an aqueous extract of either peel will have a significant but unreliable gustatory repellant effect on ants. As an olfactory repellent, cucumber water has a significant half-repulsion effect on ants, while bitter melon water does not. We then ran hexane, isopropanol, and methanol extracts of the two plants though a gas-chromatogram electroantennogram using ant antennae from worker ants of the species *Camponotus pennsylvanicus* and *Formica fusca*, to identify the exact chemicals responsible for the observed repellency and better quantify the strength of their effects. We also repeated the bioassays using pure chemical components. Our results demonstrate the use of modern methods to test folk remedies, and confirm that cucumber does have a measurable though mild repellent effect on ants.

S09-11

A defense protein MLX56 found in mulberry latex: roles in mulberry-silkworm interaction, unique mode of function, and application to pest management

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Since sericulture originated in China c.a.4,000-6,000 years ago, people have been observing the silkworm, *Bombyx mori*, feeding on mulberry, *Morus spp*. without noticing hostile interactions between them. Recently, we found that mulberry leaves are toxic to insects other than *B. mori* because of two types of defensive components in mulberry latex, sugar-mimic alkaloids and MLX56 family proteins (MLX56 and its close homolog LA-b). MLX56 is a 56 kDa protein consisting of 394 amino acids with a unique sandwich-like structure composed of an extensin domain (Gum Arabic-like domain) surrounded by two hevein (chitin-binding) domains. MLX56 inhibited the growth of *Spodoptera litura, Mamestra brassicae*, and Eri-silkworms, *Samia ricini*, in 0.01-0.04% concentrations. MLX56 has a unique mode of toxic action. MLX56 swells the peritrophic membrane (PM, thin chitin-based membrane existing between midgut epithelium and food materials) of Eri-silkworms fed MLX56 into an extraordinary thick gel-like structure that functions as obstacle to digestive processes, by binding to chitin-framework of PM with hevein domains, and swelling PM with extensin domain. Interestingly, *B. mori* is resistant to MLX56 and sugar-mimic alkaloids, suggesting the physiological adaptation in the mulberry specialist, and the involvement of the latex components in the evolution of silkworm-mulberry interactions. We are attempting to develop pest-resistant crops using MLX56. Tomato, tobacco, and *Arabidopsis*, expressing *mlx56*-gene (MLX56-protein) showed strong resistances to various important pests including *Spodoptera litura*, *Mamestra brassicae*, *Plutella xylostella* (Lepidoptera), *Henosepilachna vigintioctopunctata* (Coleoptera), and thrips (Thysanoptera) suggesting that MLX56 can be a promising substitute of *Bt* toxin in making pest-resistant crops in future.

S09-12

Correlation analysis between the shoot damages and trap catches of *Tomicus minor* Hartig in the *Pinus yunnanensis* forest

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We initiated the insect pest monitoring researches in order to clarify the relationship among the percentage of *Pinus yunnanensis* shoots with beetles and trap catches of *Tomicus minor* Hartig, and furthermore, to provide technical support for population monitoring and controlling of the *T. minor* pest in the future. The shoot damages of *P. yunnanensis* were investigated by random branch sampling method with pruner in two different damage level field sites of Pupeng and Xiazhuang, Xiangyun County, Yunnan province. The adults were trapped by aggregation pheromone of *T. minor* during the period of shoots transferring to trunk, in order to evaluate the population flight dynamics and analyze the relationship among the percentage of shoots with beetles and trap catches. There are two dominant *Tomicus* species, *T. minor* and *T. yunnanensis* in Pupeng and Xiazhuang field sites. *Tomicus minor* accounted for 49.75% with sex ratio 1.06:1, however, *T. yunnanensis* consisted of 50.25% with sex ratio 1.32:1 in Pupeng field site. In Xiazhuang field site, it accounted for 54% of *T. minor* with sex ratio 1.45:1; 46% of *T. yunnanensis* with sex ratio 1.88:1; The percentage of shoots with beetles has gradually reduced from top crown to bottom crown in the Pupeng and Xiazhuang sampling locations, where the density of Pupeng population was ca. 10 times the density of Xiazhuang populaton. The population flight dynamics of *T. minor* in Pupeng showed the same trend as that of Xiazhaung, with adult emerging in mid-November and adult flight stopping in late May of the next year. The peak of adults' flight activities ranged from the first of March to the late of April. The natural enemies followed the pests. The traps caught more number of males than females with sex ratio ranging from 1:1.09 to 1.71 (♀:♂). To analyze the correlation among the trap catches (x) and the percentage of shoots with beetles (y), the function expression was $y = 0.0024x + 0.0601$ ($R^2 = 0.67$) in high population densities area (Pupeng), and $y = 0.0032x–0.0043$ ($R^2 = 0.71$) in low population densities area (Xiazhaung). These studies clarified the distribution patterns of *T. minor* in the tree crown of Yunnan pine forest with high and low pest population densities. Furthermore, the aggregation pheromone trapping test can be regard as an effective method to monitor the population dynamic of *T. minor* in the forest which result in a positive linear correlation between the trap catches and percentage of shoots with beetles, suggesting that the number of trap catches could reveal the percentage of shoots with beetles.

S09-13

Significant role of the maxillary palps in the olfactory communication of insects

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Although the antenna is the major olfactory sensory organ in insects, the maxillary palp appears to play an important olfactory sensory role in a number of insects. In particular, dipteran species exhibit well developed olfactory sensilla on their maxillary palps, in which the presence of multiple nanoscale pores is the morphological evidence for their olfactory function. The morphology and distribution of the olfactory sensilla in the maxillary palps appears to be different from those of antennal sensilla, suggesting their function is different from that of antennal sensilla. Our recent electrophysiological and behavioral studies on two fruit fly species, *Bactrocera depressa* and *B. scutellata*, indicate that the maxillary palps are responsible for detecting long-range attractants. Such sensory role of the maxillary palps appears to be unique and species-specific. Our study clearly demonstrated that the olfactory sensory function of the maxillary palps is not limited to the detection of food-related volatiles in a short range. The significant and species-specific role of the maxillary palps in olfactory communication needs to be further investigated in wide range of insects, which may provide new opportunities to develop semiochemicals. It would also be interesting to understand how these separate olfactory sensory systems have been evolved and how the olfactory sensory inputs from the antennae and maxillary palps are processed in the central nervous system.

S09-14

Herbivore feeding and Exogenous MeJA induced terpenoid defense in *Pinus massoniana*

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The destructive pine wilt disease (PWD) is threatening the conifer forest ecosystem around the world. *Monochamus alternatus* is the main vector insect of pine wood nematode (PWN), *Bursaphelenchus xylophilus*, in southern China. However, the secondary defense in *Pinus massoniana* induced by either *M. alternatus* or the putative key signal molecular, methyl jasmonate (MeJA), hasn't been clearly determined. In present study, we compared the secondary defense in *P. masspniana* induced by *M. alternatus* adult feeding and exogenous MeJA, respectively. Visible anatomical responses occurred in cambium 6-9 days and mature resin ducts formed 21-24 days post both treatments were inoculated. After *M. alternatus* feeding, 12 monoterpenoids, 7 sesquiterpenoids and 8 diterpenoids were detected in *P. masspniana*. The terpenoid concentrations in treated *P. massoniana* varied over time with significant increase in 3 days and 12-18 days. However, MeJA treatment led to fewer terpenoid components with lower concentration in *P. masspniana* than *M. alternatus* feeding. Moreover, both treatments activated the terpenoid biosynthesis related pathways and promoted related genes transcription at certain timepoints which were normally prior to the release of corresponding compounds. Bioassay results indicated that MeJA treated *P. massoniana* greatly depressed *M. alternatus* maturation feeding and also effect PWN colonization. Our results showed that herbivore feeding and MeJA inoculation can both induce terpenoid secondary defense and change overtime, which supported that MeJA is an important signal molecular in *P. massoniana* secondary defense system. Insect feeding may trigger more complicated responses in plant defense system than MeJA only.

S09-15

Vanillin as a bioactive compound from resistant tomato root exudates affects *Meloidogyne incognita* infection

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Root knot nematodes (*Meloidogyne incognita*) are ubiquitous in soil and adversely affect tomato productivity. Various tomato cultivars have been developed to resist nematode infestation via allergic reactions to root knot nematodes and/or excretion of bioactive compounds into the rhizosphere. In this study, XianKe nematode-resistant tomatoes reduced numbers of root knot by ≥ 95.76% and inhibited egg generation on roots. The bioactive compound exuded by XianKe roots, identified as vanillin, inhibited *M. incognita* egg hatching by > 50%. Laboratory tests on second-stage juveniles (J2s) of *M. incognita* showed greater repellent behavior and mortality in response to vanillin than to deionized water. In the pot experiment, root knot numbers per tomato decreased 45.61–62.68% when vanillin was mixed into the soil, and *Mi-flp-18* and *Mi-16D10* showed upregulated expression. We conclude that vanillin applied to soil can effectively inhibit *M. incognita* infection and reproduction and regulate nematode diseases at an optimal concentration range of 4–6 m mol/l, which is safe for tomato growth. Thus, vanillin is a suitable bioactive compound derived from root exudates of nematode-resistant cultivars that is expected to improve the performance of nematode-susceptible crops.

S09-16

Isolation and identification of the aggregation pheromone in *Megalurothrips usitatus* (Thysanoptera: Thripidae)

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Megalurothrips usitatus is an important leguminous pest in South China, which has caused enormous losses to cowpea planting industry. Lures based on aggregation pheromone is one of the environmentally friendly control methods for *M. usitatus*, which would play a key role in bio-control of this pest. In this study, the behavioral responses of female and male adults of *M. usitatus* to headspace volatiles collected from female and male conspecifics were tested in a Y-tube olfactometer. Headspace volatiles released by female and male adults were collected using headspace solid-phase microextraction (HS-SPME) and hexane extraction. The active compound was identified by gas chromatography-mass spectrometry (GC-MS). The behavioral responses of female and male adults to synthetic aggregation pheromone component were tested in a Y-tube olfactometer. Behavioral results showed that both male and female adults of *M. usitatus* were attracted to the odors released by conspecific males but not by females. The volatiles from female and male adults could be extracted by both SPME and hexane extraction, but the extraction with SPME was more effective and suitable. GC-MS analysis showed that there was one major compound [(*E,E*)-farnesyl acetate] in headspace volatiles from male adults, and this compound was absent from headspace volatiles from female adults. Olfactometer results showed that both male and female adults showed significant preference to synthetic (*E,E*)-farnesyl acetate at certain doses. This study confirmed the presence of aggregation pheromone in *M. usitatus* male adults and identified its active compound as (*E,E*)-farnesyl acetate. The results provide a basis for population monitoring and pest control of *M. usitatus* using aggregation pheromone.

S10-01

Response of gut-associated bacteria to alpha-pinene of *Ips typographus*

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Spruce bark beetle (*Ips typographus*) is a harmful pest in Eurasia. The α-pinene as a main monoterpenes of spruce can protect the pines from pest attack, it could be converted to semiochemicals or other nontoxic metabolites for bark beetle.The gut microbes are very important to insect life, to explore the roles of *I. typographus* gut bacteria in the response process to α-pinene. In this study, through 16sRNA high-throughput sequencing, we find two chiral α-pinene both make microbial diversity become higher compared than control group, but the result of PCOA and cluster analysis showed that the *R*-(+)-a-pinene have more effect on gut microbiomes than *S*-(-)-a-pinene. In order to further affirm the response of gut-associated bacteria to two chiral a-pinene, we isolated and identified the bacteria in guts of *I. typographus*, the three strains *Rahnella sp., Enterococcus sp., Pesudomonas tolaasii,* could converted *R*-(+)-a-pinene to *R*-(+)-*trans*-verbenol, *R*-(+)-verbenone, but no product from *S*-(-)-a-pinene could be detected. To field behavior test, we find *R*-(+)-*trans*-verbenol is not a pheromone components that no any effect for *I. typographus.* But the *R*-(+)-verbenone could as an inhibitor to decrease the trap quantity in the field significantly. These conclusions would provide an insight to understand the coevolutionary relationships among the host, *I. typographus* and gut microbes.

S10-02

A collaborative intrusion mechanism between pine wood nematode, pine sawyer beetle and blue stain fungi

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Chemical communication is a survival strategy for biological behavioral manipulation and adaptive evolution. Through the study of the symbiosis system of "pine wood nematode – pine sawyer beetle - blue stain fungi", the mechanism of chemical signal drives the developmental consistency between symbiotic organisms is clarified. We have proposed and explained that chemical information adaption between species lead to multi-species hazard superposition. Firstly, the key to the formation of the symbiotic system between pine wood nematode and vector beetle is that the signals released during the specific developmental stages, which keep the two species at the same developmental speed. Ascarosides secreted by the dispersal third-stage nematode L_{III} larvae promote beetle pupation by inducing ecdysone production in the beetle and upregulating ecdysone-dependent gene expression. Once the beetle develops into the adult stage, it secretes ascarosides that attract the dispersal fourth-stage nematode L_{IV} larvae, potentially facilitating their movement into the beetle trachea for transport to the next pine tree. Secondly, the contact between pine wood nematode and vector beetle will cause reactive oxygen species burst, and the immune tolerance of the vector beetle is the basis of the coexistence. Thirdly, the emergence of new commensal bacteria species in introduced region inducing the host to release hormone-like signals, which enhance the reproduction and virulence of the pine wood nematode, and promoting the rapid death of pine trees. The fourth, we propose that destructive pathogenicity of pine wood nematode to pines is partly due to upregulated fecundity modulated by insulin pathway in association with ROS pathway and further enhanced by H_2O_2 oxidative stress. These findings provide a better understanding of pathogenic mechanisms in plant–pathogen interactions and adaptive evolution of invasive species.

S10-03

Diversity of ascarosides signaling in *Pristionchus* nematodes

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Pristionchus pacificus is an important model nematode which is used to study the evolution and development through comparing with *Caenorhabditis elegans*. Our prior chemical investigation on the *exo*-metabolome of *P. pacificus* indicated that *P. pacificus* produced a complex mixture of small molecules (ascarosides and paratosides) to control its life circle and phenotypic plasticity, which greatly accelerated our understanding on the chemical ecology and biology of this nematode. However, we still know nothing about the chemistry in remainder *Pristionchus* species. To understand the evolutionary metabolism of ascarosides pheromone in *Pristionchus* nematodes, we spanned from *P. pacificus* to the whole *Pristionchus* genus to examine the chemical composition of their excretomes, which led to the discovery of diverse ascarosides with intriguing chemical features and activities. Comparative metabolomics and structural characterization of these unique ascarosides signaling provided new insights into the chemical ecology of *Pristionchus* nematodes.

S10-04

Identification and field evaluation of the sex pheromone of *Orthaga achatina* (Lepidoptera: Pyralidae)

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The *Orthaga achatina* (Lepidoptera: Pyralidae) is the most serious pest of the camphor tree (*Cinnamomum camphora* (L.) Presl), an important urban tree species in south China. In the present study, the sex pheromone of *O. achatina* was analyzed by gas chromatography equipped with an electroantennographic detector (GC-EAD), and three EAD-active components were found in crude pheromone gland extracts of calling females. Further GC-MS analyses using synthetic chemicals and derivatization of the extracts identified the three components as (*Z*)-11-hexadecenol (Z11-16:OH), (*Z*)-11-hexadecenyl acetate (Z11-16:OAc), and (3Z,6Z,9Z,12Z,15Z)-tricosapentaene (Z3,Z6,Z9,Z12,Z15-23:H). This identification revealed that *O. achatina* uses both type I and type II sex pheromone components, and *O. achatina* is the third Pyraloidea species found to utilize Z3,Z6,Z9,Z12,Z15-23:H as a sex pheromone component. In field tests with different combination of the three components, male moths were strongly attracted to a mixture of Z11-16:OAc and Z3,Z6,Z9,Z12,Z15-23:H, but much less attracted to other blends. Further field test with different ratios of Z3,Z6,Z9,Z12,Z15-23:H determined the optimal ratio of this binary blend as 500:250. However, the addition of Z11-16:OH to Z11-16:OAc, or to the binary mixture of Z11-16: OAc and the pentaene could not generate significantly higher catches. The behavioral activity of Z11-16:OH needs to be further investigated.

S10-05

Effect of intra- and inter-specific exposure of sex pheromone on adult reproductive performance of *Helicoverpa armigera* and *H. assulta*

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A specialist *Helicoverpa assulta* and a generalist *Helicoverpa armigera* are two sibling noctuid species in Lepidoptera. We tested the effect of high-dose sex pheromone exposure on female reproduction performance and longevities of both sexes. The response of *H. assulta* females to high-dose and long-term sex pheromone exposure was decreasing their life-time fecundity, while response of *H. armigera* females was delay oviposition activity. Both intra- and inter-specific sex pheromone exposures could shorten the longevity of *H. assulta*males, while these exposures did not affect the longevity of *H. armigera* males.

S10-06

Enhancement of copulation by dim red light during scotophase in the yellow peach moth, *Conogethes punctiferalis*

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Environmental factors such as light conditions have great influences on insect copulation. Different photoperiods, illumination intensity and wavelengths of light could change mate choices. In artificial rearing of the yellow peach moth, a dim red light is usually provided to benefit observation. During long period of artificial rearing, we found a red light with an illumination intensity of 2.0 lux, enhanced copulation of the insect. Under red light conditions (660nm, 2.0lux), numbers of mating pairs and average egg numbers lay by females were significantly more than those of insects under dark conditions. Additionally, copulation under other light conditions including blue light (460nm, 2.0lux) and white light (wide range of wavelength, 2.0lux) were also tested. Results showed that the blue light inhibited copulation and white light had no obvious influences on mating, compared with the dark condition. Sex pheromone amounts of female moths under the red light condition were found less than those under the dark condition. And male moths under red light conditions showed higher electroantennographic responses to female pheromones than males under dark conditions. A transcriptome analysis further found differently expressed genes such as seminal fluid proteins genes between the red light and dark moths. In conclusion, dim red light in scotophase was found to enhance copulation in our artificially rearing population of the yellow peach moth. The enhancement may due to decreased amount of female pheromone secretion and male’s pheromone sensitivity.

S10-07

Romantic leaves: plant volatiles stimulated mating behavior by modulating vibrational communication in leafminers

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Herbivore-induced plant volatiles (HIPVs) synergize with the sex pheromones of herbivorous insects to facilitate mate location. However, the synergism of HIPVs and acoustic signals for sexual communication remains unknown. Here, we investigated the synergy between HIPVs and vibrational duets for sexual communication and mating in the pea leafminer (*Liriomyza huidobrensis*).

Our results indicated that adult leafminers do not produce species-specific pheromone, and female-puncture-induced plant volatiles facilitate the attraction of both sexes to host plant leaves and sexual encounters. Insect-derived cues do not participate in mate locations. Both sexes do not produce qualitatively different cuticular hydrocarbons (CHCs), and CHCs from females cannot elicit the antennal and behavioural responses of males. By contrast, induced green leaf volatiles, terpenoids and oximes elicit dramatic antennal responses in both sexes. Electrophysiological and behavioural tests consistently showed that the volatiles (Z)-3-hexenol and (Z)-3-hexenyl-acetate elicited the most intense gas chromatographic electroantennographic responses, and attracted males and females. Remarkably, these volatiles not only promoted the occurrence of vibrational duets between the sexes, but also modulated plastic strategy in duets, thereby increasing the mating success of leafminers.

Therefore, the synergism of HIPVs and vibrational signals largely promoted the mating success of leafminers, suggesting an alternative control strategy through precision trapping for non-pheromone-producing insects.

S10-08

Study on pheromone binding proteins and active components of contact pheromone in *Liposcelis entomophila*

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Chemosensory proteins (CSPs) are an indispensable part of insect olfactory system, which can recognize host plant volatiles and pheromones. *Liposcelis entomophila* was widely exists in the world in the past 20 years and have gradually become to the dominant population of stored grain pests. Therefore, from the perspective of molecular biology and chemical ecology, it is of great significance to systematically explore the mechanism of chemoreceptor proteins in the prevention and control of *Liposcelis entomophila*. The purpose of this paper is to identify the pheromone blinding protein and its special blinding contact pheromone components and their trap activity. Firstly, based on the data of transcriptome sequencing of *L. entomophila*, the present study was obtained and analyzed the open reading frame sequence of chemonsensory protein gene in *L. entomophila* (*LeCSP,* Genbank accession No.MK211168). The open reading frame length of *Le-CSP* was 411 bp, encoding 136 amino acids. The predicted molecular weight was 17.45 kDa and the isoelectric point was 9.45. *LeCSP* has a complete signal peptide located at 1-18 amino acids. There were four conserved cysteine residues in the amino acid sequence of *LeCSP*, which were 56.93% and 54.47% homologous to *Tribolium castaneum* and *Tenebrio molitor*, respectively. qPCR results showed that the expression level of *LeCSP* in different stage and tissues was significantly difference and the highest level was in the fourth larval instars. The highest express level of *LeCSP* was in male antennae and it could express in other tissues such as head, thorax and abdomen. The expression vector was successfully constructed by prokaryotic expression. The expression of *LeCSP* protein in supernatant was detected by inducing the expression of recombinant plasmid and SDS-PAGE analysis. The recombinant protein *LeCSP* was purified by Ni-NTA His Bind Resin column. The mass concentration of the recombinant protein *LeCSP* was 1 mg/mL. Using 1-NPN as a fluorescent probe, the binding ability of recombinant protein to volatiles and contact pheromone analogues of *L. entomophila* was tested by fluorescence competitive binding assay. The binding constant (K_d) of *LeCSP* was 6.351 μM. Among them, , hexadecanoic acid, oletic acid and linoleic acid have strong binding ability, but whether to recognize contact pheromone of insect-louse needs further verification. To confirm the trap activity of five candidate contact pheromone components, odor selection experiments in laboratory were carried out with “Y”-type olfactometer. At the same time, two kinds of attractants made according to specific components were tested in a warehouse in Zhengzhou City. The results of odor selection test showed that all the five attractants had trap effects on the tested insect. There were significant differences in the trap effects under different concentrations. There were certain effective ranges of different volatiles on the action concentration of the *L. entomophila*, and there were also certain differences in the action concentration of different volatiles. The results of field trapping experiment showed that the combination of hexadecanoic acid, oletic acid and linoleic acid according to 27.8:43.9:28.3 with conical traps had significant trapping effect on the *L. entomophila*. The results indicated that hexadecanoic acid, oletic acid and linoleic acid were the contact pheromone components of *L. entomophila*c. The attract lure with special ration could be used to predict the occurrence of the *L. entomophila* for a long time, and also forecast the occurrence location of the *L. entomophila* in grain warehouse.

