16th International Symposium on Insect-Plant Relationships

16th SIP - Abstract Book

University François-Rabelais, Tours, France,
2-6 July 2017

Insect Biology Research Institute
University François-Rabelais (Tours) and CNRS

Organizing structures

IRBI
Institut de Recherche sur la Biologie de l'Insecte

UNIVERSITÉ
FRANÇOIS - RABELAIS
TOURS

cnrs
dépasser les frontières

UFR
SCIENCES & TECHNIQUES

UNIVERSITE D'ORLEANS

INRA
SCIENCE & IMPACT

Supporting structures

cost
EUROPEAN COOPERATION IN SCIENCE AND TECHNOLOGY

BRITISH
ECOLOGICAL
SOCIETY

FéRI
FÉDÉRATION DE RECHERCHE
EN INFECTIOLOGIE
CENTRE - LOIRE

RÉSEAU
MiDi
Milieux & Diversité
Réseau thématique de recherche
en Région Centre Val de Loire

COMMUNAUTÉ D'AGGLOMÉRATION
Tour(s)plus

WILEY

VILLE DE
TOURS

Région
Centre-Val de Loire

Functional Ecology

Virtual Issue: Functional Ecology will publish a virtual special issue on plant-microbe-insect interactions to coincide with the conference. Any paper published in Functional Ecology from June 2013 to December 2017 will be included to this virtual issue. Please contact us as soon as possible if you are eligible to be part of this virtual issue or plan to submit a paper to Functional Ecology before December 2017.

For more information contact Alison Bennett (Alison.Bennett@hutton.ac.uk) or David Giron (david.giron@univ-tours.fr)

Previous special issue on plant-microbe-insect interactions:
http://besjournals.onlinelibrary.wiley.com/hub/issue/10.1111/fec.2013.27.issue-3/

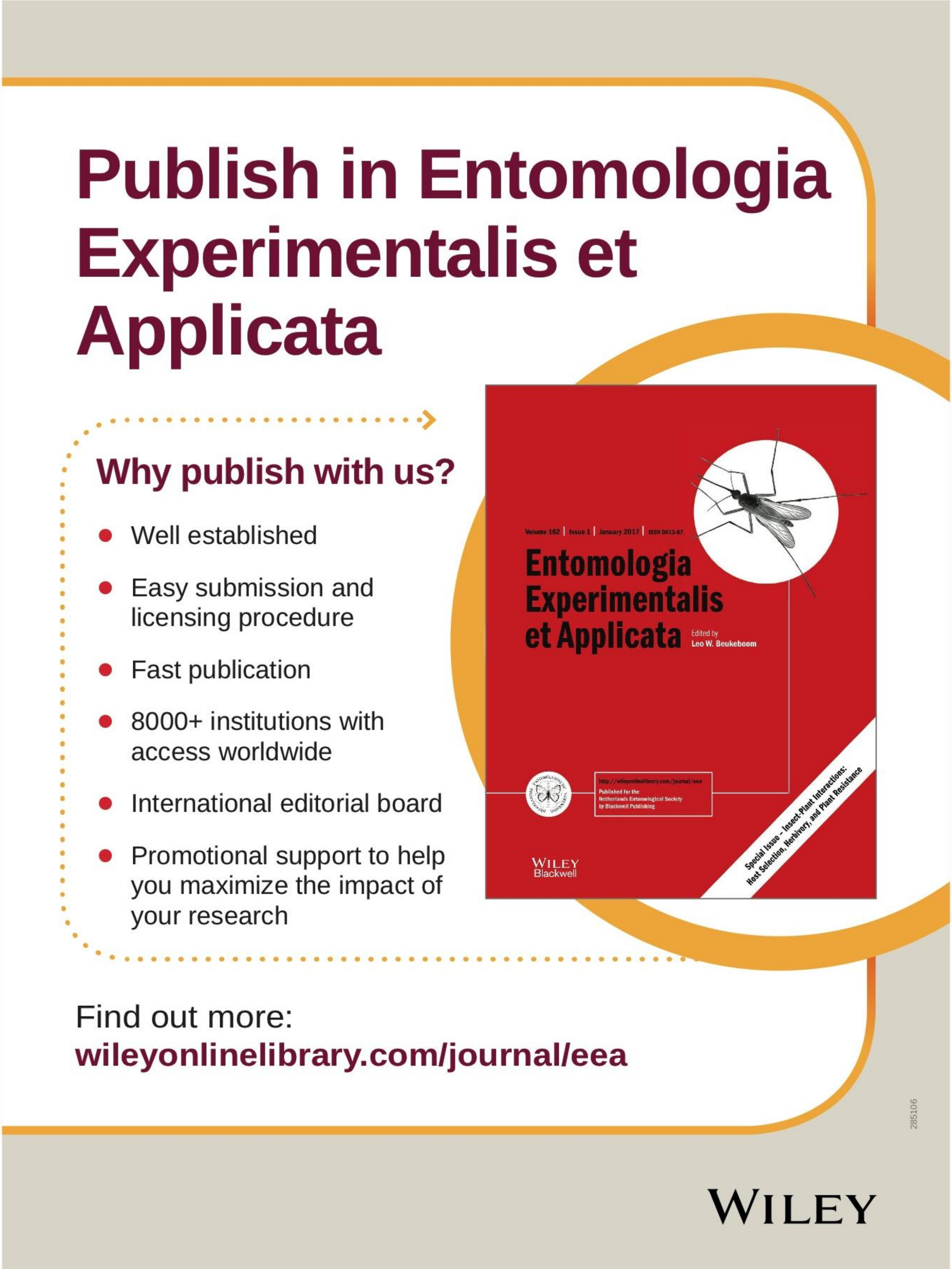
Podcast: A podcast about research on plant-insect-microbe interactions will be organized during the meeting. Please come and join us at the second poster session (Tuesday 4th of July) to answer a few questions about your research, the latest developments of this fascinating research field and the challenges ahead.