S10-09

Characterization of nine odorant binding proteins in *Diaphorina citri*

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The Asian citrus psyllid (ACP), *Diaphorina citri* Kuwayama (Hemiptera: Liviidae) is the most crucial pest of citrus worldwide. It is the vector of the extremely destructive citrus disease called huanglongbing (citrus greening disease), which is a major threat to citrus production all over the world. Therefore, it is very important control ACP effectively. The olfactory system of ACP is sensitive to diverse odors produced by citrus plants, thus it offers an opportunity to develop new attractants or repellents. The odorant binding protein (OBP) play an important role in binding and transporting chemical compounds between external environment and odorant receptor. Nine *DcitOBPs* were identified in transcriptome and multiple sequence alignment analysis showed that eight *DcitOBPs* belong to classic OBP with six conserved cysteines, only one is plus OBP. The phylogenetic analysis of several Hemiptera insects OBPs presented the consistent result with multiple sequence alignment analysis. Subsequently, nine *DcitOBPs* without signal peptide sequence were cloned into PET-30a(+) vector and expressed in *Escherichia coli*. Additionally, different tissue expressions showed that seven *DcitOBPs* highly expressed in head cuticle, which suggested that these OBPs play a key role in olfaction. Based on the amino acid sequence, homology modeling and I-TASSER methods were used to construct three-dimensional structure of *DcitOBPs*. In further study, a variety of chemical compounds will be used to dock three-dimensional structure of *DcitOBPs*, aiming to screen potential functional OBPs. Furthermore, microscale thermophoresis (MST) and RNAi methods will be employed to identify the authentic *DcitOBPs* for chemical compounds.

S10-10

Rice stripe virus infection regulates olfactory behavior of the small brown planthopper (SBPH) *Laodelphax striatellus*

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The survival of plant viruses is largely dependent on the efficient transmission to plant hosts by viral-specific vectors. The plant viruses may influence subsequent vector behavior either directly or via effect on plants, and consequently enhance their spread. However, the mechanism of plant virus-induced effect on vectors behavior directly remains unclear. Rice stripe virus (RSV), causal agent of rice stripe disease, is transmitted by the *Laodelphax striatellus* (SBPH) in a persistent manner. Here, we found that the SBPH after acquiring Rice stripe virus (RSV) prefers health rice plants, whereas noninfected SBPH did not show a significant preference. The transcriptome analysis identified 15 odorant-binding proteins (OBPs), 12 chemosensory proteins, 7 sensory neuron membrane proteins and 95 odorant receptors in SBPH, and screened the 39/36 olfactory genes with different expression between noninfected and RSV-infected female/male antennae. We confirmed that the expression of four OBPs (*LstrOBP2, 3, 4,* and *5*) was decreased in RSV-infected antennae by qRT-PCR analysis. To explore the role of four OBPs on the preference of RSV-infected SBPH to health rice, we found that the absence of the SBPH ubiquitin fusion protein (*LstrUBI*) could block RSV infecting antennae. We used dsRNA of *LstrUBI* (*dsUBI*) as a RSV inhibitor. Knockdown of LstrUBI by RNAi rescued the lower expression of *LstrOBP 3* in the RSV-infected antennae, indicating the LstrOBP 3 may play a key role in the preference of RSV-infected SBPH. Our results showed that RSV infection regulated LstrOBP 3 expression to alter olfactory behavior of SBPH. These provide new ideas for the control of insect-borne plant viral diseases.

S10-11

Neural basis underlying pollinator's decoding of floral scents

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The interactions between insects and plants, such as predation, parasitism, pollination, are fundamental cornerstones of evolution process and ecosystem stability. The key issue in dissecting these interactions is the neural bases underlying the entomic "decoding" of floristic contexts. Here, we addressed this issue by studying the olfactory neural responses of *Drosophila immigrans*, which is bamboozled by *Cypripedium bardolphianum* into performing pollination process. We find out that the orchid *C. bardolphianum* employed ET as the critical VOC to accomplish the pollinator enticement. Behavior analysis shows that ET represents a dual olfactory mimicry of food source and oviposition to attract the pollinators. And we found that ET was recognized by the gustatory receptor to active the specific glomerulus, whose volume was evolutionary augmented in the drosophilids with preference to ET, especially *D. immigrans*. What's more, in pollination field experiment of *C. bardolphianum*, two allopatric drosophilids species with the suitable body size and olfactory neural properties, successfully played a role as ecological potential orchid pollinator. These findings are a demonstration of neural processes mediating a fly's unique odor preference at behavioral and circuitry level, which allows the flies to maintain specialized plant/insect interaction in a complex environment.

S10-12

Chrysomelidae discriminates host plants by tarsal gustation

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Tarsal taste recognition is well documented in Diptera and Lepidoptera. However, in Coleoptera, the largest insect order, the role of tarsal taste recognition is unclear. In this study, we focused on tarsal taste recognition of Chrysomelidae as this family includes many agricultural pest species. First, we observed the tarsi of Chrysomelid species by using scanning electron microscope to investigate whether tarsal gustatory organs were common in this family. We found that all subfamilies of Chrysomelidae exhibited tarsal gustatory sensilla. In contrast, a tarsal gustatory sensillum was not found in the other families that we observed. Taken together, this indicated that tarsal gustatory sensilla were not common in Coleoptera as a whole. We investigated the role of tarsal taste recognition using *Galerucella grisescens* as a model species of Chrysomelidae. Through electrophysiological experiments, we found that NaCl, KCl, sucrose, brucine, and leaf surface wax of *Rumex obtusifolius*, a host plant of *G. grisescens,* were perceived by tarsal gustatory sensilla of *G. grisescens*. Additionally, in our behavioral experiments, we found that *G. grisescens* could select sucrose and tasted their host plant leaf surface wax by only their tarsi. In contrast, they did not show any behavioral responses to leaf surface waxes of their nonhost plants. These results indicate that *G. grisescens* were able to discriminate their host plants by tarsal gustation. Our results indicate that in Chrysomelidae, tarsal taste recognition was important in their host selection.

S10-13

A cyanogenic glucoside, linamarin, regulates differential oviposition on white clover by coliadine butterflies, *Colias erate* and *Eurema mandarina*

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Two coliadine butterflies, *Colias erate* and *Eurema mandarina*, are Fabaceae-feeders and use D-pinitol as a primary oviposition stimulant[1-2)]. However, although D-pinitol is omnipresent in Fabaceae, they greatly differ in host range and show different preferences for specific fabaceous plants. Although white clover (*Trifolium repens*) is a preferential host for *C. erate*, *E. mandarina* females lay very few eggs on the foliage in the field. We attempted to identify which plant chemicals in white clover deter oviposition of *E. mandarina*. The crude leaf extract and its three fractions by solvent extraction were inactive to stimulate female oviposition. Among four subfractions of the aqueous fraction, the most polar one containing D-pinitol (Tr-3-1) elicited high oviposition responses. The second most polar subfraction (Tr-3-2), when mixed with Tr-3-1, significantly decreased oviposition responses, indicating that it contains some oviposition deterrents. Chemical analyses revealed that two cyanogenic glucosides, linamarin and lotaustralin, were the major constituents of Tr-3-2. Authentic linamarin also significantly inhibited oviposition when mixed with Tr-3-1 at the natural concentration. Therefore, we concluded that linamarin acts as an oviposition deterrent for *E. mandarina*. Interestingly, linamarin and lotaustralin have been reported to synergistically induce the oviposition of *C. erate* on white clover together with D-pinitol[1,3)]. These results demonstrate that linamarin regulates differential oviposition on white clover by the two coliadine butterflies and that oviposition deterrents might play central roles in their differential host utilization within Fabaceae.

S10-14

Induced resistance of oviposition of *Micromelalopha sieversi* on two clones of *Populus* section *Aigeiros*

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Host plants can protect against pests through induced resistance, which is an important factor for ecological management of pests. The study on the induced resistance of oviposition of *M. sieversi* was conducted with two clones of section *Aigeiros*, with ‘108’ (*P.* × *euramericana* ‘Guariento’) being more attractive to *M. sieversi* than ‘111’ (*P.* × *euramericana* ‘Bellotto’). Three treatment (Oviposited plants, neighboring plants, and control plants) were set up. The oviposition amount of the three treatment plants was counted and the volatiles at 24 h, 48 h and 72 h after oviposition were collected for GC-MS analysis. In electroantennogram test of five volatile compounds on the males, females and mating females, the maximum response dose was dropped on the plants leaves to statistics the number of eggs. At the same time, the survival rate of the larva feeding with the leaves of the three treatments plants were observed. Illumina HiSeq 2000 high-throughput sequencing technology was used to analyze the transcriptome sequencing and gene expression differences in the leaves of the three treatment plants. The results show that Significantly fewer eggs were oviposited on neighboring plants compared to control plants for ‘108’ and ‘111’ after oviposition of *M. sieversi*, with more eggs being laid on oviposited and control plants of ‘108’ compared to ‘111’. In addition, once egg masses appeared on ‘108’ and ‘111’, the number of eggs basically remained unchanged until the end of the egg incubation period. The relative content of 3-carene in oviposited and neighboring plants of ‘108’ and ‘111’ was significantly higher than that of control plants at 24 h, 48 h, and 72 h after oviposition. The defense genes related to PR protein, innate immune regulation and biological stress response in the oviposited and neighboring leaves of ‘108’ and ‘111’ were up-regulated respectively, but the specific genes were different, and the genes related to photosynthetic activity were all significantly down-regulated.

S10-15

Identification of leafhopper-induced tea plant volatiles and their attraction to parasitic mymarid wasps

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In order to investigate potential role of tea plant volatiles in the host finding behavior of mymarid wasps (*Stethynium empoascae* Subba Rao and *Schizophragma parvula* Ogloblin), the egg parasitoids of the tea green leafhopper, volatiles from the fresh excised tea shoots (**ETS**), excised leafhopper-feeding damaged tea shoots (**ELFDTS**), excised tea tender stems (**ETTS**) and excised ovipositing-injured tea tender stems (**EOITTS**) were respectively collected via a custom-made push–pull aeration system with Super Q absorbent. The volatile compounds from these samples were qualitatively and quantitatively analyzed by gas chromatography-mass spectrometry (GC-MS), and were assayed in the field on the mymarid wasps. Our GC-MS analyses detected 13 and 18 volatile compounds from **ETS** and **ELFDTS**, respectively. The content of (*E*)-2-hexenal, (*Z*)-3-hexen-1-ol, (*Z*)-3-hexenyl acetate and (*Z*)-butanoic acid-3-hexenyl ester in **ELFDTS** samples seemed to be significantly higher than those in **ETS** samples; and following compounds, hexanal, (*Z*)-2-hexen-1-ol, acetic acid-hexyl ester, linalool oxide (*Z*)-furanoid, squalene, (*E*, *E*)-*α*-farnesene and (*E*)-*β*–myrcene, benzaldehyde and phenylethyl alcohol, were detected from **ELFDTS**, but not from the **ETS**. The volatiles from **ETTS** were similar to those from the **ETS**, and ovipositions on the tea stems by the leafhoppers resulted in the release of (*E*, *E*)-*α*-farnesene, benzaldehyde and (*Z*)-3-hexenyl butyrate from the **EOITTS**. At the dosage of 10^{-2} g/mL, the synthetic individual leafhopper-induced volatiles, (*E*, *E*)-*α*-farnesene, (*E*)-*β*-farnesene, benzaldehyde, linalool, (*E*)-2-hexenal and methyl salicylate, and their partial mixtures, mixture 1 [(*Z*)-jasmone and benzaldehyde at 1:1 ratio] and mixture 2 [(*E*, *E*)-*α*-farnesene and benzaldehyde and (*E*)-2-hexenal at 1:1:1 ratio] showed signficant attraction to the mymarid wasps, *St. empoascae* and *Sc. parvula,* with the mixture 2 being the most attractive, in the field trapping experiments. The jasmine yellow boards baited with the synthetic mixture 2 or (*E*, *E*)-*α*-farnesene could efficaciously attract these two species of mymarids to the target areas and enhance their parasitism on eggs of the tea green leafhoppers, therefore, could indirectly suppress the leafhopper populations.

S10-16

Impacts of CCYV-induced plant volatiles on behaviors of vector *Bemisia tabaci*

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Plant viruses can modify vector behaviors by changing the volatile composition and/or concentrations of the infected host plants. *Cucurbit chlorotic yellows virus* (CCYV) is a new plant virus (family *Closteroviridae*, genus *Crinivirus*) on cucurbit plants and many other plant species occurring in Asia, Greece and recently in California. CCYV is transmitted specifically by B and Q biotypes of tobacco whitefly, *Bemisia tabaci* (Hemiptera: Aleyrodidae), in a semipersistent manner. In this study, we investigated volatile profiles of CCYV-infected cucumber plants, and observed orientation behaviors of *Bemisia tabaci* B and Q biotypes to healthy and CCYV-infected plants. The volatile profiles of CCYV-infected plants were much different from those of heathy plants, and some volatile compounds were not found or in much lower concentrations. From the present results we can conclude that CCYV can change the vector feeding behaviors through changing host plant profiles, thereby modify the plant-insect interactions. Suppression of some plant volatile releasing by CCYV may be one of the strategies to adjust plant-vector interactions in order to facilitate virus transmission, and needs further research. In addition, *Bemisia tabaci* B and Q biotypes differentially responded to virus-induced plant volatiles which may partially explains why two biotypes have different efficiencies in transmission of CCYV.

S10-17

Root feeding larvae increase their performance by inducing leaf volatiles that attract aboveground conspecific adults

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1. Herbivore-induced changes in plant volatile emissions mediate above-belowground interactions by determining host plant colonization of different herbivores. By changing shoot-emitted volatiles, belowground herbivores may use the plant to extend their capacity to interact with aboveground con- and heterospecifics.

2. We investigated the attractiveness of *Triadica sebifera* plants infested by larvae of a specialist beetle or root-knot nematodes to aboveground herbivores. We then determined the contribution of leaf volatiles to the observed recruitment patterns using olfactometer experiments. We also identified volatiles through GC-MS and electroantennography, and conducted field experiments to confirm their effects.

3. Leaf volatiles induced by the root-feeding larvae attracted aboveground conspecific adults in laboratory and field experiments, but repelled a heterospecific specialist weevil, whereas induction by root-knot nematodes had no effects on either. Greater leaf consumption by conspecific adults increased root nutrients, decreased root defenses, and facilitated root feeding larval performance. Thus, larvae and adults appear to manipulate their host plant, which increases aggregation aboveground and feeding belowground.

4. *Synthesis*. The resulting colonization dynamics may shape the composition of plant rhizosphere and phyllosphere herbivore communities by enhancing conspecific establishment and reducing colonization by other herbivores. By modifying aboveground volatiles and aboveground herbivore behavior, root feeders could mediate plant and leaf herbivore interactions and benefit via plant responses to aboveground feeding.

S10-18

Identification, characterization and allelochemical induced expression of *CYP321A2* in *Helicoverpa zea*

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Cytochrome P450 is the most important gene family responsible for detoxification of the diversity of plant allelochemicals in insects and other animals. Here, we reported a new P450 gene *CYP321A2*, a duplicated paralog of the xenobiotic-metabolizing P450 *CYP321A1* in *Helicoverpa zea*. Very interestingly, in a laboratory strain, *CYP321A2*'s transcription was disrupted by insertion of the transposon *HzSINE*, yielding two transcripts of different length that encode an identical C terminus-truncated P450; but this truncated P450 is non-functional, as it lacks the heme-binding region. PCR survey with individual insects conformed that the *HzSINE*-disrupted *CYP321A2* allele is fixed in the laboratory colony, whereas the wild type *CYP321A2* allele prevails in two field population. Quantitative RT-PCR experiments showed that wild type *CYP321A2* and its paralog *CYP321A1* were constitutively expressed in low levels but can be differentially induced by a range of the plant allelochemicals and plant signal molecules, among which xanthotoxin, flavone and coumarin were the most prominent inducers of *CYP321A2* both in midgut and fat body, whereas flavone, coumarin and indole-3-carbinol were the prominent inducers of *CYP321A1*. Moreover, xanthotoxin- and flavone-responsive regulatory elements of *CYP321A1* were also detected in the promoter region of *CYP321A2*. Taken together, our results enrich the P450 inventory by identifying an allelochemical broadly induced *CYP321A2*. Our results support that *CYP321A2* is not a pseudogene but a functional P450 with a spontaneous *HzSINE*-disrupted null allele in the laboratory strain and *CPY321A2* could potentially be involved in the detoxification of plant allelochemicals and adaptation of *H. zea* to its chemical environment.

S10-19

The cosmopolitan phytopathogen *Sclerotinia sclerotiorum* detoxifies defensive isothiocyanates in a Brassicaceae host plant

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Glucosinolates and myrosinases constitute a two-component activated chemical defense system in plants of the order Brassicales, generating toxic isothiocyanates that contribute to broad plant resistance against diverse herbivores and pathogens. However, how this defense system acts during plant-fungal interactions is poorly understood. The necrotrophic fungal pathogen *Sclerotinia sclerotiorum* (Lib.) de Bary colonizes a range of plant species including glucosinolate-producing plants, but the adaptations allowing such generalist fungal pathogens to avoid the toxic isothiocyanates in Brassicales plants remain unclear. In this study, we used Arabidopsis (*Arabidopsis thaliana*) and the white mold *S. sclerotiorum* to demonstrate that the glucosinolate-myrosinase system is rapidly activated by fungal infection and contributes to plant resistance against this fungus. Interestingly, we found that *S. sclerotiorum* copes with exposure to isothiocyanates via the widespread glutathione conjugation pathway and a specific hydrolytic degradation pathway. This latter pathway depends on an isothiocyanate hydrolase (ITCase) from the metallo-β-lactamase superfamily that we identified as a SaxA protein. The metabolites of SaxA are not harmful to fungal growth, indicating that this protein catalyzes a detoxification reaction. Using an ITCase deletion mutant (ΔSsSaxA) we demonstrated that this degradation pathway determines fungal tolerance to host isothiocyanates and is an important virulence factor for *S. sclerotiorum* on glucosinolate-producing host plants.

S10-20

Complex ecological impacts of the giant willow aphid invasion in New Zealand

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The giant willow aphid (GWA), *Tuberolachnus salignus*, is an invasive pest species first recorded in New Zealand in 2013. Since then, it has spread rapidly, affecting over 50 species and hybrids of willow and poplar throughout the country. These trees and shrubs have high agricultural importance as forage, to stabilize slopes and river banks, to prevent soil erosion, and as sources of nectar and pollen for bees. The GWA affects its surroundings in multiple ways, not only by reducing plant vigour, but by releasing copious amounts of honeydew that promotes the growth of sooty mould, attracts unwanted insects (such as wasps, ants, and flies), causes bee honey to crystalize (affecting apiculture), and alters soil composition and biota. Due to the extent of the invasion, eradication is no longer feasible, so there is a need to assess the environmental impact of this pest species and develop sustainable control strategies to mitigate it. This talk will present preliminary results of a semi-field study using 15 different willow clones, including the characterisation of plant volatile emissions, changes in soil enzyme activity due to honeydew deposition, and the effect of different host-plants on the chemical composition of aphid honeydew.

S10-21

Increasing flavonoids enhance the AM fungal colonization in an invasive plant

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As an important group of symbiotic fungi in soil, arbuscular mycorrhizal fungi (AMF) has been got more and more attention in invasive plants, because lots of studies support that they play huge role on the plant invasion. However, how does the invasive plants regulate the relationship of AMF and plants is still poorly known. Here, in order to make clear this question, we carried out a common garden experiment on the Chinese tallow tree (*Triadica sebifera*) by examining the difference of plant's AMF, biomass, and secondary metabolite in invasive and native populations, as well as their relationship. The results showed that the flavonoids were positive correlated to AMF colonization significantly and there was significantly positive relationship between AMF colonization and aboveground biomass. What's more, the relationship between the flavonoids and AMF depended on the origin (native range and invasive range) significantly. Therefore, the increase of the flavonoids in invasive populations promoted the growth of hypha and attracted to more AMF hypha on their roots, which resulted in the increase of the aboveground biomass and total biomass significantly. These findings will provide guidance on the further study of the mechanism of invasive plants and the evolution of the relationship between plants and AMF.

S11-02

Pheromone synthesis with my mentor, Prof. Kenji Mori

Shigefumi Kuwahara

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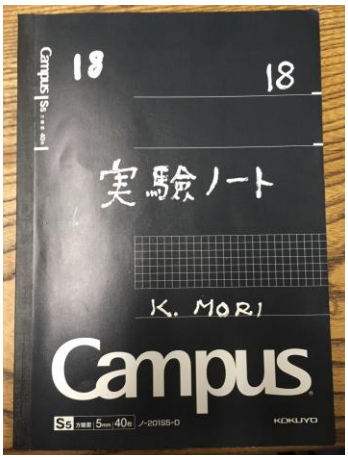
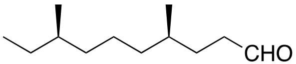
My beloved mentor, Prof. Kenji Mori, passed away at the age of 84 at the University of Tokyo Hospital on the morning of April 16, 2019. In November, last year, he was diagnosed as advanced bile duct cancer, but the direct cause of his death was cardiac infarction. The first heart attack hit him on January 24, 2019, and the second one that took place late at night on April 15 carried him off.



His last laboratory notebook ends on January 22, 2019.

I studied pheromone synthesis, as a student and as an assistant professor as well, for 11 years from 1979 under his mentorship. The year 1979 was his second year as a full professor at the University of Tokyo. He was incredibly vigorous and hardworking, and loved to talk a lot with students while drinking endlessly. In this symposium, I would like to speak about some of his early pheromone syntheses that I really enjoyed with him.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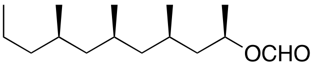
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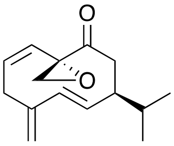
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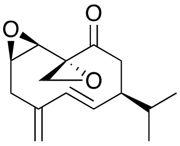
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S11-03

Teachings of Prof. Mori sensei for scientists who work for a company

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I began to work at Fuji Flavor in 2003 after getting a doctoral degree at Okayama University. The very first time that I met Prof. Mori sensei was at Fuji Flavor. He worked for Fuji Flavor from January, 2002 to June, 2006. He was a technical advisor of our chemist team and synthesized various pheromones based on requests. He didn’t synthesize chemical substances himself for 16 years. He resumed synthesis of pheromones at Fuji Flavor and gave presentations and submitted papers. He really enjoyed research.

He was a true scientist but he had a standpoint as a manager. He said to me, “You should become a scientist in a company who get your own salary by yourself”. He emphasized both basic and applied science. He often said “Happy” at places other than a drinking party. It meant a win-win relationship. We, scientists give outcome to the society and get value that is appropriate for it from the society.

I learned a lot from Prof. Mori sensei. I’d like to think of Prof. Mori sensei, looking backward to memories and episodes with him.

S12-01

Root exudate analysis of buckwheat and oat in the presence of redroot pigweed

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Allelopathic cover crops as an ecological weed management technique are of great interest for farmers. Several studies have been performed to evaluate the effect of cover crop biomass on weed suppression. However, little is known about the impact of allelopathy on weed growth in a cover crop stand.

Our experiments combine field trials and a metabolic approach with the aim to identify chemical compounds produced as the result of the interaction of a cover crop and a weed. For this, we studied buckwheat (*Fagopyrum esculentum*) and black oat (*Avena strigosa*) root exudation in the presence and absence of the weed redroot pigweed (*Amaranthus retroflexus*) with a splitroot system allowing to collect specifically the buckwheat and black oat root exudates. We could show that the two cover crop species modify their root exudation in the presence of redroot pigweed. Buckwheat root exudates lead to pigweed root growth reduction.

Our results suggest that allelopathy is a factor to be considered in weed management by cover crops. Inducible allelopathic root exudates could provide a growth advantage to allelopathic crops.

S12-02

The influence of peanut/maize intercropping on jasmonates biosynthesis and secretion of root and its physiological and molecular mechanism in improving peanut iron nutrition

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Intercropping is an efficient technology in resource-limited agricultural systems with low inputs. Our previous works revealed that peanut/maize intercropping system could enhance the iron (Fe) nutrition of peanut. The increased deoxymugineic acid (DMA), secreted by intercropped maize, is vital for this improvement because peanut could absorb Fe(III)-DMA. The biosynthesis and signal transduction of jasmonic acid (JA) were promoted in intercropping. However, the role of JA in improving peanut iron nutrition by intercropping remains unclear. Here, we found that JA participated in root-root interaction and promoted DMA secretion. The DMA secretion and the endogenous JA biosynthesis of maize roots were enhanced gradually by intercropping, which owed similar dynamic variation. Moreover, several jasmonates (JAs) were incrementally secreted to the rhizosphere by intercropped peanut. One of those JAs was methyl dihydrojasmonic acid, which has been proven to increase endogenous JA biosynthesis. The biosynthesis and secretion of DMA in maize were increased by JA. Furthermore, an overlap was found between the DMA biosynthesis and secretion genes up-regulated by intercropping and those by JA treatment. Besides, although Fe(II) uptake of peanuts was inhibited by JA, there was no obvious relationship between endogenous JA concentration and Fe absorption progress in intercropped peanut roots. Taken together, our results suggested that the DMA secretion of intercropped maize roots was increased by the elevated endogenous JA, which may be the result of more jasmonates secreted by peanuts. This feedback of peanut to maize to peanut may play a key role in improving peanut Fe nutrition.

S12-03

The parasite *Cuscuta australis* with a streamlined genome mediates inter-plant systemic signals

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Cuscuta spp. (dodders) are stem parasites that naturally graft to their host plants to draw water and nutrients, and multiple adjacent hosts can often be parasitized by a dodder plant simultaneously, forming dodder-connected plant clusters. Whether ecologically meaningful signals can be transferred between dodder and hosts and among hosts in the dodder-connected plant clusters remains unclear. We show that when two host plants are bridge-connected by *Cuscuta* parasites, insect herbivory on one host induced strong defense-related responses in the dodder-connected other hosts, and these hosts exhibited increased resistance to insects. Furthermore, using ^{15}N labeling experiments, we found that dodder can transfer N from a N-replete host to dodder-connected N-deplete host, and importantly, dodder mediates N-systemic signaling between the N-replete and N-deplete hosts bidirectionally. These data indicate that dodder facilitates ecologically meaningful systemic signaling and even transfers nutrients between different host plants and influences host interaction with environmental factors. To gain insight into the evolution of dodder genome, a high-quality reference genome sequence of the dodder *Cuscuta australis* was generated. It was found that *C. australis* genome experienced a large scale of gene reduction, including important genes involved in photosynthesis, stress resistance, flowering, and circadian regulation, indicating that during the long interaction with host plants, *Cuscuta* lost root and leaf, as well as genes important for regulating root and leaf functions. The genome of *Cuscuta* provides important insight into the evolution of parasitic plants.

S12-04

Structure and origin of phenolic compounds that mediate the signaling interactions of parasitic plants with host plants

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Parasitic plants form a specialized organ, the haustorium, to infect host plants. After initiation, haustorium invade host tissue and connect the xylem of parasite with that of host for initiation of water and nutrients uptake. Host infection mediated by haustorium, therefore, involves multiple layers of signaling interactions between host plant and parasitic plant. Some parasitic plants in Orobanchaceae family, including *Striga* spp. and *Orobanche* spp., are among the major agricultural constraints worldwide by infecting important staple crops such as rice, maize, millet and sunflower. Many Orobanchaceae members induce haustorium on the root by perceiving host-derived chemicals, collectively called haustorium inducing factors (HIFs). These HIFs are simple aromatic compounds that include quinones as well as flavonoids and lignin monomeric compounds derived from phenylpropanoid pathway. Although these phenolic compounds have been shown to induce haustorium in vitro, a key question remains for their synthetic pathway from host in vivo. To address this question, we investigated the role of host lignin biosynthetic pathway of HIFs production. Various lignin-related phenolics, quinones and lignin polymers, together with host plants that have altered lignin compositions, were tested for their haustorium-inducing activity in two Orobanchaceae species, a facultative parasite, *Phtheirospermum japonicum*, and an obligate parasite, *Striga hermonthica*. Structural specificities exist in these phenolic compounds to be able to induce haustorium in both parasites. Transgenic *Arabidopsis* with altered lignin composition showed reduced haustorium induction compared to the wild type, indicating that host lignin biosynthetic pathway plays an important role in the production of HIFs.

To gain insights into how lignin-related phenolics act as signals to trigger haustorium induction in parasitic plants, we further investigated cellular accumulation of monolignols in the haustorium using fluorescence-tagged monolignols, which appeared to be able to induce haustoria in *Striga*. Our results show that, upon haustorium induction, monolignols are immediately incorporated into the cell wall of haustorial epidermis, indicating that they are polymerized into lignin at haustorial surface. Supportively, H_2O_2 and peroxidases required for oxidative radical coupling of monolignols into polymer were highly induced in haustorium during the development and peroxidase inhibitor largely compromised the cell wall incorporation of monolignols. These results show the unanticipated localization of exogenous monolignols in the haustorium and imply the specific feature of haustorial epidermal cells in inducing functional lignification, which may be beneficial for host invasion by making physical boundary with host tissue. Our studies demonstrate that phenolic compounds derived from host lignin biosynthetic pathway is an important player in host plant-parasitic plant interaction.

S12-05

Molecular evidence of (-)-loliolide induced the production of defensive metabolites in plants

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The production of defensive metabolites in plants can be induced by signaling chemicals. Plant-derived signaling chemicals have focused mainly on volatiles as airborne signals. However, soilborne signaling chemicals in plant-organism belowground interactions are largely unknown. Our previous study revealed root-secreted the most ubiquitous lactone (-)-loliolide as a soilborne signaling chemical for plant neighbor detection and allelochemical (2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one, DIMBOA) response from a model system of allelopathic wheat with 100 interacting plant species. Here, we experimentally demonstrate (-)-loliolide-triggered plant defensive responses and the corresponding molecular evidence. (-)-Loliolide induced the production of various defensive metabolites including phenolic acids (ferulic acid, caffeic acid, chlorogenic acid), flavonoids (daidzein, genistein, luteolin, tricin), terpenoids (artemisinin, momilactone B), alkaloids (nicotine, nornicotine) and cyanogenic glycosides (sinigrin) in multiple plant systems. Furthermore, (-)-loliolide induced the expression of the biosynthesis genes of wheat allelochemical BIMBOA. This induction was regulated by the upstream JA signaling pathway. Not limited to defensive metabolites, (-)-loliolide also induced the gene expression of the defensive proteins including PI, PPO, PR3 and Defensin. The determination of reactive oxygen species (ROS) indicated that (-)-loliolide improved the antioxidant enzyme activities but did not generate an excessive amount of ROS, resulting in the increase of resistance in wheat root. The rice root transcriptome profiling revealed that (-)-loliolide activated a series of pathways in relation to plant defense responses. Therefore, (-)-loliolide is a belowground signaling chemical to elicit the production of defensive metabolites in plants, participating in the defense of plants against herbivores or pathogens and other plant competitors.

S12-06

Potential control of paddy and invasive weeds by mimilactones A,B,E and 7-ketostigmasterol isolated from rice husk

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There were four bioactive compounds including momilactone E (ME), 7-ketostigmasterol (7KS), momilactone A (MA), and momilactone B (MB) were isolated by column chromatography (CC) to yield 2.7, 0.3, 11.7, and 8.3 mg/kg rice husk, respectively. The structures of the isolated compounds were identified and confirmed by spectroscopic techniques consisting of ^{1}H and ^{13}C nuclear magnetic resonance (NMR), electrospray ionization mass (ESI), high-resolution mass spectrometry (HR-MS) and infrared spectroscopy (IS). An advanced quantitative method for MA and MB was achieved to increase the detectable yields of MA and MB in rice husk to 51.96 and 42.33 µg/mL, respectively. Results showed that both MA and MB exhibited stronger inhibitory activity than ME and 7KS. MB exerted greater inhibitions than MA but the mixture of MA and MB (1:1, *v/v*) possessed a similar level of inhibition to MB. On the other hand, although ME and 7KS presented non-significant inhibition, their mixture of ME-7KS (1:1, *v/v*) displayed a remarkable inhibition on the growth of *S. altissima*. Findings of this study revealed that MA, MB, and the mixture ME-7KS had the potential to control the invasive plant *S. altissima* and the noxious paddy weed *E. crus-galli*.

S12-07

Allelochemicals: promiseful sources of natural products with ecologically functions

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It is well recognized that allelopathic interactions are an important factor in determining species distribution and abundance within plant communities in nature- and agro-ecosystem. With the beneficial or detrimental effects contributed by the allelochemicals, of which the production is affected by biotic factors and abiotic factors, allelopathy plays important roles in plant biodiversity and sustainable agriculture. Allelochemicals with negative allelopathic effects are an important part of plant defense against herbivory and pest management. Besides the direct promotion or inhibition effects on the target organisms and the community, our recent approaches have confirmed that the release of allelochemicals affect the composition and diversity of rhizosphere soil microbial communities to some extent in the soil environment. Allelopathic interactions between the allelochemicals and soil enzyme activities, environmental factors, rhizosphere soil bacterial communities contribute to the species ecological adaptability within plant communities. On the other hand, autotoxic allelopathy has been thought to be one of the critical factors in replant problems in agriculture. The degradation of the allelochemicals by developed microbial agents provides an efficient strategy to eliminate the replant problems in agriculture.

S12-08

Antioxidant response mechanism of freshwater microalgae species to reactive oxygen species production: a mini review

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Microalgae are able to utilize dissolved CO_2 and CO_3^{2-} for their biomass production as such found in freshwater and marine water. The production of reactive oxygen species (ROS) by microalgae is unavoidable because ROS is a by-product of metabolism. ROS is beneficial to microalgae at low concentration, but injurious at higher concentration leading to oxidative stress. In order to annul any effect resulting from ROS, microalgae have developed antioxidant system which involves enzymatic and non-enzymatic pathways. This mini review is aimed at providing the progress and future prospect of the antioxidant responses exhibited by algae to counter the effect of excess ROS production. The mini review summarizes the process of ROS formation in the mitochondria, endoplasmic reticulum, chloroplast etc. The effect of algae cell size, cell density, light intensity, growth stage and temperature on production of ROS were analyzed. The review extensively looks at the role of ROS to the ecology of freshwater algae and the role of algae enzymatic and non-enzymatic antioxidant responses towards combating oxidative stress resulting from excess production of ROS. The mini-review shows that the production of ROS and antioxidant response to ROS production (enzymatic and non-enzymatic antioxidant) varies across species of freshwater microalgae and is dependent on cell size, cell shape, cell density, growth stage and a biotic factor such as light, nutrient and temperature. It is recommended that more research should be done on more species of algae in order to determined how factors such as algae cell size, light intensity, intra-specific and inter-specific etc. affect the production of ROS by algae and how antioxidant response differ from one species of organism to the other in order to know more species that can be utilized for the production of natural antioxidants.

S13-01

Comparison of different heterologous expression systems for studies of genes involved in moth pheromone biosynthesis

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The integral membrane fatty acyl desaturases (FADs) in the Lepidoptera have evolved to function not only in normal cellular lipid metabolism, but also in the biosynthesis of moth sex pheromones. Pheromone biosynthesis-related desaturases are key enzymes that have evolved unusual regio- and stereoselectivity that contribute to the diversity of chemical structures used for mate communication in moths. Since the Δ11 desaturase gene involved in pheromone biosynthesis in the cabbage looper *Trichoplusia ni* was characterized heterologously in yeast (Knipple et al., 1998), there has been a massive number of studies using yeast, *E. coli*, insect Sf9 cells, and plant chassis as expression systems to study fatty acyl desaturase from various lepidoptera. We compare the advantages and limitations of each expression system, summarize the main achievements of these desaturase studies, and highlight some of the desaturases that have the potential to broaden our "toolbox" for biotechnological production of pheromones. The optimal choice of expression system depends on the species and pheromone under study.

S13-02

Odorant receptor 25 is narrowly tuned to the floral volatile eugenol and methyleugenol attracting pollinator *Eupeodes corollae*

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Flowering plants have evolved some strategies to attract pollinators. Floral scents, especially those aromatic compounds emitted by flower, can be accurately perceived by olfactory sensory system of pollinators. Syrphid fly is the largest flower visiting insect in Diptera, but little is known about how they detect aromatic compounds at molecular level. In this study, we analyzed functional profiles of odorant receptors (ORs) from *Drosophila melanogaster*, one of them, DmelOR46a, are only tuned to 4-methyl phenol being a part of aromatic compounds. Next, phylogenetic analysis showed that DmelOR46a belonged to relatively conserved OR clade, and was homologous with OR25 of *Eupeodes corollae*. The full-length gene encoding *EcorOR25* expressed in antennae of both sexes was functionally characterized. The result showed that EcorOR25 was narrowly tuned to two structurally-related floral scent volatiles, eugenol and methyleugenol. At last, choice behavior assay confirmed that eugenol and methyleugenol elicited significantly behavioral attraction of both sexes in *E. corollae* adults. In summary, our study preliminarily demonstrated a molecular mechanism of floral scent detection in pollinators, inferring that EcorOR25 may be involved in flower foraging and pollination of Syrphid flies.

S13-03

A gustatory receptor tuned to coumarin in the cotton bollworm *Helicoverpa armigera*

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Gustation plays a critical role in host-plant selection of phytophagous insects. It is commonly believed that plant acceptability is mainly based on a balance between stimulating and deterrent compounds in plants. Gustatory receptor neurons housed in taste sensilla recognize primary and secondary plant compounds. Gustatory receptors (GRs) tuning to deterrents experienced an expansion in the polyphagous species *Helicoverpa armigera*. However, the functions of these GRs remain to be elucidated. In this study, we analyze the transcriptome of taste organs in *H. armigera* and find that HarmGRx is highly expressed in antennae, proboscis and tarsi of adults, and the mouthparts of larvae. Using the *Xenopus laevis* oocyte expression system and two-electrode voltage-clamp recording, we discover that the oocytes expressing HarmGRx respond specifically to coumarin among 25 plant secondary compounds. This GR is not homologous to BmGr53, BmGr16 and BmGr18, which are GRs tuned to coumarin in *Bombyx mori*. Coumarin is a common secondary compound in many plant species. The two-choice behavioral assays show that coumarin is a feeding deterrent of *H. armigera* larvae, and such an effect is dose-dependent. The further RNAi experiments are carried out to validate the function of HarmGRx in host-plant selection of *H. armigera*.

S13-04

Characterization of DHCR24 orthologs in the phytophagous insect, *Bombyx mori*

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Because insects fail to biosynthesize cholesterol *de novo*, sterol compounds must be exogenously acquired. In particular, phytophagous insects must acquire cholesterol by conversion of phytosterols. Previous studies have demonstrated that conversion enzymatic processes from phytosterols to cholesterol are composed of four steps in lepidopteran species. Of the contributing enzymes, an enzyme catalyzing the final step has been identified as 24-dehydrocholesterol reductase (DHCR24) which reduces a double bond at C-24 of desmosterol. Meanwhile, characterization of insect DHCR24s have not been completely reported so far. Therefore, we aimed to identify and characterize insect DHCR24 in the phytophagous silkworm *Bombyx mori*. Database searches revealed the presence of two DHCR24 homologs, BmDHCR24-1 and BmDHCR24-2. To know which subtype contributes to the enzymatic activity, we therefore performed following experiments. RT-PCR analyses indicated that both subtypes are predominantly expressed in the midgut of *B. mori* larvae but in different manners. Analyses of subcellular localization of BmDHCR24-1 and BmDHCR24-2 expressed in HEK293 cells revealed that both subtypes were localized mainly in ER, corresponding to those of mammalian DHCR24s. Analyses of conversion activity from desmosterol into cholesterol using HEK293 cells expressing BmDHCR24s revealed that BmDHCR24-1 exhibited its enzymatic activity in the presence of NADPH. The optimal pH and optimal temperature for BmDHCR24-1 were consistent with those of microsomal fraction derived from *B. mori* larval midgut. Together, we concluded that BmDHCR24-1, but not BmDHCR24-2, functions as the DHCR24 in *B. mori*, possibly contributing partly to conversion of phytosterols into cholesterol.

S13-05

Production of insect pheromone precursor in the oil crop *Camelina sativa*

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Camelina sativa is a short-seasoned and fast-growing crop that can grow in diverse climates and most soil types. As a distant relative to rape, Camelina produces high amount of seed oil, making it ideal as a source of industrial oil for various uses. Over the years, researches on Camelina have been focused on making e.g. heart-heathy oil that is rich of omega-3 fatty acids or renewable jet fuel. By introducing biosynthetic genes of different origin, we have proved that gene-modified Camelina can also be a plant factory to produce insect pheromone precursors with specific carbon-chain lengths, double bond positions and configurations. We performed continuous selection over generations and got a transformed line, in which the target compound (*Z*)-11-hexadecenoic acid production was above 20% of the total fatty acids. Processing of the seed oil extract by a combination of short-path distillation and urea-complexation further increased the purity of the pheromone precursor before it was transformed into volatile pheromone compounds by simple chemical conversions. Finally, the field activity of Camelina seed oil-derived pheromones was evaluated and compared favourably with conventionally produced synthetic pheromones.

S13-06

The locust odorant-binding protein *Lmig*OBP1 is involved in detection of host plant odorants

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Locusts, *Locusta migratoria* (Orthoptera: Acrididae), are extremely destructive agricultural pests, but very little is known of their molecular aspects of perception to host plant odorants including related odorant-binding proteins (OBPs), though several OBPs have been identified in locust. To elucidate the function of *Lmig*OBP1, the first OBP identified from locust, RNA interference was employed in this study to silence *Lmig*OBP1, which was achieved by injection of dsRNA targeting *Lmig*OBP1 into the hemolymph of male nymphs. Compared with *Lmig*OBP1 normal nymphs, *Lmig*OBP1 knockdown nymphs significantly decreased food (maize leaf, *Zea mays*) consumption and electro-antennography responses to five maize leaf volatiles, ((Z)-3-hexenol, linalool, nonanal, decanal, and (Z)-3-hexenyl acetate). These suggest that *Lmig*OBP1 is involved in perception of host plant odorants.

S13-07

Functional characterization of fructose gustatory receptors in *Plutella xylostella* and *Spodoptera litura*

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Insect gustatory system plays important roles in multiple behaviors including feeding, mating, and oviposition. Gustatory receptors (GRs) are crucial in peripheral coding of non-volatile compounds, but remain poorly understood in lepidopteran pests. In the present work with *Plutella xylostella* and *Spodoptera litura,* two important crop's pests worldwide, we cloned and functionally characterized a fructose GR gene in each of the two species. In *P. xylostella,* the fructose GR gene *PxylGR43* has two spliced variants (*PxylGR43a-1* and *PxylGR43a-2*); both variants were highly expressed in antennae and less highly in heads of adults, while *PxylGR43a-2* was also weakly expressed in other tested tissues; functional analyses using the *Xenopus* oocyte system showed that both variants responded specifically to D-fructose among 12 tested sugar compounds, but PxylGR43a-2 was more sensitive than PxylGR43a-1. In *S. litura,* the fructose GR gene *SlitGR8* (orthologous to *PxylGR43* in *P. xylostella)* was highly expressed in antennae of both male and female adults, as well as in larva of 1st, 5th and 6th instars. Functional analyses showed that SlitGR8 responded specifically to D-fructose, similar as the two PxylGR43 variants. In addition, the behavioral assays confirmed that both female and male moths of the two species could respond with proboscis extension behavior to D-fructose applied onto the antenna, and females showed higher sensitivity than males. Our study contributes to elucidate the molecular mechanisms of fructose reception and provides potential target genes for development of GR based pest control techniques.