The podcast will appear on the Functional Ecology website.

For more information contact Alison Bennett (Alison.Bennett@hutton.ac.uk) or David Giron (david.giron@univ-tours.fr)

Social Media: Follow the latest developments about plant-microbe-insect interactions at the 16th SIP meeting on Twitter.

@IRBI_Tours
@FunEcology



Entomologia, Experimentalis et Applicata

Wiley-Blackwell and the editors of *Entomologia Experimentalis et Applicata* have agreed to publish the proceedings of SIP-16 as a special issue of the journal, as has been the case for previous SIP meetings. The papers to be included will be subjected to the journal's standard reviewing procedures. All contributions accepted for publication will become freely available on the EEA website.

Invited keynote speakers and presenters of oral communications and posters are all invited to submit their review-type or full research papers. Preparation of manuscripts should follow the guidelines of *Entomologia Experimentalis et Applicata* as set out in the Author Guidelines.

Authors may submit the manuscript before or during the symposium.

Manuscripts must be submitted at latest by 6 July 2017.

Entomologia
Experimentalis
et Applicata

WILEY
Blackwell

Guest Editors:
David Giron
Géraldine Dubreuil
Sylvain Pincebourde

Assistant editors:
Franck Dedeine
Elisabeth Huguet
Carlos Lopez-vaamonde
Aurélien Sallé
Jean-Christophe Simon

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The MiDi network

Habitats & Diversity

The MiDi (Habitats & Diversity [Milieux & Diversité]) network is a **Thematic Research Network** in the Centre-Val de Loire Region. An extension of the RESONAT Cluster since 2014, it has brought together the laboratories of INRA, BRGM, the Universities of Tours and Orléans, IRSTEA and CNRS involved in the **observation and management of natural resources**. It develops its activity in close relation with the DREAM cluster.

Its Ambitions

- in the Region, promote **cross-disciplinary** and **integrated** activities in the **BioGeosciences** and the **Human Sciences** on the theme of **interactions between Habitats, Biodiversity and Society;**
- **strengthen the international visibility of the** Region's **academic competences** relating to this theme**;**
- promote implementation in relation with socioeconomic and territorial partners.

Its Scientific & Technical Perimeter

On the basis of the competences present in the Region on habitats, biodiversity and societal dynamics, MIDI has defined 3 directions of activity:

- **The dynamics of natural resources** concerns their composition, functioning and utilisation (economic, social and political dimensions) under conditions of global change.
- **Adaptation mechanisms** of living organisms to variations in habitats subject to anthropic forcing, and the impacts of these adaptations on habitats (retroaction).
- **The technical and social engineering** of habitats and biodiversity, and **decision aids** for the sustainable management of natural resources.

Its key figures

MiDi has forged a network of more than 1500 researchers in the academic world, including **7 research organisations (**INRA, CNRS, IRSTEA, BRGM, MNHN, the Universities of Tours and Orléans), **24 units** and **7 partners** (DREAM cluster, SATT Grand Centre, Intelligence des patrimoines (I-PAT), the Zone Atelier Loire (ZAL), Labex Voltaire, the Natural Regional Park of Loire Anjou Tourraine (PNR LAT), the Conservatory of Natural Areas of Centre-Val de Loire (CEN).