S13-08

Functional conservation and divergence underscore the flexibility of Lepidoptera odorant receptors

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Odorant receptors (ORs) are essential for olfactory detection, and functional characterization of OR repertoires is necessary to understand how animals interact with their surrounding odor scape. In insects, there have only been a few reports of such studies outside *Drosophila melanogaster*. Here, we report comprehensive profiling of the functions of an unprecedented number of ORs in a lepidopteran, the cotton bollworm *Helicoverpa armigera*, using a highly flexible and sensitive analytical platform. The *in vitro* functional screen of 44 *H. armigera* ORs (HarmORs) with a large diversity of 67 plant volatiles revealed robust responses of 28 HarmORs. Functional and phylogenetic comparison with ORs from another moth, *Spodoptera littoralis*, revealed that tuning of orthologue ORs can differ substantially, with only a small number of ORs demonstrating a conserved function. These function-conserved orthologues were spread in different clades in the phylogeny. One striking example of functionally conserved ORs between the two species is HarmOR42 and its *S. littoralis* orthologue, specifically tuned in both species to phenylacetaldehyde (PAA), a plant volatile commonly emitted by flowers. *In vivo* studies through CRISPR/Cas9 knock-out of HarmOR42 combined with electrophysiological and behavioral experiments predict that this receptor is essential for sensing this plant volatile. Our research provides an important reference for comparative functional analyses that will pave the way to understanding structure-function relationships and the evolution of Lepidoptera ORs.

S13-09

A cytochrome P450 from mustard leaf beetles hydroxylates geraniol, a key step in iridoid biosynthesis

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Larvae of the leaf beetle *Phaedon cochleariae* synthesize the iridoid chysomelidial via the mevalonate pathway to repel predators. The normal terpenoid biosynthesis is integrated into the dedicated defensive pathway by the ω-hydroxylation of geraniol to 8-hydroxygeraniol. Here we identify and characterize a P450 monooxygenase, CYP6BH5, as the geraniol 8-hydroxylase using integrated transcriptomics, proteomics and RNA interference (RNAi). In the fat body, 73 cytochrome P450s were identified, and CYP6BH5 was among the ones that expressed highly specifically in fat body. Double stranded RNA mediated knock down of *CYP6BH5* led to a significant reduction of 8-hydroxygeraniol-glucoside in the hemolymph and, later, of the chrysomelidial in the defensive secretion. Heterologously expressed CYP6BH5 converted geraniol to 8-hydroxygeraniol. In addition to geraniol, CYP6BH5 also catalyzes other monoterpenols, such as nerol and citronellol, into the corresponding α, ω-dihydroxy compounds.

S13-10

Semiochemical carrier proteins in ticks and mites

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Detection of odorants and pheromones, from bacteria to mammals, is mediated by soluble carrier proteins at the peripheral level. In insects, three classes of soluble proteins, OBPs (odorant-binding proteins), CSPs (chemosensory proteins) and NPC2 (Niemann-Pick proteins) act as carriers for semiochemicals, while in other arthropods only NPC2, together with so-called OBP-like (OBP-L) proteins seem to be active for such tasks. OBP-L are similar to insect OBPs in their sequences, but the positions of the six cysteines, an element considered important for assigning proteins to the OBP family, are not conserved.

In this study we report structural and functional properties of the 6 OBP-L encoded in the genome of the mite *Varroa destructor*, a major per for honey bees.

We have expressed all 6 OBP-L in bacteria and purified them using conventional protocols. Ligand-binding assays performed with two fluorescent probes, 1-aminoanthracene (1-AMA) and N-phenyl-1-naphthylamine (1-NPN) failed with most proteins. However, we were able to measure affinities of some ligands, monitoring the quenching of intrinsic fluorescence of tryptophan. OBP-L1 was crystallized and its three-dimensional structure solved. The folding of this proteins appears to be new with respect to that of insect OBPs, with a different arrangement of the three disulphide bridges.

We propose that both OBP-L of Arachnida and OBPs of insect derive from a still unidentified common ancestor. While the first proved to be a failed attempt to make carrier proteins (as also indicated by their poor binding properties), insects succeeded in making very successful binding proteins, that were adopted through all species of this group of arthropods. Only half dozen or less OBP-L are predicted from the genomes of Arachnida, from spiders to ticks and mites, while the number of NPC2, while being highly variable, can be very high, with more than 40 members in the herbivorous spider mite *Tetranychus urticae*.

All these elements seem to suggest that generally OBP-L in Arachnida represent a failed attempt, and NPC2 are probably the most important semiochemical carrier proteins in this class.

S13-11

Strigolactones activate defense against the stem-boring weevil *Trichobaris mucorea* via their interactions with jasmonates and auxin

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Strigolactones (SLs) regulate shoot branching, parasitic plant seed germination and symbiosis with arbuscular mycorrhizae. Do SLs play a role in herbivore defense? Larvae of the *Tricobaris mucorea* weevil*,* attack the root-shoot junction (RSJ) to feed in the stems of *Nicotiana attenuata* plants in nature, growing into larger larvae in plants silenced in MORE AXILLARY GROWTH 2 (ir-max2), DWARF 14 (ir-d14) and CAROTENOID CLEAVAGE DIOXYGENASE 7(ir-CCD7). The RSJ of SL-insensitive and SL-deficient plants have more branches and elevated jasmonate (JA) and auxin responses. The repressors of SLs signaling (NaSMXL6/7) and JA signaling (NaJAZs) physically interact, leading to the JAZb degradation and higher chlorogenic acid (CGA) and phenolamides in SL-insensitive and SL-deficient plants. However, the greater larval performance results from lower nicotine levels which in turn, result from higher auxin levels; decapitation decreases auxin levels, increasing nicotine, independently of JA signaling, decreasing larval performance. SL signaling mediates weevil-resistance of stems by tailoring cross-talk among hormones, including JAs and auxin.

S13-12

An inhibitor for mating in cotton bollworm, *Helicoverpa armigera*

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Mating is critical for the successful survival of many agriculture pests, and during the past few decades, many chemical compounds have been used as behavioral regulators to control these pests. *Helicoverpa armigera* is a serious agriculture pest for many cultivated crops all over the word, and how to efficiently control it remains a big problem. Currently, some efficient methods, such as food attractants and sex pheromones for *H. armigera* control have been developed depending on the studies of their behaviors including foraging, mating, oviposition and so on. Here, we found an important chemical compound MSP1 significantly inhibits the mating behavior of *H. armigera*. We used video camera to observe the mating behavior of 3-4 days old adult *H. armigera* that existed in MSP1 surrounding or not. The result showed that the mating rate decreased when MSP1 was presented. Next, we checked whether MSP1 can avoid *H. armigera* by a two-choice olfactometer box. The result showed that MSP1 can not avoid female or male adult *H. armigera.* Then, we tested the EAG response of female and male moths to different concentrations of MSP1, and the results showed that both female and male antennae respond to MSP1. Moreover, the EAG response of female and male moths have no significant difference. However, our results indicated that MSP1 perception in *H. armigera* was not increased with elevated MSP1 concentretion. We anticipated there were two or more ORs played important role in detecting MSP1.

S13-13

Functional characterization of odorant receptors in the moth *Eriocrania semipurpurella*: a comparison of results obtained with the *Xenopus* oocyte and HEK cell systems

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The *Xenopus* oocyte and the Human Embryonic Kidney (HEK) 293 cell expression systems are frequently used for functional characterization (deorphanization) of insect odorant receptors (ORs). However, the inherent characteristics of these heterologous systems differ in several aspects, which raises the question of whether the different systems provide comparable results, and how well the results correspond to the responses obtained from olfactory sensory neurons *in vivo*. Five candidate pheromone receptors were previously identified in the primitive moth *Eriocrania semipurpurella* (Esem) and their response profiles were characterized in HEK cells. In the current study, we re-examined the responses of these five EsemORs in *Xenopus* oocytes. We showed that in both systems, EsemOR1 specifically responded to the plant volatile β-caryophyllene. EsemOR3 responded stronger to the pheromone component (*S,Z*)-6-nonen-2-ol than to its enantiomer (*R,Z*)-6-nonen-2-ol, the second pheromone component. However, EsemOR3 also responded secondarily to the plant volatile β-caryophyllene in the oocyte system, but not in the HEK cell system. EsemOR4 did not respond to any tested compound in the HEK cell system, but responded primarily to (*R,Z*)-6-nonen-2-ol followed by (*S,Z*)-6-nonen-2-ol in the oocytes, representing a discovery of a new pheromone receptor in this species. EsemOR5 was broadly tuned to pheromone components, behavioral antagonist and nonan-2-one in both systems. EsemOR6 showed no response to any compound in either system. We compared the results obtained in the two different heterologous systems with the activity previously recorded *in vivo*, and performed *in situ* hybridization to localize the expression of these OR genes in the antennae. In spite of overall similar results, differences in OR responses between heterologous expression systems were observed, and conclusions about the function of individual ORs may thus differ depending on the system used for deorphanization.

S13-14

Sterol composition analysis of the two-spotted crickets, *Gryllus bimaculatus*

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Cholesterol is a compulsory material for living organisms, however, there is not a universal way of obtaining cholesterol. There are still unsolved puzzles about the sterol compositions and sterol conversions, especially in arthropods, which are unable to bio-synthesise sterols for growth and development. Although there are evidences showing most phytophagous insects obtain cholesterol through converting phytosterols to desmosterol, the complete process is not clearly understood. Here, we analysed the sterol composition of various tissues in the two-spotted crickets (*Gryllus bimaculatus*) to address the sterol metabolism in omnivorous insects. The crickets were given diets composed of different concentrations of sterols, mainly cholesterol and phytosterols, and their tissues were dissected out for quantification of sterols. GC/MS analysis revealed that dietary sterols, such as cholesterol, phytosterol, desmosterol and lathosterol, altered the sterol components in tissues. Meanwhile, we found that there are potential limits on the sterol absorption by tissues. In addition, when an excess of cholesterol was given to crickets, only a small proportion of dietary sterols was taken up and most of them were excreted in their original forms. Contrarily, when a low sterol diet was provided to crickets, almost all dietary sterols were absorbed, including phytosterols and cholesterol, the dominant sterol in crickets. Furthermore, accumulations of lathosterol and cholestanol were observed in midgut and fat body, which indicated the possibility of conversions between lathosterol, cholestanol and cholesterol. Additionally, we discovered the presence of 7-dehydrocholesterol in midgut, hence, we hypothesised that midgut is the site of conversion between cholesterol and 7-dehydrocholesterol.

S13-15

Production of (Z)-11-hexadecenal by a metabolically engineered yeast

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(Z)-11-hexadecenal, which is main component in sex pheromones of *Helicoverpa armigera*, is being used as an attractant for pest control, which is widely considered to be an environmentally friendly approach. In order to optimize synthesis of the compound, we present an *in vivo* total synthesis approach to prepare (Z)-11-hexadecenal in an engineered yeast. First, a *Saccharomyces cerevisiae* chassis was constructed to improve titres of free fatty acids (FFAs) by knocking out essential genes using CRISPR/Cas9. As a result, production of FFAs in converted strain reached over 350 mg/L, which provided sufficient substance for further biosynthesis. Then, several heterologous Δ11 fatty-acyl desaturases (FADs), which is responsible for precursor of (Z)-11-hexadecenal, were cloned from several species of insects and their activities were compared in same chassis. After fermentation in shake flask, an engineered strain equipping with a plasmid carrying FAD from *Helicoverpa armigera* could produce over 60 mg/L (Z)-11-hexadecenoic acid, over 70% of which was intracellular. Subsequently, introduction of a carboxylic acid reductase (CAR) into further constructed strains brought near 50 μg/L (Z)-11-hexadecenal. Extra adjustments in metabolic pathway is on the road to improve yield of the final compound.

S01-P-01

A neuropeptide inhibits feeding behavior by modulating sweet chemosensory in the brown planthopper

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The brown planthopper, *Nilaparvata lugens*, is one of the most economically important pest of the rice. They cause rice damage directly by feeding. However, the mechanism that modulates feeding behavior in the brown planthopper remains largely elusive. Here, we showed that a neuropeptide could reduce food uptake and reflected food satiety in *N. lugens*. After silencing this neuropeptide and its receptor gene, we detected some feeding related genes was up- or down-expressed. Interestingly, this neuropeptide negatively regulated gustatory receptor for sugar taste gene expression that inhibited the feeding of brown planthopper. Our work provides a foundation for further investigation of neuropeptide regulation of vital behavior associated with feeding and are believed to present promising targets for new insecticides.

S01-P-02

Olfactory responses of the antennae and maxillary palps to parapheromone and plant volatile compounds in the striped fruit fly, *Bactrocera scutellata*

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We investigated the responses of the antennae and maxillary palps of the striped fruit fly, *Bactrocera scutellata* (Hendel) (Diptera: Tephritidae), a serious pest of pumpkin and other cucurbitaceae plants, to parapheromone and plant volatile compounds. The electroantennogram (EAG) and electropalpogram (EPG) responses of *B. scutellata* were sex-specific and organ-specific. Male and female *B. scutellata* displayed significant EAG responses to a plant volatile compound, 3-octanone, and methyl eugenol, whereas they did not show any significant EAG responses to cue lure, raspberry ketone and zingerone that are known to attract several other species of *Bactrocera* fruit flies. In contrast, the maxillary palps exhibited the largest EPG responses to cue lure among the five compounds tested in male and female *B. scutellata*, with only small EPG responses to 3-octanone. This indicates that the maxillary palps are responsible for detecting cue lure and raspberry ketone in this species. In subsequent field trapping experiments, significant number of male *B. scutellata* were captured in the traps baited with cue lure or raspberry ketone. In a series of GC-EAD experiments using mixture of synthetic plant volatile compounds and headspace extracts from host plants, the profiles of EAD-active compounds were different from those of EPD-active compounds. Some of the EAD-active and EPD-active compounds appeared to be sex-specific. Our study indicates that the behavioral attraction of *B. scutellata* to cue lure and raspberry ketone is mediated by the olfactory sensory neurons present in the maxillary palps, and the olfactory sensory roles for detecting plant volatiles are different between the antennae and maxillary palps.

S01-P-03

Identification and expression profile analysis of olfactory receptor gene in *Apriona germari* (Hope)

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The *Apriona germari* (Hope) (Coleoptera: Cerambycidae) is a destructive pest in China that infests a wide range of broadleaved trees, especially *Populus* spp, resulting in massive environmental damages and economic losses. The olfactory system is a key physiological trait for insect survival and reproduction. Insect olfactory receptors, including odorant receptors (ORs) and ionotropic receptors (IRs), are essential for the recognition of ligands at peripheral neurons. We conducted RNA sequencing analysis of the antennae of adults of *A. germari*. We identified 42 ORs and 3 IRs from the transcriptome of female and male antennae. Tissue expression analyses showed that 26 ORs displayed an enriched expression in female antennae, suggesting that this receptors may be involved in some female specific behaviors. *Ager*OR2, *Ager*OR5, *Ager*OR9, *Ager*OR22 and *Ager*OR27 were highly expressed in labial palps. IRs expressed profiles showed that *Ager*IR2 were strongly expressed in labial palps. These results confirm the authenticity of the transcriptome data. This study lay a solid foundation for further studies on the molecular mechanisms of olfaction in *A. germari*, and indicate novel targets for control of *A. germari* in future.

S01-P-04

Ultrastructural observation of the antennae of the *Zele chlorophthalmus*

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Zele chbrophthalmus (*Hymenoptera: Braconidae*) is an important larval parasitoid of *Loxostege sticticalis L.* (*Lepidoptera: Crambidae*) larval pests. To better understand the host location mechanism, we describe the morphology, ultrastucture and distribution of sensilla on the antennae of both male and female adults using scanning electron microscopy. Observations determined that the antennae of *zele chbrophthalmus* were thredlike and the flagella were composed of 37 sub-segments. Antennae of male and female of the *zele chbrophthalmus* are 7361.86±227.87µm and 7234.63±71.16µm in length and consist of scape, pedicel, and flagellum, respectively. Totally, there were eight types of sensilla found on the antennae. They were identified as *Sensilla trichodea, Sensilla chaetica, Sensilla basiconica, Sensilla coeloconicum, Sensilla placodea, Sensilla campaniformia, Bōhm bristles and Sensilla* obscura, respectively. The S.trichoded were the most abundant sensilla and distributed over the entire antennae. We compared number, morphology, and distribution of sensilla, The sensilla trichodea may be involved in mechnosensation.

S01-P-05

Sweet sensation inhibit texture discrimination in *Drosophila* egg-laying behaviour

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When choosing among options that each present more than one behaviorally relevant sensory stimulus during decision-making, it is advantageous for animals to integrate the different sensory stimuli associated with each option such that these options can be compared more easily. Drosophila females are known to be able to “choose the greater of two goods” when selecting for egg-laying sites and are sensitive to both the chemosensory (e.g., sweetness) and the mechanosensory properties (e.g., hardness) of potential options; however, how they integrate these two important sensory properties of potential options when making egg-laying decisions is not known. Here we show that detection of sweetness on substrates by Drosophila females modifies how they choose between two egg-laying substrates of different hardness. Specifically, females switch from clearly preferring the softer substrate when both substrates are sucrose-free to being less selective between them when both contain sucrose. Such sucrose-induced indifference between substrates of different hardness critically depends on functional sweet-sensing neurons, and, curiously, the mechanosensitive neurons that express the evolutionarily conserved Transmembrane Channel-like (TMC) protein, which was previously shown to be required for substrate hardness discrimination during feeding. Further, axons of sweet neurons contact with and can increase Ca^{2+} influx into axons of TMC-expressing neurons. These results uncover one mechanism by which Drosophila integrate chemosensory and mechanosensory information during egg-laying decisions and reveal how texture sensing by the TMC-expressing mechanosensitive neurons contributes differently to discrimination and selection of substrates of different hardness when flies are making feeding vs. egg-laying decisions.

S01-P-06

Identification of volatile compounds from rectal gland and headspace extracts of female *Bactrocera correcta*

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The guava fruit fly, *Bactrocera correcta*, is one of the major pests affecting mango (*Mangifera indica*) and guava (*Psidium guajava*) production in China. The compound β-caryophyllene was identified from the rectal gland extracts of wild *B. correcta* males and was demonstrated to be a more specific and potent male lure than methyl eugenol (ME) for *B. correcta*. In order to find potential additional pheromone attractants for the monitoring and mass-trapping of this fruit fly, a series of chemical and flight tunnel assays were conducted in this study. Five major compounds (i.e., ethyl dodecanoate, ethyl tetradecanoate, ethyl *(E)*-9-hexadecenoate, ethyl hexadecanoate, and ethyl *(Z)*-9-octadecenoate) in high quantities, and other compounds (i.e., octanal, N-(3-methylbutyl) acetamide, (*Z*)-9-tricosene, ethyl octadecanoate, and ethyl eicosanoate) in trace amounts were identified from the rectal glands of virgin females. The compounds were identified as octanal, (R)-(+)-limonene, N-(3-methylbutyl) acetamide, decanal, 3-ethylacetophenone, 4-ethylacetophenon, pentadecane, ethyl dodecanoate, ethyl tetradecanoate, ethyl (*E*)-9-hexadecenoate, and ethyl hexadecanoate in headspace extracts of the females. In the flight tunnel bioassays, female *B. correcta* displayed significantly greater levels of upwind oriented flight to sources with octanal, (R)-(+)-limonene and ethyl tetradecanoate, respectively, compared with other single compounds and multicomponent blends. Collectively, these results will contribute to the understanding of pheromone communication in *B. correcta* and may provide important information for improving existing monitoring and control methods for this pest.

S01-P-07

A mechanosensitive channel modulates egg-laying in the brown planthopper *Nilaparvata lugens* and the fruit fly *Drosophila melanogaster*

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Many agricultural pests oviposit on plant and fruit causing large cost to agriculture. Insect females laid her eggs by distention and contraction of females' internal reproductive tract. However, which genes or mechanosensitive channels take part in insect egg-laying behavior is still unknown. . Here, we showed that a mechanosensitive channel plays important role in the egg-laying of brown planthopper *Nilaparvata lugens* and fruit fly, *Drosophila melanogaster.* The mechanosensitive channel is highly expressed on the internal reproductive tract of the *N. lugens*. And silencing of this gene significantly reduced the egg-laying number of *N. lugens*. The same phenotype was also observed in the *D. melanogaster.* Our results may provide mechanistic insights into the functions of mechanosensation in insect egg-laying behavior.

S02-P-08

The involvement of an herbivore-induced acyl-CoA oxidase gene, *CsACX1*, in the synthesis of jasmonic acid and its expression in flower opening in tea plant (Camellia sinensis)

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Abstract: The biosynthesis of jasmonic acid (JA) in plant peroxisomes requires the action of acyl-CoA oxidase (ACX; EC 1.3.3.6). Multiple isoforms of ACXs have been identified in various annual herbaceous plants, but the genes encoding these enzymes in perennial woody plants are yet to be fully investigated. In this study, an ACX gene named *CsACX1* (GeneBank accession: KX650077.1) was isolated from tea plant (*Camellia sinensis* L.). *CsACX1* was predicted to consist of 664 amino acid residues. Transcriptional analysis revealed that *CsACX1* can be induced by mechanical wounding, JA application, and infestation by the tea geometrid Ectropis obliqua Prout and the tea green leafhopper *Empoasca* (*Matsumurasca*) *onukii* Matsuda. To further elucidate the function of *CsACX1*, it was heterologously expressed in a bacterial system and characterized. Recombinant *CsACX1* showed preference for C12- ~ C16-CoA substrates. The constitutive expression of *CsACX1* can rescue woundrelated JA biosynthesis in Arabidopsis mutant acx1. *CsACX1* was expressed in different organs, predominantly in flowers. Notably, *CsACX1* transcripts were detected up-regulated during flower opening, and the JA levels were correlated with *CsACX1* expression. All these results enrich our knowledge of the regulatory pathway involved in the JA biosynthesis in tea, and helps further understand the defense mechanism of tea plant against insects.

S02-P-09

Bt* rice plants may protect neighboring non-*Bt* rice plants against the striped stemborer *Chilo suppressalis

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The area planted with insect-resistant genetically engineered crops expressing *Bacillus thuringiensis* (*Bt*) genes has greatly increased in many areas of the world. Given the nearby presence of non-*Bt* crops (including those planted as refuges) and non-crop habitats, pests targeted by the *Bt* trait have a choice between *Bt* and non-*Bt* crops or weeds, and their host preference may greatly affect insect management and management of pest resistance to *Bt* proteins. In this study we examined the oviposition preference of the target pest of *Bt* rice, *Chilo suppressalis*, for *Bt* vs. non-*Bt* rice plants as influenced by previous damage caused by *C. suppressalis* larvae. The results showed that *C. suppressalis* females had no oviposition preference for undamaged *Bt* or non-*Bt* plants but were repelled by conspecific-damaged plants whether *Bt* or non-*Bt*. Consequently, *C. suppressalis* egg masses were more numerous on *Bt* plants than on neighbouring non-*Bt* plants both in greenhouse and in field experiments due to the significantly greater conspecific damage on non-*Bt* plants. We also found evidence of poorer performance of *C. suppressalis* larvae on conspecific-damaged rice plants when compared to undamaged plants. GC-MS analyses showed that larval damage induced the release of volatiles that repelled mated *C. suppressalis* females in wind tunnel experiments. These findings suggest that *Bt* rice could act as a dead-end trap crop for *C. suppressalis* and thereby protect adjacent non-*Bt* rice plants. The results also indicate that the oviposition behavior of target pest females should be considered in the development of *Bt* resistance management strategies.

S03-P-10

Screening of chemical cues during the host searching process of weevil *Curculio chinensis*

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Curculio chinensis is an important pest on *Camellia oleifera*, which mainly destroy the leaves and fruits of *C. oleifera*. Lots of chemical pesticides have been used for its management, but using of pheromone attractants for its control has not been reported. In the current study, the choice behavior of the male and female adults of *C. oleifera* to the leaves and fruits of *C. oleifera* was determined by Y-tube olfactometer. Results showed that host leaves and fruits strongly attracted the both male and female of *C. chinensis*. There was no significant difference for the choice behavior between male and female either to leaves or fruits. The main chemicals influences the choice behavior of *C. chinensis* were determined by GC-EAD and GC-MS. There are four main active substances that induce the electrophysiological reaction of the weevil, which are n-octadecane, stearaldchyde, (Z)-1,19-eicadiene and cis-9-docosene. Octadecane was identified by standard products, and the other three peaks were determined by comparing their mass spectrum with NIST library. N-octadecane cause significantly repellent behavior against weevil, and the effects of other three chemical to *C. chinensis* will be studied next step. The results of this study will provide important basis for the development of attractants or repellent for *C. oleifera* management.

S03-P-11

Tea geometrid-induced biosynthesis of polyphenol oxidase is regulated by the jasmonate pathway in tea plant

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Plant polyphenol oxidase (PPO) is assumed to be involved in defense against herbivorous pests in myriads of plants. Our previous results have shown that jasmonic acid (JA) treatment resulted in increases in PPO activity of tea plant (*Camellia sinensis*) and decrease in the weight gain of tea geometrid (*Ectropis obliqua*) that fed on them, which depended on the JA dosage. However, the regulation mechanisms of this process are poorly understood. Here, we detailedly investigated the role of JA signaling pathway in regulating PPO biosynthesis of tea plants that infested by the tea geometrid. In this study, we pretreated tea saplings with MeJA and sodium diethyldithiocarbamate (DIECA), an inhibitor of JA pathway, 24h before infestation with larva of tea geometrid. As expected, the levels of PPO activity were higher at 24 hour post infestation, by up to 3-fold, and the transcript levels of PPO synthesis genes *CsPPO2* by qRT-PCR was significantly increased at 6 hour post infestation, by up to 6-fold, in MeJA-treated plant compared with the corresponding mock-treated plants. The stronger transcriptional induction of PPO biosynthetic genes is consistent with MeJA-dependent regulation of PPO activity. Whereas the levels of PPO activity were lower, by down to 1.7-fold, in DIECA-treated plant compared with the mock-treated plants. We concluded that jasmonate signal pathway activates biosynthesis of PPO, conferring defense responses to tea geometrid.

S03-P-12

Molecular dissection of early defense signaling underlying volatile-mediated defense regulation and herbivore resistance in rice

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Herbivore-induced plant volatiles prime plant defenses and resistance, but how they are integrated into early defense signaling and whether a causal relationship exists between volatile defense priming and herbivore resistance is unclear. Here, we investigated the impact of indole, a common herbivore-induced plant volatile and modulator of many physiological processes in plants, bacteria, and animals, on early defense signaling and herbivore resistance in rice (*Oryza sativa*). Rice plants infested by fall armyworm (*Spodoptera frugiperda*) caterpillars release indole at a rate of up to 25 $ng*h^{-1}$. Exposure to equal doses of exogenous indole enhances rice resistance to *S. frugiperda*. Screening of early signaling components revealed that indole pre-exposure directly enhances the expression of the leucine-rich repeat-receptor-like kinase *OsLRR-RLK1*. Pre-exposure to indole followed by simulated herbivory increases (i.e. primes) the transcription, accumulation, and activation of the mitogen-activated protein kinase OsMPK3 and the expression of the downstream WRKY transcription factor gene *OsWRKY70* as well as several jasmonate biosynthesis genes, resulting in higher jasmonic acid (JA) accumulation. Analysis of transgenic plants defective in early signaling showed that *OsMPK3* is required and that *OsMPK6* and *OsWRKY70* contribute to indole-mediated defense priming of JA-dependent herbivore resistance. Therefore, herbivore-induced plant volatiles increase plant resistance to herbivores by positively regulating early defense signaling components.

S03-P-13

An intrinsically disordered protein regulates the resistance in rice to brown planthopper (*Nilaparvata lugens*)

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Intrinsically disordered proteins (IDPs) have been reported that they control important cellular functions via transcriptional regulation, chaperone formation, and enrichment of regulatory capacity, under abiotic stress conditions. However, how IDPs participate in herbivory-induced defenses of rice is still poorly understood. Here, we identified an intrinsically disordered protein gene from rice (*Oryza sativa*), *OsIDP1*, which could be strongly and promptly induced by wounding and infestation by gravid female adults of rice brown planthopper (BPH, *Nilaparvata lugens*). We generated rice lines (*ir-idp1*) with reduced expression of this gene via the RNA interference (RNAi) approach and observed that it can regulate transcript levels of defense-related *OsWRKYs* under gravid BPH female infestation. The silencing of *OsIDP1* promoted BPH-induced levels of jasmonic acid (JA), jasmonoyl-isoleucine (JA-Ile) and salicylic acid (SA) but decreased levels of ethylene (ET). These changes resulted in decreases in the hatching rate of BPH eggs and survival rate of BPH nymphs. Moreover, adult females preferred to feed and lay eggs on wild type plants when wild-type and *ir-idp1* plants were exposed to the same colony gravid BPH females. Our study reveals that OsIDP1 plays an important role in herbivore-induced defenses in rice.

S03-P-14

The feeding preferences of *Apolygus lucorum* (Heteroptera: Miridae) by the PCR-based analysis of plant DNA

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The mirid bug *Apolygus lucorum* (Meyer-Dür) (Heteroptera: Miridae) is a severe pest of cotton and other crops in China. The feeding preferences of this pest are unclear due to its frequent movement among different host plants and the inconspicuous signs of its feeding.Here, we present results of a field trial that used direct observation of bug densities and a PCR-based molecular detection assay to detect plant DNA in bugs to explore relationships between *A. lucorum* population abundance and its feeding preference between two host plants, *Humulus scandens* (Loureiro) Merrill and *Medicago sativa* L. The field-plot samples showed that *A. lucorum* density was significantly higher on flowering *H. scandens* than on seedlings of *M. sativa*, and, similarly, mirid bug density was also higher on flowering *M. sativa* than on seedlings of *H. scandens.* In the laboratory, we designed two pairs of species-specific primers targeting *trn*L-F region for *H. scandens* and *M. sativa*, respectively. The detectability of plant DNA generally decreased after feeding, and the half-life of plant DNA detection in the gut was estimated as 6.26 h for *H. scandens* and 3.79 h for *M. sativa*. In mirid bugs exposed to seedlings of *H. scandens* and flowering *M. sativa*, the detection rate of *M. sativa* DNA in *A.lucorum* guts was evidently higher than that of *H. scandens*. Meanwhile, in mirid bugsexposed to seedlings of *M. sativa* and flowering *H. scandens*, a higher detection rate of *H.scandens* DNA was found. Our current finding provides evidence of a strong positiverelationship between population abundance and feeding preference of *A. lucorum* between different plants.

S03-P-15

Chemical mechanisms of the preferential attraction of the sugarcane stem borer, *Chilo sacchariphagus*, to the trap crop *Erianthus arundinaceus*

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Sugarcane yield losses due to the sugarcane stem borer, *Chilo sacchariphagus*, are reduced when plants of *Erianthus arundinaceus*, a close relative to sugarcane, are dispatched at the border of sugarcane fields. Previous studies showed that *C. sacchariphagus* females lay preferentially their eggs on *E. arundinaceus* and that newly emerged larvae are unable to reach adulthood. *E. arundinaceus* is currently used in La Réunion Island as a trap crop in an integrated agricultural system reminiscent of the push-pull system introduced in Kenya to control maize stem borers. We explored the chemical mechanisms underlying this insect-plant interaction. The volatile compounds released by intact plants were collected at dusk and analyzed with a thermodesorber, a gas chromatograph (GC), and a mass spectrometer. This protocol was repeated on seven accessions of *Erianthus* and one sugarcane cultivar susceptible to *C. sacchariphagus*. We identified 91 compounds, 15 that were sugarcane specific and two (noted compounds A and B) that were *Erianthus* specific (ANOVA, $p<0.05$, $n=10$ per accession and species). We then tested the electroantennographic (EAD) response of *C. sacchariphagus* to compounds A and B and found that both sexes are sensitive to compound A only (response threshold: 10^{-2} dilution, $p<0.01$ sign rank test, $n=10$). Further GC-EAD recordings revealed no additional differences in the olfactory sensitivity of *C. sacchariphagus* to sugarcane and to *E. arundinaceus*. Finally, we tested the olfactory orientation behavior of gravid *C. sacchariphagus* females in a Y-olfactometer at dusk. These insects spend significantly more time in the branch of the olfactometer with compound A than in the branch with clean air (bootstrap test, $p<0.01$, $n=14$). Our study suggests that compound A might be a key compound in the attraction of *C. sacchariphagus* by *E. arundinaceus*. This mechanism might be targeted to improve the strategies of management of *C. sacchariphagus* in infested areas.

S03-P-16

The molecular cloning and characterization of *CsMYC2*, a bHLH transcription factor from tea plants (*Camellia sinensis*)

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Jasmonic acid (JA) has been proven to regulate defense response to *Ectropis obliqua*, an important pest insect in tea plant (*Camellia sinensis*). However, transcription factors of JA signaling pathway in tea plants and their role in resistance to tea geometrid have not been fully investigated. Here, we identified a basic helix-loop-helix (bHLH) family TF in tea plants, *CsMYC2*, shared high identity with AtMYC2 and SlMYC2, master transcriptional factors in the other species. Sequence alignments showed that CsMYC2 contained the conserved JID domain in N-terminal, which responsible for the interaction with the family of JAZ repressors and a C-terminal bHLH domain involved in forming an oligomer and recognizing DNA. Expression of *CsMYC2* was specifically high in leaves of tea plants. Feeding of tea geometrid rapidly increased the transcripts of *CsMYC2* as soon as 1.5h. Wounding and JA treatment also up-regulated the accumulation of *CsMYC2* at early stage. Yeast two-hybrid assay proved that CsMYC2 interacted with CsJAZ1, a repressor in JA signaling pathway. Together, these results indicate that *CsMYC2* is involved in the induced defense response in tea plants through a JA-dependent manner.

S03-P-17

Functional characterization of herbivore resistance-related gene *OsJMJ28* in rice

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OsERF3, a member of AP2/ERF transcription factors, acts as a central switch in regulating defense responses of rice against chewing or piercing/sucking herbivores. However, the underlying mechanisms of OsERF3 remained elusive. Here, we identified a jumonji C (jmjC) domain-containing protein, OsJMJ28, which interacts with OsERF3 *in vivo* and *in vitro*. We further proved that OsJMJ28 serves as an E3 ligase to ubiquitinate OsERF3 *in vitro*. Functional analyses showed that either overexpression or silencing *OsJMJ28* increased resistance of rice *Oryza sativa* to the brown planthopper (BPH) *Nilaparvata lugens* by regulating BPH-elicited jasmonic acid (JA), jasmonoyl-isoleucine (JA-Ile), salicylic acid (SA) and abscisic acid (ABA) biosynthesis. On the other hand, the striped stem borer (SSB) *Chilo suppressalis* caterpillars gained more mass on *OsJMJ28* mutants than those fed on wild type plants. These results suggested that OsJMJ28 plays an important role in herbivore-induced rice defense.

S04-P-18

Various bee pheromones binding affinity, exclusive chemosensillar localization, and key amino acid sites reveal the distinctive characteristics of odorant-binding protein 11 in the eastern honey bee, *Apis cerana*

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Odorant-binding proteins (OBPs) are the critical elements responsible for binding and transporting odors and pheromones in the sensitive olfactory system in insects. Honey bees are representative social insects that have complex odorants and pheromone communication systems relative to solitary insects. Here, we first cloned and characterized OBP11 (*AcerOBP11*), from the worker bees antennae of Eastern honey bee, *Apis cerana*. Based on sequence and phylogenetic analysis, most sequences homologous to AcerOBP11 belong to the typical OBPs family. The transcriptional expression profiles showed that AcerOBP11 was expressed throughout the developmental stages and highly specifically expressed in adult antennae. Using immunofluorescence localization, AcerOBP11 in worker bee's antennae was only localized in the sensilla basiconica (SB) near the fringe of each segment. Fluorescence ligand-binding assay showed that AcerOBP11 protein had strong binding affinity with the tested various bee pheromones components, including the main queen mandibular pheromones (QMPs), methyl p-hydroxybenzoate (HOB), and (*E*)-9-oxo-2-decanoic acid (9-ODA), alarm pheromone (n-hexanol), and worker pheromone components. AcerOBP11 also had strong binding affinity to plant volatiles, such as 4-Allylveratrole. Based on the docking and site-directed mutagenesis, two key amino acid residues (Ile97 and Ile140) were involved in the binding of AcerOBP11 to various bee pheromones. Taken together, we identified that AcerOBP11 was localized in a single type of antennal chemosensilla and had complex ligand-binding properties, which confer the dual-role with the primary characteristics of sensing various bee pheromones and secondary characteristics of sensing general odorants. This study not only prompts the theoretical basis of OBPs-mediated bee pheromones recognition of honey bee, but also extends the understanding of differences in pheromone communication between social and solitary insects.

S04-P-19

Functional characterization of pheromone receptors in codling moth *Cydia pomonella*

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Odorant receptors (ORs) are essential for many behaviors during insect life, such as locating host plant, mate partners, oviposition-site and so on. Pheromone receptors (PRs), a monophyletic clade in the OR phylogeny, are usually highly expressed in male antennae, with the function of detecting sex pheromones. In this study, four PRs were characterized in codling moth *Cydia pomonella*, a worldwide pest causing great harm to a variety of pome fruits every year in China. Among them, male-specific expressions were confirmed in the antennae for *CpomOR1*, *CpomOR**A***, *CpomOR7,* while *CpomOR**B*** was male-biased expressed in the male antennae. In addition, functional analysis of these PRs was carried out by *Xenopus oocyte* ectopic expression system. As the results, CpomOR**B** and CpomOR**A** specifically responded to (E, E)-8, 10-dodecadien-1-yl acetate (codlemone acetate), while CpomOR1 and CpomOR7 did not respond to any pheromone components. Interestingly, our results demonstrated that CpomOR**B** was more sensitive to high concentration of codlemone acetate (EC50=1.663×10^{-6} M), but CpomOR**A** basically more sensitive to low concentration (EC50=1.379×10^{-8} M). This study provides a deeper understanding for the molecular mechanisms of sex communication in codling moth and may help for developing new pest control strategies via pest chemosensory system.

S04-P-20

Sensilla trichodea-biased EoblPBP1 binds sex pheromones and green leaf volatiles in a geometrid moth pest *Ectropis obliqua* Prout that uses Type-II sex pheromones

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Pheromone-binding proteins (PBPs) are considered to play critical roles in sex pheromone detection. Lepidopteran moths can be divided into two taxa, those that use Type-I sex pheromones, such as C10-C18 unsaturated aldehydes, alcohols and acetates, and those that use Type-II pheromones, which are C17-C23 polyunsaturated hydrocarbons and their epoxide derivatives. To date, nearly all the characterized PBPs have been reported in moths with Type-I sex pheromones, and the physiological functions of PBPs in moths that use Type-II sex pheromones remains unclear. In the present study we functionally examine EoblPBP1 in *Ectropis obliqua* Prout, an important geometrid moth pest that uses Type-II sex pheromones. The phylogenetic analysis of the sequence indicated that EoblPBP1 clustered together with ScerPBP1, a geometrid PBP for detecting Type-II sex pheromones. Fluorescence *in situ* hybridization revealed that EoblPBP1 was primarily expressed at the base of pheromone-sensitive sensilla trichodea (Str-I). A comparative binding assay showed that recombinant EoblPBP1 bound three sex pheromone components of *E. obliqua*, demonstrating its involvement in the detection of Type-II sex pheromones. Besides, EoblPBP1 also highly bound unsaturated acetates pheromones and the green leaf volatiles. These results indicate that PBP1 is associated with detecting Type-II sex pheromones in *E. obliqua* but cannot differentiate Type-II sex pheromones from Type-I sex pheromones or green leaf volatiles.

S04-P-21

Functional differentiation of pheromone-binding proteins in *Hyphantria cunea* (Drury).

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As an invasive species, the fall webworm moths, *Hyphantria cunea* (Drury), is widely spread in China. Managements of this species are very difficult and rear. Pheromones and other semiochemicals play a crucial role in today's integrated pest management strategies. Here we functional studied the three pheromone binding proteins (PBPs) with four sex pheromone compounds (type I and type II sex pheromone included) and 24 plant volatiles by prokaryotic expression system, histidine label protein Ni magnetic bead purification and fluorescence competitive binding assay.The results showed that the binding ability of three PBP to Type I sex pheromone components ($K_i < 1.0$ μM) was significantly different from that of Type II sex pheromone components. Among them, the binding ability of HcunPBP2 to Type II sex pheromone components 1,Z3,Z6-9S,10R-epoxy-21Hy was strong, HcunPBP3 had moderate binding ability, but HcunPBP1 had no binding ability. Both HcunPBP1 and HcunPBP3 had moderate binding ability to Type II sex pheromone components Z3,Z6-9S,10R-epoxy-21Hy, but HcunPBP2 had no binding ability. In addition, among the 24 plant volatile compounds tested, three PBP could selectively bind to some plant volatiles and had strong binding ability ($K_i < 10.0$ μM). Our study reveals that HcunPBPs have distinct functional differentiation and are different from moths that use Type I sex pheromones, which could helps better understanding the molecular mechanism of sex pheromone detection in *H.cunea*, and also provides important ideas for resolving the difference mechanism of type I and type II sex pheromone chemoreception.

S04-P-22

Sensory neuron membrane protein 1 (SNMP1) reinforces receptivity of male *Helicoverpa armigera* (Lepidoptera: Noctuidae) to sex pheromone components

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Sex pheromones emitted from female moths can be efficiently recognized by conspecific males using their precise and specific olfactory sensory system. Sex pheromone receptors (PRs) expressed on the dendritic membrane of olfactory receptor neurons (ORNs) and pheromone binding proteins (PBPs) expressed in sensillum lymph, are particularly significant for sex pheromones detection. Besides, sensory neuron membrane protein 1 (SNMP1), a family member of the CD36, has been reported to participate in male pheromone cVA detection in Drosophila melanogaster. In Lepidopteran insects, it is firstly detected in the silk moth *Antheraea Polyphemus*. Although SNMP1 is supposed to be indispensable for perception of pheromone in moths, little is known about its precise and specific function *in vivo*. In this study, the tissue expression profile revealed that HarmSNMP1 was specifically expressed in antennae, a major olfactory organ, inferring its function may be involving in olfaction. Subsequently, *SNMP1*$^{-/-}$homozygous mutant line in H. armigera with 8-bp insertion had been obtained using CRISPR/Cas9. Further EAG recording results showed the whole antennae of *SNMP1*$^{-/-}$ mutant line weakly responded to major sex pheromone component Z11-16:Ald and minor component Z9-16:Ald, than those of wild type. Comparatively, no obviously different response to general plant volatiles were recorded between *SNMP1*$^{-/-}$ mutant and wild type. At last, mating behavior confirmed that mating rate of *SNMP1*$^{-/-}$ mutant line remarkedly decreased in comparison to wild type. In summary, our study demonstrated a molecular mechanism of pheromone detection reinforced by HarmSNMP1, indicating that the HarmSNMP1 is indispensable for pheromonal communication of male *H. armigera*.

S04-P-23

The evolution pattern of the production and processing of short chain cuticular pheromones in genus *Drosophila*

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Pheromones, which are generally considered as species-specific cuticular hydrocarbons (CHCs), play important roles in communication and aggregation behaviors in insects. Response to those chemical signals has been suggested to help these insects to find mating partners, thus purge a great selective pressure on species speciation. Here, we investigated the cuticular pheromones of Drosophila species, and found several short chain esters including ethyl tiglate, ethyl hexanoate, etc. These compounds are male-specific volatile esters and occur in subgenus Drosophila. Behavioral experiments showed that the pheromone ethyl tiglate triggers aggregation response in subgenus Drosophila, while the odor did not attract the species in subgenus Sophophora. Our result firstly revealed the evolution pattern of the production and processing of the male-specific short chain pheromones, which could be an ancestral trait of subgenus Drosophila.

S05-P-24

Electroantennogram responses of *Diaphania caesalis* Walker (Lepidoptera: Pyralidae) to volatile matters elicit from *Artocarpus heterophyllus* Lam

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For determination the Electroantennogram responses of *Diaphania caesalis* Walker to volatile matters elicit from jackfruit, *Artocarpus heterophyllus* Lam. The host species and feeding characteristics were illuminated by indoor host selection and non-selection tests. Moreover, the types and relative contents of volatile components in flowers and leaves of jackfruit were identified by headspace solid-phase microextraction combinded with GS-MS. Furthermore, the olfactory sensitivity of *D. caesalis* to the volatile matters was tested using EAG technique. The result showed that *D. caesalis* preferred to eat *Artocarpus heteroyllus* (Lam.), *Artocarpus champeden* (Spreng.) and *Artocarpus altilis* (Fosberg.). GC-MS result indicated that there were seven kinds of chamicals in leaves and nineteenth in flowers. EAG result showed that *D. caesalis* presented obvious electrophysiology to the twelve kinds of chemicals selected from flowers, leaves and ripening fruits, and the intensity of the reaction increased with the concentration rising. Females appeared significant reaction to 100mg/ml of isovaleric acid with the relative reaction value of 234.66, which was 4.85 times as the same concentration of alpha-pinene, and 2.13 times as the value of males. However, Males showed significant response to 100mg/ml of isoamyl acetate with its relative reaction value of 236.14, slightly higher than that of females. Therefore, we concluded that isovaleric acid and isoamyl acetate were speculated to be the important compositions of plant original modifiers for *D. caesalis*. This study will provide a theoretical basis for the development of insect behavior regulator and a reference for field prevention and control.

S06-P-25

Genotypic diversity interacts with predation risk to influence on arthropod richness, evenness and diversity in poplar plantation

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Hybrid poplars (*Populus* spp.) have important value in commercial development and ecological function. Given these applications of poplars plantation, it behooves us to understand the structure of arthropod community diversity, analysis of tritrophic interactions involved in host plant-herbivore-predators system in order to improve pest management in these systems. In early May 2016, we planted four domination hybrid poplars- *P.simonii×P.nigra*, *P.nigra×P.simonii*, *P.nigra×P.simonii*, *P.alba×P.berolinensis*) -in eastern-northern province, Heilongjiang, China. We constructed two treatments: genotypic monocultures (one hybrid poplar genotype) and genotypic polycultures (four hybrid poplars genotypes). Total number of 2880 three-year-old seedlings were planted in four blocks each containing 5 plots randomly allocated to monocultures and polycultures of poplars. To test whether the adult of *Arma chinensis* (Fallou) which was the predator of many defoliators was more attracted to mixtures or monocultures, we used a static-air choice arena for paired choice test. In this study, we demonstrated that (1) the structure of arthropod richness, evenness and diversity was be altered by mixture of poplars compared with monocultures. (2) Leaf damage on poplars were significantly lower in polycultures than in monocultures. (3) There were no significant differences in the growth rate of poplars between monocultures and polycultures. (4) In the predator choice assay, increasing genotype diversity significantly affected predator tropism. Our results provide insight into the potential value of genotypic diversity within poplars for improving management of herbivorous insect population. The exact mechanisms responsible for these effects and the relative importance of genotypic diversity in poplars plantation warrant further investigation.

S08-P-26

The OsmiR396–OsGRF8–OsF3H-flavonoid pathway mediates resistance to the brown planthopper in rice (*Oryza sativa*)

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MicroRNAs (miRNAs) are emerging as key modulators of plant–pathogen interactions. Although the involvement of some miRNAs in plant–insect interactions has been revealed, the underlying mechanisms are still elusive. The brown planthopper (BPH) is the most notorious rice (Oryza sativa)-specific insect that causes severe yield losses each year and requires urgent biological control. To reveal the miRNAs involved in rice–BPH interactions, we performed miRNA sequencing and identified BPH-responsive OsmiR396. Sequestering OsmiR396 by overexpressing target mimicry (MIM396) in three genetic backgrounds indicated that OsmiR396 negatively regulated BPH resistance. Overexpression of one BPH-responsive target gene of OsmiR396, growth regulating factor 8 (OsGRF8), showed resistance to BPH. Furtherrmore, the flavonoid contents increased in both the OsmiR396-sequestered and the OsGRF8 overexpressing plants. By analysing 39 natural rice varieties, the elevated flavonoid contents were found to correlate with enhanced BPH resistance. A BPH-responsive flavanone 3-hydroxylase (OsF3H) gene in the flavonoid biosynthetic pathway was proved to be directly regulated by OsGRF8. A genetic functional analysis of OsF3H revealed its positive role in mediating both the flavonoid contents and BPH resistance. And analysis of the genetic correlation between OsmiR396 and OsF3H showed that down-regulation of OsF3H complemented the BPH resistance characteristic and simultaneously decreased the flavonoid contents of the MIM396 plants. Thus, we revealed a new BPH resistance mechanism mediated by the OsmiR396–OsGRF8–OsF3H–flavonoid pathway. Our study suggests potential applications of miRNAs in BPH resistance breeding.

S09-P-27

Functional analysis of three olfactory protein genes in *Galeruca daurica* (Coleoptera: Chrysomelidae) by RNAi and electroantennography

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Odorant-binding proteins (OBPs) and Chemosensory proteins (CSPs) play a fundamental role in insect olfaction. *Galeruca daurica* (Joannis) is a new pest with outbreak status in grasslands of Inner Mongolia, northern China. In this study, three olfactory protein genes (*GdauOBP15, GdauOBP20* and *GdauCSP5*) were induced by constructing prokaryotic expression system, and the binding affinity were measured for 13 volatiles from the host plant (*Allium mongolicum*) by the fluorescence competitive binding assays. To further verify their olfactory functions, RNA interference (RNAi) and electrophysiological recording were conducted. Ligand-binding assays showed that three recombinant proteins displayed different degrees of binding affinities to various volatiles. GdauOBP15 bound to dimethyl disulfide specifically. GdauOBP20 showed strong binding affinity to p-xylene and 1,3,5-cycloheptatriene. GdauCSP5 could bind dimethyl disulfide and 2-hexenal. qPCR analyses revealed that RNAi reduced the transcript expression levels of *GdauOBP15*, *GdauOBP20* and *GdauCSP5* to 2.93%~28.65% within 48 hours in *G. daurica*. The EAG values of *G. daurica* to most tested volatiles were decreased when the *GdauOBP20* gene was silenced by RNAi. It was found that there were different EAG responses between males and females when the *GdauOBP15 and GdauCSP5* genes were silenced. Among them, the EAG values of females were decreased while those of males were increased. It was suspected that these three genes are involved in finding host plants, and may have different functions in odor perception between males and females in *G. daurica.*

S09-P-28

Effects of jasmonic acid seed treatment on tobacco resistance to *Spodoptera litura*

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To test whether application of jasmonic acid (JA) to seeds influence the resistance of tobacco (Var. Yunyan87), the herbivore performance of *Spodoptera litura*, as well as the contents of JA and JA-Ile of the Yunyan87 plants were measured. The caterpillars feeding on the Yunyan 87 plants from JA-treated seeds gained 15% less weight than those grown on the control plants. After simulated *S. litura* larval feeding, JA and JA-Ile (a bioactive signal which can induce defenses to arthropod herbivores) were 41% and 42% more accumulated in tobacco plants from JA-treated seeds, respectively. Meanwhile, several JA-Ile-dependent direct defensive metabolites including caffeoylputrescine, dicaffeoylspermidine, nicotine, diterpene glycosides, and the activity of trypsin proteinase inhibitors increased 60%, 79%, 19%, 29%, and 80%, respectively, in tobacco grown from JA-treated seeds. Importantly, the JA treatment to seeds did not influence the growth of plants: the dry weight of 6-week-old plants grown from the JA-treated seeds was not reduced. We conclude that application of JA to seeds increases tobacco resistance to *S. litura*, but not reduce the yield.

S09-P-29

Study on the odorant binding proteins (OBPs) and odorant receptors (ORs) of *Bactrocera minax*

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Bactrocera minax (Diptera: Tephritidae) is a devastating pest to citrus plants. The pest has one generation a year and mainly distributed in citrus producing areas such as Sichuan, Hunan and some other Provinces in China.Adult stage is the key period for controlling *B. minax* because its egg, larva and pupae stages are hidden. Olfactory system of insects plays an important role in their survival and adaptation to the environment such as host location, feeding, mating and avoiding enemies. OBPs and ORs play a role in insect recognition and coding of odor molecules and behavior regulation. Using olfaction to regulate the adult behavior is the most important method to control the fruit flies. In order to find the key odor of *B. minax* looking for its host plant citrus, we verified the active components from the volatiles of citrus plants by GC-EAD and olfactory behavior test. Based on antenna transcriptome sequencing, we identified 39 OBPs and 61 ORs of *B. minax*. Study on the binding ability of BminOBPs to the components of citrus volatiles by fluorescence binding assay, and identification of the BminORs function by two-electrode voltage clamp techniques. We found the BminORx may related to identify undecanol, 1-octene-3-ol or linalool by *B. minax*, and the BminOBPx may be involved in the transport of citral and some other odor chemicals.Then, we combined with single sensillum recording (SSR) to determine the antenna sensilla type and function which responds to the volatiles of host plant citrus. Studying the olfactory mechanism of *B. minax* will help us to control this pest more environmentally friendly and efficient.

S09-P-30

Silicon inhibits the resistance of rice stem borer to chlorpyrifos

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Rice (*Oryza sativa*) is an important food crop for a third of the world’s population. Striped stem borer (SSB, *Chilo suppressalis*, Lepidoptera) is one of the most destructive pests of rice. Silicon (Si) is the second most abundant element in the earth's crust. Previous studies have found that Si increases rice resistance against SSB by enhancing both physical and chemical defenses. However, little is known about effects of Si addition on responses of SSB. In this study, we determined the growth and mortality of SSB larvae fed on rice plants cultivated in the nutrient solution with different Si concentrations and reared on artificial diets with different Si concentration. After damage by the SSB, LOX activity and TrypPI content were significantly higher in rice plants treated with higher Si concentration than those treated with lower Si concentration. The similar pattern was observed for the expression levels of defense related genes such as *OsAOS*2, *OsMPK*3, *OsMPK*6, *OsWK*53 and *OsWK*70. Different concentrations of silicates were incorporated into artificial diet respectively. Weight gain of SSB fed on artificial diets with higher Si concentration was significantly lower than the control. Moreover, the mortality of SSB larvae fed on either plants treated with higher Si concentration or artificial diets with higher Si concentration was significantly higher than that in the corresponding controls with lower Si after chlorpyrifos treatment. Activities of detoxifying enzymes including GST, AChE and P450 in midguts were lower in Si-treated larvae than those in Si-untreated larvae reared in the artificial diets. Our results suggest that silicon enhances rice resistance by both increasing rice defense and inhibiting insect detoxification.

S09-P-31

The suppressing effect of leaf-radish living mulch on cabbage pests

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Some studies have shown that living mulches depress insect pest populations in crop fields. In this study, we evaluated the suppressing effect of living mulch using leaf radish, *Raphanus sativus* var. *longipinnatus*, on Plusiinae pests, *Autographa nigrisigna* and *Anadevidia peponis*, and a Pieridae pest, *Pieris rapae*, on cabbage crops, *Brassica oleracea* var. *capitata*. First, we evaluated the effect of leaf-radish living mulch in a field test during the fall of 2018 at Miyagi, Japan. Egg and larval densities of the lepidopteran pests on the crops in the field with the living mulch were lower than those in the field without the living mulch. These results indicate that leaf-radish living mulch reduced the occurrence of cabbage pests. Second, to clarify the effect of leaf radish on oviposition on cabbage plants by *Autographa nigrisigna*, we released adult moths in a screenhouse in which potted cabbage plants were grown with or without potted leaf-radish plants. The number of eggs on the cabbage plants grown with or without leaf-radish plants nearby were compared. The number of eggs on the cabbage plants with leaf-radish plants nearby were lower than that of cabbage without leaf-radish plants nearby. The presence of leaf-radish plants seems to have a suppressing effect on certain species of lepidopteran insects in cabbage cultivation.

S09-P-32

JA-Ile-macrolactones induce both herbivore *Ectropis obliqua* and pathogen *Colletotrichum camelliae* resistance responses of *Camellia sinensis*

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Jasmonates (JAs), the group of lipid-derived hormones were found to control the growth-defense tradeoffs in a myriad of plants. Meaningfully, the pioneer studies with JA-Ile-macrolactones, two diastereomers of macrolactones of 12-hydroxy jasmonate isoleucine (JA-Ile), open the possibility of uncoupling growth and defense in plants. However, little to nothing has been known about the induced defense response of JA-Ile-macrolactones on non-model plants, let alone its underlying mechanisms. Here, we investigated the induced resistance of JA-Ile-macrolactones in tea plant (*Camellia sinensis*) to insect *Ectropis obliqua* and pathogen *Colletotrichum camelliae*, and their preliminary reasons. JA-Ile-macrolactones-treated tea plants significantly influenced the growth rate of *E. obliqua* larvae and infection of *C. camelliae*. On the 8 day and 10 day after the start of feeding, weight gains in larvae fed on control plants were 2.13-fold and 1.13-fold higher than those in larvae fed on 5b, one of the two JA-Ile-macrolactones-treated tea plants. Meanwhile, on the 4 day after the start of inoculation, the infection area of *C. camelliae* in 5b-treated tea plants was inhibited in 31% to those in control plants. Furthermore, the expression level of *CsOPR3* and *CsPR5* were significantly induced by JA-Ile-macrolactones application. In conclusion, our study proved that JA-Ile-macrolactones could induced the woody plant defense response both to herbivore *E. obliqua* and pathogen *C. camelliae*, which may act through activating both JA and SA signaling pathway.

S09-P-33

Cuticular hydrocarbon of the Japanese carpenter ant is useful in pest management on the Argentine ant (*Linepithema humile*)

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Today, the threat of Argentine ant (*Linepithema humile*) is expanding in the many countries, not only in the US but also Japan or Australia. They invade living area of humans, destroy local ecosystems and cause indirect economical loss. In their invaded area, peoples have been trying to deracinate Argentine ant or decrease their threat of quick expansion, but those efforts are not successfully resulted. Thus, we attempted to separate this ant species from human living area by a species-specific repellent. In the previous study, we observed in a behavioral test that *L.humile* show “urgent avoidance behavior (Argentine ants immediately recede from CHC, dragging their antennae.)” when they contact cuticular hydrocarbons (CHCs), (*Z*)-9-tricosene, (*Z*)-9-pentacosene and (*Z*)-9-hexacosene derived from the Japanese carpenter ant (*Camponotus japonicus*). Now, we conducted next experiments, focusing on (*Z*)-9-tricosene. First, we carried out electrophysiological and immunohistochemical experiments in order to elucidate peripheral and central responses to (*Z*)-9-tricosene, and then the repelling effect of (*Z*)-9-tricosene was investigated on some other ant species. Currently used many insecticides kill insect species indiscriminately, not only invasive but also native species. This is a big ecological problem. If a species-specific repellent was developed, we think we can control the invasive ant species without disturbing native ecosystem.

S10-P-34

Differential host choices of *Helicoverpa armigera* and *H. assulta* to tomato volatiles

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A specialist *Helicoverpa assulta* and a generalist *Helicoverpa armigera* show differential responses to tomato.Dichloromethane and *n*-hexane could extract the active volatiles responsible for deterring *H. assulta* females from tomato leaves, while ethyl ether could not. All the three extracts exhibited significant ovipositional attractiveness to ovipositing females of *H. armigera*. The major components contained in the dichloromethane extracts of tomato leaveswere identified as: (Z)-3-Hexen-1-ol (16.27%), (+)-4-carene (12.97%), eugenol (8.61%), benzyl alcohol (6.86%), benzeneactaldehyde (6.54%), *trans*-2-hexenal (6.20%), 1-hexanol (5.62%), 2-phenylethyl alcohol (4.19%), β-phellandrene (3.82%), *trans*-2-hexen-1-ol (3.24%), β-caryophyllene (3.12%), *p*-cymene (2.5%), (+)-α-pinene (2.44%). D-limonene was the most abundant component in the headspace volatiles of tomato seedling. We prepared four volatile blends based on different biosynthetic pathways (acetate-malonate pathway, acetate-mevalonate pathway, and shikimic acid pathway) and the natural ratios (GC-MS): green leaf volatile-typed blend (*trans*-2-hexenal : (Z)-3-Hexen-1-ol: *trans*-2-hexen-1-ol: 1-hexanol = 8 : 21 : 4 : 8), aromatic-typed blend (benzyl alcohol : benzeneactaldehyde : 2-phenylethyl alcohol :eugenol = 10 : 10 : 6 : 13), terpene-typed blend ((+)-α-pinene : (+)-4-carene : β-phellandrene : *p*-cymene : β-caryophyllene = 4 : 20 : 7 : 4 : 5), and a full blend with all the above-mentioned mixed in natural ratios. The results show that all the blends were deterrent to *H. assulta* females, among which the full blend showed the strongest effect. Only the aromatic-typed blend and the terpene-typed blend showed ovipositional attractiveness to *H. armigera* females.

S10-P-35

Rhizosphere responses to environmental conditions in *Radix pseudostellariae* under continuous monoculture regimes

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The root exudates of *Radix pseudostellariae,* working as a rhizospheric intermediary between plants and microbes, can deteriorate the microbial community in the rhizosphere in a consecutive monoculture system. We assessed the effects of artificially applied *R. pseudostellariae* root exudates on *R. pseudostellariae* seedling growth, rhizosphere soil microbial communities, and soil physicochemical properties. We found that phenolic acids and organic acids acted as a driver of changes in the microbial community. High-throughput sequencing and qRT-PCR analysis demonstrated that treatment with phenolic acids significantly decreased the relative abundance of *Trichoderma*, *Penicillium*, *Pseudomonadales*, *Xanthomonadales*, and *Streptomycetales*. Organic acids had a significant negative effect on the relative abundance of *Pseudomonadales* and *Streptomycetales* and significantly increased the abundance of *Fusarium, Xanthomonadales*, *Micrococcales*, and *Gemmatimonadales*. Analysis based on the noninvasive microtest technique indicated that root exudates increased H^+ efflux and plasma membrane H^+-ATPase activity in the pathogenic fungi and decreased them in the beneficial fungi. These phenomena created an acidic environment for the inhibition of beneficial bacteria and accumulation of specialized plant pathogens. This study explains the mechanisms underlying the shift in microflora and structural disorder caused by root exudates in continuously monocultured *R. pseudostellariae* rhizosphere soil through responses to environmental conditions.

S10-P-36

The morphological development of antennal sensilla and corresponding expression of OBP3/7/9 after emergence in the grain aphid *Sitobion miscanthi*

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The secondary rhinaria of aphid, a main olfactory sensillum, is responsible for aphid alarm pheromone (EBF) detection. And the candidate EBF binding proteins have been narrowed to 3 odorant binding proteins (OBPs), OBP3/7/9. However, the evidence leads to any specific OBP(s) as the EBF binding OBP(s) *in vivo* is still lacking. Here we report: 1. the morphological development of the antenna sensilla in *Sitobion miscanthi*, a dominant wheat aphid in China (widely mis-reported as *Sitobion avenae*) . 2. the corresponding expression of OBP3/7/9. There are mainly 5 types of antennal sensilla in antennae, namely the primary rhinaria, secondary rhinaria, type I and type Ⅱ trichoid sensillum, coeloconic pegs and campaniform sensillum. The only difference between winged (migratory strain) and wingless (sedentary strain) aphids is the number of secondary rhinaria. Which of the migratory strain is 6-12, and the sedentary strain is 1-4. The morphology of the secondary rhinaria were not full developed until 2 hours after emergence. SmisOBP3 widely expressed in various tissues and its expression in antennae increased since 2nd hour after emergence. SmisOBP7 specially expressed in antenna and its expression increased since 6th hour after emergence, 4 hours behind the full development of secondary rhinaria. And SmisOBP9, another specially expressed antennal OBP remained high and stable expression after emergence. In summary, the secondary rhinaria, which is responsible for EBF detection takes around 2 h to full develop after emergence. OBP7 might be a focused functional protein involve in the EBF detection.

S10-P-37

Development of regional attractants for *Spodoptera frugiperda* (Smith) based on sex pheromones and its application

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Spodoptera frugiperda (Smith), which belongs to Noctuidae (Lepidoptera), originating in tropical and subtropical America. It is a major local agricultural pest and an FAO global warning, migratory pests of country transboundary, which is prevalent in nearly 100 countries around the world. This pest migrated beyond the borders to Southeast and South China and is migrating to North China. It seriously damages widespread host, generates universality, and diffusively migrates. The Ministry of Agriculture has deployed the monitoring and controlling to its migratory and diffusive in nationwide, surveying and monitoring its population and implementing a serious pest information reporting system. Facing the outbreak of this important invasive pest, it urgently needs to develop a safe and efficient pest monitoring and control technology to achieve this pest control. Therefore, we have screened and developed a sex attractant, field trapping experiment in Guangdong. The two major sex pheromone compounds of *S. frugiperda* are Z9-14: Ac and Z7-12: Ac. Screening was performed to assay the best attractants of different formulas of chemical synthetic pheromone components in corn field of Guangdong Province. The research and development of suitable regional attractants is expected to play an important role in the ecological control technology of *S. frugiperda*.

S10-P-38

Detoxification of plant chemical defenses is an important virulence factor for the cosmopolitan phytopathogen *Sclerotinia sclerotiorum*

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Plants synthesize various secondary metabolites in response to pathogen infection, some of which may also serve as chemical defenses. Despite these chemical defenses, the non-specific plant pathogen, *Sclerotinia sclerotiorum*, can still cause disease on a wide range of host plants, suggesting that it has strategies to overcome them. In order to investigate how this fungal pathogen circumvents plant chemical defenses, we studied changes in important secondary metabolites in Brassicaceae including flavonoids, glucosinolates and isothiocyanates during infection by *S. sclerotiorum* in model plant *Arabidopsis thaliana*. In this study, we found reduced levels of flavonol glycosides and isothiocyanates (ITCs) during late infection stages in *A. thaliana* leaves. *In vitro* assays revealed that this fungus cleaved the sugar moieties from the flavonol glycosides and subsequently degraded the aglycones. We then identified a quercetin 2, 3-dioxygenase (*SsQDO*) in *S. sclerotiorum*. Deletion of *SsQDO* from the genome of *S. sclerotiorum* not only limited fungal growth on flavonols in artificial medium, but also decreased the virulence of the fungus on plants. Moreover, we identified a number of fungal ITC-degradation products and a *SsSaxA* gene encoding a isothiocyanate hydrolase enzyme in *S. sclerotiorum*. The *SsSaxA* deletion mutant, ΔSsSaxA, exhibited decreased tolerance to ITCs *in vitro* and was less pathogenic compared to the wild-type fungus on *A. thaliana* Col-0, underlining the significance of ITC degradation for fungal pathogenicity. Taken together, our results clearly demonstrate that detoxification of plant chemical defenses contributes to virulence of *S. sclerotiorum* on one of its host plants.

S10-P-39

Electroantennographic responses of *Artona martini* Efetov (Lepidoptera: Zygaenidae) to its dorsal abdomine extracts

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Artona matini has been known as the most notrious bamboo feeding zygaenid species in estern China and Japan. In Korea, we also found numerous larvae on the bamboo, which fed it. At Halla mountain, Jeju, Korea, bamboo is expanding its habitat and taking away the havitat of other protective plants. *A. martini* could be a good biological control agent against bamboo. Behavior control agent for *A. matini* is needed for safety before using as a biological control agent. The aim of this study is to identify the pheromone and to develop mating disrupt for controlling population of *A. matini*. The termincal abdominal tips and dorsal abdomine were extracted with hexane. The extracts were subjected to electroantennography (EAG) and GC-MS analysis. In EAG, the dorsal abdomine extracts evoked 6 times higher responses than the termincal abdomine extract. The extracts were sperated by open-column chromatography. 1% hexane-ether fraction evoked the strongest EAG response among other fractions. GC-MS analysis of the dorsal abdomine extrats of male and female revealed that the female extracts had a specific peak. We are trying to identify this female specific compound.

S10-P-40

Host recognition of the cabbage bug, *Eurydema rugosa* (Hemiptera: Pentatomidae), and its sucking stimulant(s) from the host plant, *Brassica juncea* var. *cernua* (Brassicaceae)

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In general, phytophagous insects can detect plant chemicals to find their preferable food sources and suitable oviposition sites. The cabbage bug, *Eurydema rugosa*, completes its life cycle on brassicaceous plants, for example, cabbage, radish and bitter cress. Although little attention has been given to the host recognition cues in *E*. *rugosa*, we hypothesized that this bug species can discriminate between brassicaceous and other plants by detecting brassicaceae-specific chemical(s) like a brassicaceae-specialist herbivore, *Pieris rapae*. First, we evaluated the host preference of *E*. *rugosa* by field observation and found that the adult bugs, which can fly and move between plants, clearly preferred brassicaceous plants over other plants. Second, we tested whether the adults of *E*. *rugosa* can be specifically attracted to the brassicaceous plants in the laboratory. The adult bugs could reach the brassicaceous plants more quickly and stayed longer on those plants than other plants. This suggests that *E*. *rugosa* adults perceive the brassicaeae-specific chemicals to find their host plants. Then, we tested the responses of *E*. *rugosa* adults to the methanol extracts of *Brassica juncea* var. *cernua*, one of their host plants. The adult bugs were not attracted to the crude extracts, but when they touched to the filter paper containing the extract, they stretched their proboscis and began to suck the extracts. This suggests that the extracts contain the sucking stimulant(s) of *E*. *rugosa* adults. Bioassay-guided fractionation and chemical analysis revealed that sinigrin, a characteristic secondary metabolite of brassicaceae, stimulated the sucking behavior of *E*. *rugosa* adults.

S10-P-41

Pheromones, plant-gall allelochemicals, and division of labor in a social aphid

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Social insects build large colonies, which consist of many individuals with elaborate division of labor, inside the enclosed nests. Although their pheromonal communications have been well studied, the roles of allelochemicals involving in the processes are not fully understood. Here, we identified two plant allelochemicals emitted from the galls of the social aphid *Tuberaphis styraci* with sterile soldier caste: the "home sweet home" signal (linalool) constantly released from gall tissues to ensure the stability of colony members; and the alarm signal (trans-2-hexenal) rapidly released from damaged gall tissues to mediate defensive communications. We also identified two pheromones of *T. styraci*: the corpse-recognition pheromone (linoleic acid) that triggers housekeeping behaviors; and the alarm pheromone (trans-β-farnesene) that mediate defensive communications. Young soldiers mainly responded to the corpse-recognition pheromone by performing gall-cleaning behavior, while aged soldiers exclusively responded to the alarm pheromone by performing attacking behavior, which highlighted an age-related division of labor. However, when the concentration of each pheromone or allelochemical was elevated, some soldiers performed all kinds of tasks regardless of their age. Notably, middle-aged soldiers responded to the two pheromones as well as the alarm signal, the latter of which promoted their attacking response. In contrast, the "home sweet home" signal inhibited the alarm response and thus appeared to relax the aphids inside the galls. *T. styraci* regulated task allocation by utilizing an array of pheromones and allelochemicals, thereby regulating a flexible division of labor. We discuss the chemical signaling mechanisms that coordinate the aphid social system.

S10-P-42

Two chemical defensive lines in leaf beetles: P450s are involved in the biosynthetic pathways

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Chrysomelina beetles are chemically protected throughout their life cycles. In larvae of these leaf beetles, for example *Phaedon cochlearia*, two chemical defensive systems co-exist. One is based on the repellent iridoid stored in the dorsal defensive glands, and the other depends on the toxin 3-nitropropanoic acid (3-NPA) that is stored as non-toxic isoxazolin-5-one glucoside ester in the hemolymph. In the fat body of *P. cochleariae*, a cytochrome P450, CYP6BH5, was identified as the geraniol 8-hydroxylase in iridoid biosynthesis. In addition to geraniol, CYP6BH5 catalyzes hydroxylation of other monoterpenols, such as nerol and citronellol to the corresponding α, ω-dihydroxy compounds. Homology modeling suggested that the -OH group of the substrate plays an important role in coordination the substrates with CYP6BH5's catalytic center. A second cytochrome P450, CYP347W1, was proved involved in the production of the 3-NPA moiety in the 3-NPA based defensive line. Moreover, *P. cochleariae* from different life stages except eggs was showed to share the same enzymatic system for 3-NPA production. This β-alanine and P450-dependend 3-NPA synthetic tactic in *P. cochleariae* is different from the aspartic acid and flavin-dependent oxidoreductase based biosynthetic mechanism in prokaryotic organisms. This indicates that different organisms may choose their favorable amino acids and enzymes to produce the same products, which contributes to the ubiquitous occurrence of 3-NPA in eukaryotic and prokaryotic kingdoms.

S10-P-43

Responses of nutrient elements in red clover to aluminum stress

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Aluminum toxicity is one of the main reasons that acid soil restricts the growth of crops. About 30%-40% of the world's arable land is acidic soil, and the acidic soil in the south of China accounts for about 21% of the root area. Red clover which is an important grass in South China, can grow well in acidic soil. But the effect of aluminum on the nutrient composition of red clover is rarely reported. In this study, the effects of 30 days aluminum stress on the nutrient elements in three varieties (Dory, Brilliant and Haifa) were studied. Al^{3+} treatment had significant negative effects on the nutrient elements in red clover. In root, the contents of P declined more than 50% at 1 mmol/L Al^{3+}. The content of K significantly increased by 13.27% and 20.78% respectively in Dory and Brilliant, while Haifa only decreased by 0.12%. The contents of Ca in Dory and Haifa increased by 32.43% and 10.87%, while Brilliant decreased by 47.36%. The Mg content of Dory, Brilliant and Haifa decreased by 1.70%, 3.97% and 2.43%, respectively. In leaf, the contents of P also decreased by 30.47%, 37.87% and 31.99% in Dory, Brilliant and Haifa, respectively. The content of K in Dory and Haifa increased 6.22% and 5.56%, while Haifa only decreased by 1.17%. The content of Ca in Dory and Haifa increased by 11.10% and 5.22%, while Brilliant decreased by 4.89%. The P contents in the plant were reduced obviously under Al stress, and meanwhile the increases of K and Ca levels were observed and thought as one of the aluminum resistance mechanisms coping with plant losses under stress.

S10-P-44

The relationship between soil nutrient elements and chemical constituents of *Apocynum venetum* L.

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Apocynum venetum L. (AV) is traditional Chinese medicinal plant widely used as health tea and antihypertensive medicine. With the rising demand for AV, artificial cultivation becoming the main source instead of wild. Nutrient management plays important role in artificial cultivation. But the influences of soil nutrient elements on the chemical composition of AV are still unknown. Here we investigated the relationship between the plant metabolites and soil nutrient elements in three AV from different habitats (Honggou, Yanhu and Tushan) in Altay, Xinjiang. Increasing the contents of flavonoids in AV is used to enhance the antioxidant activities and medical values. It was observed that the total flavonoids content of AV was positively correlated with soil organic carbon, total nitrogen, total phosphorus and available potassium, meanwhile negatively correlated with soil pH. In addition, the contents of soil nutrients and essential amino acids, polyunsaturated fatty acids were positively correlated but not significant. The moderate salt stress is conducive for the accumulation of flavonoids in the leaves of AV. At the same time, improving soil organic, nitrogen and P fertilizer, and lowering soil pH can lead to the cultivation of higher flavonoids content of AV.

S10-P-45

Comparative efficacy of the entomopathogenic fungus, *Beauveria bassiana* (Bals.) Vuill. and *Metarhizium anisopliae* (Metchnikoff) Sorokin on larval mortality, enzyme inhibition of *Spodoptera litura* Fab. and their non-target activity against *Eudrilus eugeniae* Kinb

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Biopesticides are necessary for the regulation of endemic and invasive pests impacting India, including those that are emerging as a result of climate change and farming intensification. Entomopathogenic fungi are feasible both as systems for the control of insect pests in agriculture with a growing market and as an important model for studies of host-pathogen interaction. At the same time, important progress has occurred in the understanding of the molecular aspects of the pathogenesis and in the development of tools to validate putative virulence factors by the construction of over-expressing or knock-out strains. In the present study is focused on the comparative efficacy of entomopathogenic fungi *Beauveria bassiana* (Bals.) Vuill. and *M. anisopliae* against *S. litura* (Fab.) through the assessment of larvicidal and antioxidant enzyme inhibition and the non-target screening of entomopathogenic fungi against the beneficial earthworm, *E. eugeniae*, in comparison to commercial pesticides. The entomopathogenic fungus exposure resulted in the modification of the levels of detoxification enzymes as well as significant increases in Superoxide Dismutase (SOD) and Catalase (CAT) activity after exposure of entomopathogenic fungus. Bioassay results showed that *B. bassiana* and *M. anisopliae* affect third and fourth instar larvae of *S. litura*. The artificial soil assay of non-target beneficial organism, the soil indicator earthworm E. eugeniae, with fugal culture of *B. bassiana* (5×10^8 conidia/ml/kg) and *M. anisopliae* (5×10^8 conidia/ml/kg) showed no toxicity compared to Monocrotophos at the dosage of 10 ppm/kg. Current results suggest that mycotoxins of *M. anisopliae* and *B. bassiana* are able to significantly reduce the lepidopteran pests while having only low toxicity to other beneficial species.

S10-P-46

Direct and indirect modification of *Bemisia tabaci* feeding behavior by *Cucurbit chlorotic yellows virus*

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Cucurbit chlorotic yellows virus (CCYV) (genus *Crinivirus*) is an emergent RNA plant virus and is transmitted specifically by biotypes B and Q of tobacco whitefly, *Bemisia tabaci* (Gennadius), in a semipersistent manner. It is known that plant viruses can affect vector's behaviors in order to enhance viral transmission. However, there have been few reports on whether or how a semipersistent plant virus manipulates the feeding behaviors of its whitefly vectors. In the study, the electrical penetration graph (EPG) was used to investigate the effect of CCYV on the feeding behaviors of *B. tabaci* biotypes B and Q on cotton plants (CCYV non-host) and cucumber plants (CCYV host). The results showed that CCYV altered feeding behaviors of both biotypes and sexes of *B. tabaci* with different degrees on both plants. CCYV had stronger direct effects on feeding behaviors of biotype Q than those of biotype B, by increasing duration of phloem salivation and sap ingestion both on cotton plants, on cucumber plants, respectively. CCYV could differentially manipulate feeding behaviors of males and females in both *B. tabaci* biotypes on cotton plants, with more phloem ingestion in biotype Q males and more non-phloem probing in biotype B males than their respective females. However, CCYV increased non-phloem probing and phloem salivation more on females than on males of biotype Q, and increased phloem salivation more on females than on males of biotype B on cucumber plants. In addition, CCYV had stronger indirect effects, via virus-infested cucumber plants, on biotype B than on biotype Q by enhancing phloem sap ingestion and feeding bouts. CCYV increased non-phloem probing and feeding bouts more on males than on females of biotype B, and decreased phloem sap ingestion more on males than on females on biotype Q indirectly. The results clearly indicated that the effect of CCYV on *B. tabaci* biotype Q was stronger than that on biotype B, which may lead to increased ability of the *B. tabaci* for CCYV transmission.

S10-P-47

Effects of Volatile on the Feeding and Mating Behaviors of *Sitophilus zeamais* and *Sitophilus oryzae*

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The maize weevil, *Sitophilus zeamais* Motschulsky, and rice weevil, *Sitophilus oryzae* Linnaeus, are two world-wide grain storage pests. They can attack a wide range of crop products, including maize, rice, wheat, oats, sorghum and barley, which may cause serious economic losses. Here, we studied the effect of paddy, maize and wheat on feeding and mating behaviors of maize weevil and rice weevil. We found that the maize weevil preferred maize, followed by paddy and wheat. Compared to maize and paddy, however, the rice weevil preferred wheat. Analyze the volatile components of paddy, maize and wheat found that the content of limonene and (+)-Δ-cadiene in paddy was higher than in others grain, and the content of 2-ethylhexanol and piperonone was higher in maize, while the content of cubene and 2-ethylhexanol in wheat was higher than in others grain. The 3.5 mmol/L 2-ethylhexanol, 0.35 mmol/L of (+)-Δ-cadiene, and 3.5 mmol/L of piperonone had significant attractive effects on maize weevil, and 35 mmol/L 2-ethylhexanol, 35 mmol/L (+)-Δ-cadiene, 35 mmol/L of piperonone and 3.5 mmol/L of limonene could attract more rice weevil than other concentrations of these compounds. The combination of 3.5 mmol/L 2-ethylhexanol with maize weevil males had stronger attraction to maize weevil females than combinations of 350 mmol/L of piperonone with maize weevil males and 0.35 mmol/L(+)-Δ-cadiene with maize weevil males. The combination of 35 mmol/L (+)-Δ-cadiene with rice males and 35 mmol/L 2-ethylhexanol with rice weevil males has stronger attraction to rice weevil females than combinations of 35 mmol/L pepperone with rice weevil males and 3.5 mmol/L limonene with rice weevil males. In addition, 3.5 mmol/L 2-ethylhexanol and 0.35 mmol/L (+)-Δ-cadiene significantly increased the mating rate of 15-day-old maize weevil, and 35 mmol/L 2-ethylhexanol, 35 mmol/L (+)-Δ-cadiene and 3.5 mmol/L limonene significantly increased the mating rate of 15-day-old rice weevil. The results showed that the volatile components in paddy, maize and wheat could significantly affect the feeding and mating behavior of maize weevil and rice weevil, and helpful to develop effective integrated control measures for grain storage pests.

S10-P-48

Effects of salicylic acid concentration and post-treatment time on the direct and systemic defense responses in maize (*Zea mays* L.) after exogenous foliar application

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To investigate whether there were concentration and timing effects existed on the defense responses of direct impact in treated part and systemic impact in non-treated part. We examined effects of Salicylic Acid (SA) concentration and time since foliar application on defense responses. *Zea mays* cultivar 5422 with two fully expanded leaves was pretreated with SA concentrations of 0.1, 0.5, 1.0, 2.5, 5.0 mM, presence of defense chemicals and enzymes was measured in leaves and roots at 3, 12, 24, 48, 72 h. Direct and systemic changes were related to SA concentration and time of pretreatment. In leaves, DIMBOA, total phenolics, H_2O_2 contents and polyphenol oxidase, superoxide dismutase activities were enhanced by 0.5~5.0 mM SA; peroxidase and catalase activities were increased by 1.0~5.0 mM SA. In roots, DIMBOA, H_2O_2 contents and PPO activity were enhanced systematically by 0.1~5.0 mM SA. In leaves and roots, the defense chemicals and enzyme activities increased at 3~24 h. The pretreatment of 1.0 and 2.5 mM SA decreased the chlorophyll a content and biomass of aboveground or belowground at 24~48 h. These findings suggest that 2.5 mM SA foliar pretreatment produces strong defense responses with the optimal induction time at 24 h. In either 9×10^8 mL^{-1} *Ralstonia solanacearum* (roots) or 8×10^5 mL^{-1} *Exserohilum turcicum* (leaves) inoculation after 2.5 mM SA foliar pretreatment at 24 h, the activities of PPO, POD, SOD and defense chemicals contents were enhanced in maize leaves and roots, nevertheless, the CAT activity, the contents of chlorophyll a or b and biomass were decreased.

S10-P-49

Microbial community structure and its temporal changes in *Panax ginseng* C.A. Maye rhizospheric soils monocultured for different years

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Panax ginseng C.A. Maye is a perennial herb belonging to the family Araliaceae and is highly valued in traditional Chinese medicine. The continuous cropping obstacle of *P. ginseng* is a bottleneck that restricts the sustainable development of ginseng industry. The main cause of soil deterioration during continuous cropping of *P. ginseng* may be the disturbance of soil microbial community mediated by the ecological effects of root exudates. In order to determine the effects of *P. ginseng* monoculture on the rhizospheric soil microbial community, high throughput sequencing was used to examine changes in the structure and composition of microbial community in *P. ginseng* rhizosphere soil with vorious cultivation ages. The results revealed a distinct separation between the primitive soil sample which was not planted ginseng and the rhizosphere soils of four-year(FOS), five-year(FIS) and six-year(SS) ginseng. The species of fungi in ginseng rhizosphere soils were significantly higher than primitive soil, monoculture of ginseng led to a significant increase in relative abundance of *Ascomycota*, reaching 42-66% in different years, particularly pathogens such as *Fusarium* and *Cylindrocarpon*, but a significant decrease in the relative abundance of *Russula* by the Alpha-diversity analyzing. Tree map analysis showed that the similarity of fungal community between six-year ginseng soil and five-year ginseng soil was high, while that between forest soil and ginseng soil was low. The species of bacteria in ginseng rhizosphere soils were slightly less than primitive soil, the relative abundance of *Verrucomicrobia*, *Thaumarchaeota*, *Chloroflexi* and *Firmicutes* were significant increased, while the dominant bacteria of primitive soil was *Proteobacteria*.

S10-P-50

No detrimental effects of Bt maize in aphid-ladybeetle systems

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Genetically-engineered (GE) *Bacillus thuringiensis* (Bt) crops can successfully control certain Lepidoptera and Coleoptera pests. The widespread use of Bt crops secures yield and reduces pesticides input. In the second generation of GE plants, Bt maize has been developed with several stacked Cry and other Bt proteins. The effects of Bt maize on non-target arthropods have been, and continue to be, a subject of ecological risk assessment and public debate. In this presentation, two laboratory experiments are reported that evaluated the transfer of Bt protein from three Bt maize hybrids, 5422Bt1 (event Bt11) and 5422CBCL (MON810) producing Cry1Ab and SmartStax maize expressing Cry1A.105, Cry1F, Cry2Ab, Cry3Bb1, Cry34Ab and Cry35Ab1, to aphids (*Rhopalosiphum maidis*, *Rhopalosiphum padi*) and ladybeetle predators (*Propylea japonica*, *Harmonia axyridis*). Furthermore, the impact of Bt maize on the biological parameters of the aphid and ladybeetle species were investigated. In the Cry1Ab maize- *R. maidis*- *P. japonica* system, Cry1Ab levels in the aphid contained concentrations lower than 2% of the leaves for Cry1Ab and no traces of Cry1Ab were detected in ladybeetles preying on Bt maize-fed aphids. In the stacked Bt maize- *R. padi*- *H. axyridis* system, aphids feeding on Bt maize contained no measurable amounts of Cry1A.105 and Cry2Ab2, and concentrations lower than 0.3% of the leaves for Cry1F, Cry3Bb1 and Cry34Ab1; *H. axyridis* fed with aphids contained either no detectable Cry protein or values lower than 0.17% of the leaves for Cry1F, Cry3Bb1 and Cry34Ab1. In addition, detrimental effects of Cry1Ab-producing maize and SmartStax maize on the survival and development of aphids and ladybeetles were not observed. We therefore conclude that aphids on Bt maize pose no risk to ladybeetles.

S10-P-51

Pathogenicity of the Fungus *Isaria fumosorosea* Strain (Ifu13a) against the aphid *Aphis gossypii* and on the predator *Harmonia axyridis*

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The control effect of *Isaria fumosorosea* strain (Ifu13a) against the sucking pest Aphid gossiping and its safety to the natural enemy Harmonia axyridis were determined in greenhouse and field experiments. The results showed that in the #1 treatment: 25±1°C temperature and 85±5% relative humidity was maintained for 2 days after the fungal spray, followed by normal field humidity (humidity range of 60%-94%) for 8 days, the adjusted accumulated mortality of the aphid inoculated with fungal conidia suspension of $1.0×10^8$, $1.0×10^7$ and $1.0×10^6$ conidia/ml was 85.5%, 84.6% and 50.0%, respectivit.. The median lethal times (LT_{50}) of A.gossypii were obtained from a regression-probit value was 4.35, 4.51 and 7.12 days, respectively. While in the #2 Treatment, at a totally unnipulated natural field temperature and humidity, the ajusted accumulated mortality of the aphid inoculated with the fungal conidia suspension of $1.0×10^8$, $1.0×10^7$ and $1.0×10^6$ conidia/ml decreased to 62.9%, 46.3% and 26.7%, respectively and the LT_{50} of I. fumosorosea was obtained as 5.61, 7.25 and 10.00 days, respectively. Under greenhouse conditions, the corrected hatching inhibition rate of the eggs of H.axyridis was 70.5%, 58.5%, 41.2%, the Corrective eclosion inhibition rate of the pupae of H.axyridis was 27.9%, 22.1%, 17.7%, respectively, at 25±1°C temperature and 95±5% relative humidity , inoculated fungal conidia at $1.0×10^8$, $1.0×10^7$ and $1.0×10^6$ conidia/ml of Ifu13a, respectively. The strain Ifu13a had no significantly negative effect on the larvae and adults of H.axyridis. Research conclusion: It is concluded that keeping high humidity for 2 days after fungal spraying treatment leads to high control potential on the aphid-sucking pests. In the greenhouse experiment, Ifu13a posed some effect on the eggs and pupae of its natural enemy H. axyridis. it is recommended that the entomopatogenic fungus could be safely used when the ladybug H.axyridis is in its larvae and adult stage, and a cooperative control against aphids is expected.

S10-P-52

Effects of exogenous jasmonic acid on leaf defense response and expression profile of Bt and conventional maize seedlings

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Bt maize, the most commercialized pest-resistant transgenic crop, is genetically modified to express insecticidal crystal protein from the bacterium *Bacillus thuringiensis*. Evaluating the difference in induced defense responses between Bt maize and conventional maize has become an important component to assess the ecological risk of Bt maize. Jasmonic acid (JA) is a vital signaling substance involved in plant induced defense responses processes. It can play an important role in the resistance to plant insect pests. In the present study, we examined the changes of Bt protein content, defense chemicals (DIMBOA and total phenol) contents, defense enzymes (polyphenol oxidase, peroxidase, catalase and superoxide dismutase) activities, expression profile in the leave of Bt maize varieties 5422Bt1 (event Bt11) and 5422CBCL (event MON810) and their conventional maize 5422 after applying exogenous 100 µM JA to simulate insect pest onto the leaf surface for 24 h. The objectives were to study the effects of exogenous JA on leaf defense response and expression profile of Bt and conventional maize seedlings. The results indicated that the polyphenol oxidase and catalase activities of conventional maize 5422 were increased significantly. Bt protein content and polyphenol oxidase, peroxidase activities of Bt maize 5422Bt1 were increased significantly; polyphenol oxidase, peroxidase, catalase activities of Bt maize 5422CBCL were also increased significantly after the leaf of maize was treated by JA. The results of expression profile analysis showed that the numbers of genes significantly up-regulated in 5422, 5422Bt1 and 5422CBCL leaves treated with jasmonic acid were 102, 16 and 243, respectively, whereas most of the growth-related genes were down-regulated. Compared with the control, jasmonic acid treatment to Bt maize 5422CBCL significantly increased the expression of DIMBOA mediated genes (such as *Bx3*, *Bx5*, *Bx7* and *Bx8*) and phenolics mediated genes (such as *PTAL*, *4CL* and *TAT*) in leaves, but the response of conventional maize and 5422Bt1 was not obvious. It can be concluded that Bt gene introduction and endogenous inductive defense response of maize act synergistically during the exogenous JA induced defense response. At the same time, the induced defense response of JA to maize requires growth cost.

S12-P-53

Seed soaking with sodium silicate primes salt tolerance of rice seedlings without physiological cost

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Rice is one of the most important cultivated cereal crops and is susceptible to salinity stress. Silicon (Si) has the great potential for improvement of biotic and abiotic stress tolerance in crops and rice has been considered as an effective Si accumulator. However, whether seed soaking with Si could enhance the tolerance of rice plants against salinity stress is unclear. In this study, rice seeds were pretreated with different levels of sodium silicate and then the hydroponic rice seedlings were exposed to sodium chloride. Our results showed that seed soaking with Si significantly improved the growth of rice seedlings under salinity-stress, evidenced by the enhancement in fresh weight, dry weight, leaf relative water content (LRWC), photosynthetic pigment level, soluble protein content, as well as the activities of POD, CAT and SOD enzymes. Moreover, Si-pretreated seeds showed accelerated seed germination, increased seedling heights and reduced root length. Furthermore, the contents of proline and MDA in Si-pretreated plants were lower compared to the untreated control plants. Our results indicate that seed priming with Si enhances seedling tolerance to salinity stress without physiological cost and can be used as an effective strategy to improve rice tolerance against salinity stress.

S12-P-54

Nutrient-induced shifts in fine roots architecture reflect alternate root foraging strategies in *Cunninghamia lanceolata*

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Predicting the response of fine roots to nutrient supply and forest practices has important implications for understanding plant physiology and to scale ecosystem properties such as carbon (C) and nutrient cycling in plantation ecosystems. Fine-root system architecture is known to play an important role in how trees acquire soil nutrients in changing environments. However, the effects of N and P fertilization on the fine-root system architecture of trees and their linkages with root foraging strategy remain unknown. We investigated the architectural traits related to nutrient foraging for fine roots following nitrogen (N) fertilization, phosphorous (P) fertilization, N plus P fertilization treatments in a young Chinese fir (*Cunninghamia lanceolata*) plantation in subtropical China. We measured fifteen traits of fine-root system architecture under the four treatments (Control, N, P, N plus P addition) and determined relationships between the architectural traits and nutrient foraging behaviors (precision and sensitivity). Compared with the control, fertilization significantly increased dichotomous branching index (DBI), while fertilization decreased the traits of attitude, link length (LL) and link average surface area (LSA). Fine roots exhibited higher foraging sensitivity and precision (expressed as relative fine root length difference) in response to P fertilization than to N and N plus P fertilization treatments. Fine-root foraging sensitivity and precision were correlated positively with DBI, but negatively with Topological index (TI). Furthermore, the trait syndromes (Altitude, external path length EPL, Forks and TI) is arrayed well along the positive part of the first axis, whereas the opposite trait syndromes (Crossings, DBI, Precision and Sensitivity) is along the negative part of the first axis with a principal component analysis (PCA). Variation in fine-root traits in response to P fertilization mainly explained by a set of predictor variables combining traits (link characteristics, LBA, LD and LSA), opposing the traits variation in response to N fertilization mainly explained by the traits of Altitude, EPL and TI. Our findings emphasize the importance of fine-root architectural plasticity in response to long term fertilization and suggest that shifts in fine-root architecture may reflect alternate nutrient foraging strategies in response to N and P availability.

S13-P-55

Behavioral, physiological and molecular responses to cadmium in the Asian corn borer, *Ostrinia furnacalis*

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Intake of heavy metals such as cadmium (Cd) from the environment results in many detrimental effects in living organisms and accumulates in the body for a long time. Many species of insects and other animals living in polluted areas have been shown to accumulate cadmium which causes developmental defects and behavioral changes. To explore the impacts of the heavy metals Cd on development, reproductive behaviors, and potential changes in gene expression in the Asian corn borer (ACB), *Ostrinia furnacalis*, the neonate larvae were fed with artificial diets containing the heavy metals Cd at a concentration of 5 mg/kg, and a control diet without any heavy metals, under laboratory conditions. The resulted showed that cadmium increased larvae and pupae developmental durations and lowered the survival rate of pupae. The calling frequency and the time of continuous calling of the survival female moths were also significantly decreased when the larvae were exposed to cadmium. Less than 24% of survival male moths under Cd stress landed on normal calling female moths, while above 53% of the control males contacted with normal calling females. Whether it is a control female moth or a cadmium female moth, they produced fewer eggs after mating with the cadmium male moths. However, cadmium females produced as many eggs as control females when they mated with control males. To investigate the molecular changes underlying such physiological and behavioral changes, RNA-Seq was used to examine transcriptomic changes upon cadmium exposure and showed that 123 transcripts were differential expressed (122 up and 1 down). Using Pac-Bio sequencing, a full-length reference sequence set was also sequenced and assembled in order to annotate and analyze the functions of these differentially expressed genes. Then two metallothionein genes were annotated in ACB. To determine whether these two metallothionein genes have different function in binding different metal ions, the gene expression of these two genes were tested in different heavy metal treatments. The results indicated that *O. furnacalis* may be a good model insect to understand how heavy metal pollution can affect pest insect populations.

S13-P-56

Diterpenoids from the roots of *Lonicera macranthoides*

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Lonicera macranthoides Hand.-Mazz., a plant of genus Lonicera in family Caprifoliaceae, is mainly distributed in the southwest of China. Recently, we reported the occurrence of diterpenoids (e.g. labdane, aphidicolane, and *syn*-pimarane) and submitted a paper about two new prenyleudesmanes in the roots of the plant for the first time. The absolute configurations of *syn*-pimarane and prenyleudesmanes were evidenced by X-ray diffraction data. We also discussed the biosynthesis relationship of diterpenoids in the roots.

S13-P-57

Odorant receptors for toxicants in *Ostrinia furnacalis*

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Insects have a complex olfactory system for searching host plants and mating partners by recognizing plant volatile organic compounds (VOCs) or sex pheromones. In addition, to avoid feeding or laying eggs on the non-host plants, especially some species contains toxic components which could cause negative effects to insect growth and development, the insect olfactory system should contain several genes that are sensitive for perception of toxicants. Odorant receptors (ORs) are the main gene family that detect plant VOCs and sex pheromones and expressed on the dendrites of olfactory receptor neurons. In the present study, we identified a VOC from asteraceae weeds which is toxic and can be used as a repellent to the Asian corn borer *Ostrinia furnacalis*. In addition, the corresponding odorant receptors were screened out using *Xenopus* oocyte ectopic expression system. This study indicated a molecular mechanism on chemosensation for avoiding toxic plants for insects and provided a new compound that could applied as an insecticide or a repellent for environmental friendly pest management.

S13-P-58

Research progress on insect ionotropic receptors

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Chemosensation is essential for the survival and reproduction of animals. As the largest group in animal kingdom, insects have evolved a complex repertoire of olfactory receptors in response to volatile chemicals in the environment, including the odorant receptors (ORs) and the ionotropic receptors (IRs). The IR gene family is evolved from ionotropic glutamate receptors (iGluRs). IRs are known to play a specific biological roles in perception of wide range of stimuli, such as odorants, temperature and humidity. At least three co-receptors have been found in IR gene family, and each IR requires at least one IR co-receptor to function. Different odor-binding IR can be co-expressed in a same olfactory neuron, and the combination of IR may lead to changes in the odor response. Although progress has been made in this area, many of the functions and mechanisms of IRs still remain unclear. In this paper, insect IRs' structure, evolution, gene identification, expression and function are reviewed.

S13-P-59

Cloning and expression of α-farnesene synthase gene from tea plant

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Terpenoids play an important role in the exchange of information between many species of plants and between plant and insect. α-Farnesene could efficaciously attract parasitic wasps to the target areas and enhance their parasitism rate. α-Farnesene synthase is the direct rate-limiting enzyme in the synthesis of α-farnesene, which has a very important regulatory effect on the synthesis of α-farnesene. Degenerate primers were designed based on the conservative *FAS* gene sequence of other plants in the GenBank to clone the full-length cDNA of *FAS* genes of the tea plant by using the RACE and RT-PCR methods. It is deposited to the GenBank (Accession NO. MH686504). The full-length gene is 2082 bp with a 75 bp 5’ UTR, a 1683 bp ORF, a 324 bp 3’ UTR and poly (A) tail, which encoded a total of 560 amino acids. The putative molecular weight is 65 kDa and the *pI* is 5.73. The encoded amino acid sequence contained an RR (X8) W region and a DDXXD region. Prokaryotic expression recombinant vector, pET32a(+)/FAS, was successfully constructed. SDS-PAGE assay showed that the target was highly expressed in BL21(DE3) and the molecular weight of fusion protein was similar to the predicted molecular weight. It indicated that *Cs*FAS was expressed correctly in BL21 (DE3). It was found that the recombinant protein existed in the form of inclusion bodies.

S13-P-60

Identification of olfactory genes and functional analysis of GOBP2 in *Clostera restitura*

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Clostera restitura Walker (Lepidoptera: Notodontidae) is one of the most destructive defoliators of poplars in China. We identified large amount of olfactory genes by constructing an antennal-transcriptome, characterized the expression profiles of odorant binding proteins, got recombinant protein and constructed functional analysis by fluorescence competitive binding assay, using homology modeling and molecular docking method predicting the ligand binding of GOBPs. Finally, EAG analysis was constructed to find out plant volatiles components which have stimulation activity to adults.

A total of 165 olfactory genes were identified, including 43 OBPs, 13 CSPs, 78 ORs, 15 IRs, 13 GRs, and 3 SNMPs. The relative expression levels of CresGOBP1, CresGOBP2, CresOBP9, CresOBP 10, CresOBP 16 and CresOBP21 were significantly higher expressed in antennae than in heads (antennae excluded), wings and legs suggesting their essential role in antennal recognition processes. Western Blot analyses showed single protein bands at 15 - 18 kDa which determine the target protein to CresGOBP2. Fluorescent competition binding experiment showed that CresGOBP2 has a narrow binding spectrum, it could combine with (E) - 2 - heptene aldehyde, trans - 2, 4 - sebacic olefine aldehyde, benzoic acid, beta ionone, dibutyl phthalate and diisobutyl phthalate within 29 volatiles. Docking results showed CresGOBP2 formed hydrogen bonds by THR 9, TRP 37 and SER 56, which tend to be key amino acid sites. EAG results showed that both male and female antennae reacted to (E)-2-Heptenal 、 Cis-3-Hexen-1-ol,hexanal,Cis-3-Hexenyl acetate, 2-Hydroxybenzaldehyde and Trans-2,4-Decadienal strongly.

S13-P-61

Neuropeptides in the brain of adult male cotton bollworm and their expressions at different ages

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Olfaction serves as a crucial role in insect sensory system and mediates many behavioral contexts, such as finding sexual partners, locating food and detecting oviposition sites. Odorants first detected by periphery olfactory system as a chemical signal then transformed to electrical signal and finally integrated in central olfactory system-the brain. Different physiological states significantly affect this process so that formed the neuronal plasticity. Neuropeptides has been reported to play the critical role in physiological state related olfaction plasticity. Here, the genes encoding neuropeptide precursors in the brain of male *Helicoverpa armigera* were identified by transcriptomic analysis and were used to identify potential targets for disruption of physiological processes and the protection of crops. 40 families including subfamilies of candidate genes were found to encode the neuropeptide precursors for known insect neuropeptide. Typical neuropeptides which reported as olfaction related were found, such as CCHamide, Insulin, NPF, sNPF and Tachykinin. Compare to the reported genes pool from *Bombyx mori* and *Chilo suppressalis*, we did not find Adipokinetic hormone 2, Allatostain C, Apis-ITG, Ecdysis triggering hormone, Glycoprotein hormone2 and Natalisin. Alternative splicings were found in CCHamide1, NPF1, Orconin, Ion transported peptide by transcriptome and genome data. DEG analysis indicated that candidate genes encoding Adipokinetic hormone 1 and Insulin-like peptide were up regulated whereas Ecolosion hormone and Bursicon A were down regulated as the age increase. Those genes might be critical in age related olfactory plasticity and could be the target for developing new technique in plant protection.

S13-P-62

Odorant binding protein and chemosensory protein genes in *Cacopsylla chinensis* (Hemiptera: Psyllidae)

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Chemosensory systems play an important role in insect behavior, and some key associated genes have potential as novel targets for pest control. *Cacopsylla chinensis* is an oligophagous pest and has become one of the main pests of pear trees, but little is known about the molecular-level means by which it locates its hosts. In this study, we assembled the head transcriptome of *C. chinensis* using Illumina sequencing, and 63,052 Unigenes were identified. A total of 23 candidate chemosensory genes were identified, including 12 odorant binding proteins (OBPs) and 11 chemosensory proteins (CSPs). The number of these chemosensory genes is consistent with that found in other Hemipteran species, indicating that our approach successfully obtained the chemosensory genes of *C. chinensis*. The tissue expression of all genes using quantitative real-time PCR (qRT-PCR) found that some genes displayed male head, female head, or nymph-biased specific/expression. Our results enrich the gene inventory of *C. chinensis* and provide valuable resources for the analysis of the functions of some key genes. This will help in developing molecular targets for disrupting feeding behavior in *C. chinensis*.

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Transcriptome analysis of sex pheromone glands in *Mythimna separate* (Walker) (Lepidoptera: Noctuidae)

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Insects use sex pheromones which are usually produced by females and detected by males for mating of other sexual behaviors. *Mythimna separate* Walker, an important lepidopteran pest, is widely distributed in eastern Asia and Australia, damaging wheat, maize, rice and other crops during the past thousands of years. Sex pheromones have been used as a good attractant for pest management in this species but the pheromone synthesis pathway is still unclear. In this study, to identify the genes involved in pheromone synthesis in *M. separate*, RNA-seq was carried out using pheromone glands collected from female adults at the first day (sample D1) and the fourth day (sample D4) after eclosion in *M. separate*. In total, 53456 unigenes and 52836 unigenes were yielded from D1 and D4, respectively. Compared to D1, expressions of 967 genes were up-regulated and 1218 genes were down-regulated in D4. Among them, 60 genes with the highest expression differences were selected for the conformation of tissue-specific expressions. As the results, 2 genes were tissue-specific expressed in the female sex gland. Interestingly, we also found 1 gene was specifically expressed in the male sex gland, which may be involved in male pheromone synthesis. This study could provide preliminary information for pheromone synthesis pathway in *M. separatez*.

S13-P-64

Identification and sex-biased profiles of candidate olfactory genes in the antennal transcriptome of the parasitoid wasp *Cotesia vestalis*

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Cotesia vestalis (Hymenoptera: Braconidae) is an endoparasitoid wasp that attacks larvae of the diamondback moth, *Plutella xylostella* (Linnaeus), one of the most important pests of cruciferous plants in the world. This natural enemy has been used to control populations of *P. xylostella*. To more fully understand the molecular mechanisms of olfactory reception in *C. vestalis*, the transcriptomes of male antennae, female antennae, and mixed female and male legs were systematically analyzed, and the chemosensory genes were identified. A total of 253 olfactory genes, including candidates of 158 odorant receptors (ORs), 12 ionotropic receptors (IRs), 48 gustatory receptors (GRs), 22 odorant binding proteins (OBPs), 11 chemosensory proteins (CSPs), and two sensory neuron membrane proteins (SNMPs), were systematically identified and subjected to sequence and phylogenetic analysis. Then, the differentially expressed genes (DEGs) within female and male antennae were analyzed to obtain expression information on the candidate olfactory genes at the transcriptional level. The expression levels of 25 ORs, nine OBPs, eight GRs, and three IRs were significantly different between male and female antennae.Our results provide valuable information for further studies on the chemoreception mechanisms in *C. vestalis*, to ultimately improve the pest control measures by using natural enemies.

S13-P-65

Mouthparts enriched odorant binding protein AfasOBP11 plays a role in the gustatory perception of *Adelphocoris fasciaticollis*

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The *Adelphocoris fasciaticollis* (Hemiptera: Miridae) has become one of the key pests along with the large-scale cultivation of transgenic Bt cotton in China, causing serious damage in cotton fields. Insect odorant binding proteins (OBPs), one of the most important groups of odor carriers, are believed to play essential roles in chemoreception. In our study, the expression profile of *AfasOBP*11 was studied. The expression profile showed that *AfasOBP*11 was mainly expressed in the mouthparts of *A. fasciaticollis*. Additionally, two types of sensilla, sensilla trichodeum and sensilla basiconicum, were found on the mouthparts of bugs. Moreover, anti-AfasOBP11 antiserum strongly labeled the sensilla basiconica. In fluorescence binding assays, recombinant AfasOBP11 displayed much stronger binding abilities to non-volatile secondary metabolite compounds than to volatile odors. After RNA interference of target AfasOBP11, *A. fasciaticollis* bugs spent a longer time and pierced more frequently on the artificial diet containing 2.0% gossypol, indicating that RNAi treated bugs reduced sensitivity to gossypol. Our findings suggest that AfasOBP11 may play a vital role in chemoreception of *A. fasciaticollis*, especially in gustatory perception. This work provides valuable insights into the exploration of gustatory roles of OBPs in bugs.

S13-P-66

The identification, expression profile and functional analysis of chemosensory genes in legs of *Apolygus lucorum* (Hemiptera: Miridae)

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Increasing studies focus on the functions of antennae to illuminate the mechanism of insects chemical communication. However, there are less explorations on the function of legs in chemical communication, which play roles as one of the most important insect gustatory organs. In our study, we identified the candidate chemosensory genes from forelegs, middle legs, and hind legs of adults of both sexes. We have identified 20 odorant binding proteins (OBPs), 8 chemosensory proteins (CSPs), 1 odorant receptor (OR), 2 ionotropic receptors (IRs), 1 sensory neuron membrane protein (SNMP). Furthermore, the expression characteristics of candidate genes in forelegs, middle legs, and hind legs of both sexes were clarified. What was different from our normal thinking cognition is that the forelegs, middle legs and hind legs genes were the same. It suggests that the bugs' forelegs, middle legs, and hind legs may be all involved in chemical communication. To illuminate the close chemical communication mechanism, scanning electron microscopy was conducted to observe the sensilla types on the forelegs, middle legs and hind legs of *Apolygus lucorum*. As a result, the sensilla types and distribution of forelegs, middle legs and hind legs were basically consistent. Additionally, sensilla basiconica with pores were found in the legs. In our study, the highly expressed chemoreceptor proteins in legs had extensive binding ability to host volatile and non-volatile compounds. Our work will provide a morphological basis for understanding the process of host habitat location and basic knowledge for the gustatory perception of *Apolygus lucorum*.

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