Its actions

1. **Bring the laboratories in the Region that focus on environmental themes to work in a network** so as to facilitate meetings and exchanges between the researchers and the different actors.
2. **Create scientific and technical events of national and international scale** to promote and give prominence to the research carried out in the Region.
3. **Favour interactions between the region's research and socioeconomic activities.** The objective for the academic and socioeconomic worlds and the Region is to permit the **production of scientific knowledge**, **share and disseminate** knowledge to drive the **emergence of new concepts in the environmental sciences**, the emergence of collaborative platforms, and **technology transfers.**

The network's organisation

Contact: www.reseau-midi.fr; Coordination : **Alexia Soussen** alexia.soussen@univ-tours.fr; Management: **Catherine Hénault** (catherine.henault@inra.fr), **Denis Martouzet** (denis.martouzet@univ-tours.fr)

The Federation for Research in Infectiology

The **FéRI**, Federation for research in infectiology, is supported by the Région Val de Loire, and federates the activity of over 300 researchers in the fields of fundamental research, therapeutic applications and public health in order to prevent and cure infectious diseases by developing and using innovative diagnostic and therapeutic methods . Another goal of the FéRI is to highlight research in infectiology to inform the public and to create collaborations with other research domains and industry.

The **FéRI** is recognized by the Ministry of Higher Education and Research.

The **FéRI** is composed of **15 research institutes** specialized in infectiology and animal and human immunity, belonging to the universities of Angers, Limoges, Poitiers, Tours, the INRA, INSERM, CNRS and CHRU. The FéRI is co-directed by **Denys Brand** (INSERM U966, Université of Tours) and **Nathalie Winter** (Infectiologie et Santé Publique Institute, Centre INRA Val de Loire).

The **FéRI** is supported by several experimental platforms:
-Molecular Modelling Platform
-Experimental infectiology platform
-Platform of molecular and cellular biomarkers, microscopy and genome analysis
-Platform of genome and transcriptome analysis
-Platform of surgery and imaging

The **FéRI** also hosts the National reference centre for HIV and the International centre of microbial ressources dedicated to bacterial pathogens.

https://www.infectiologie-regioncentre.fr/

COST Action FA1405

EUROPEAN COOPERATION IN SCIENCE AND TECHNOLOGY

Using three-way interactions between plants, microbes and arthropods to enhance crop protection and production

Crop plants interact with both arthropods and microorganisms, including pests that reduce yields (in Europe up to 20% annually) and mutualists that promote yield. Direct and indirect interactions between microorganisms and arthropods on crops can strongly modify their impacts on yield. For instance, herbivores and pathogens can facilitate each other, causing additional yield loss. On the other hand, beneficial microorganisms can induce defenses that protect plants against herbivores.
There is thus potential to enhance crop production and reduce pesticide use if we can better predict and manage Crop-Arthropod-Microorganism (CAMo) interactions to our advantage. Currently, knowledge of CAMo interactions is limited due to historical separation of the involved research fields.

This COST Action therefore combines existing expertise on CAMo interactions in Europe, from basic and strategic research to agri-R&D companies, and forms an interdisciplinary platform and incubator for research on mechanisms, impacts and utilization of CAMo interactions on crop yield.

The COST Action also seeks to strengthen the careers of both female and young researchers, connect the newest research in the field with its applied use, and develop new monitoring and management support systems and CAMo-based applications.

Chair of the Action: Dr Arjen Biere, Netherlands, Institute of Ecology, Wageningen NL (A.Biere@nioo.knaw.nl)

Coordination: Sabine van Wegen (S.vanWegen@nioo.knaw.nl)

http://www.cost-fa1405.eu/

Scientific Committee

David Giron* - Université François-Rabelais/Centre National de la Recherche Scientifique, France.

Alison Bennett* - James Hutton Institute, United Kingdom.

Matthias Erb* - Université de Bern, Switzerland.

Marcel Dicke* - Wageningen University, The Netherlands.

Marion Harris - North Dakota State University, USA.

Atsushi Kawakita - Kyoto University, Japan.

Carlos Lopez-Vaamonde - Institut National de la Recherche Agronomique, France.

Aurélien Sallé - Université d'Orléans, France.

Jean-Christophe Simon* - Institut National de la Recherche Agronomique/Université de Rennes 1/Agrocampus Ouest, France.

Arthur Woods - University of Montana, USA.

Noah Whiteman - University of California Berkeley, USA.

Organizing Committee

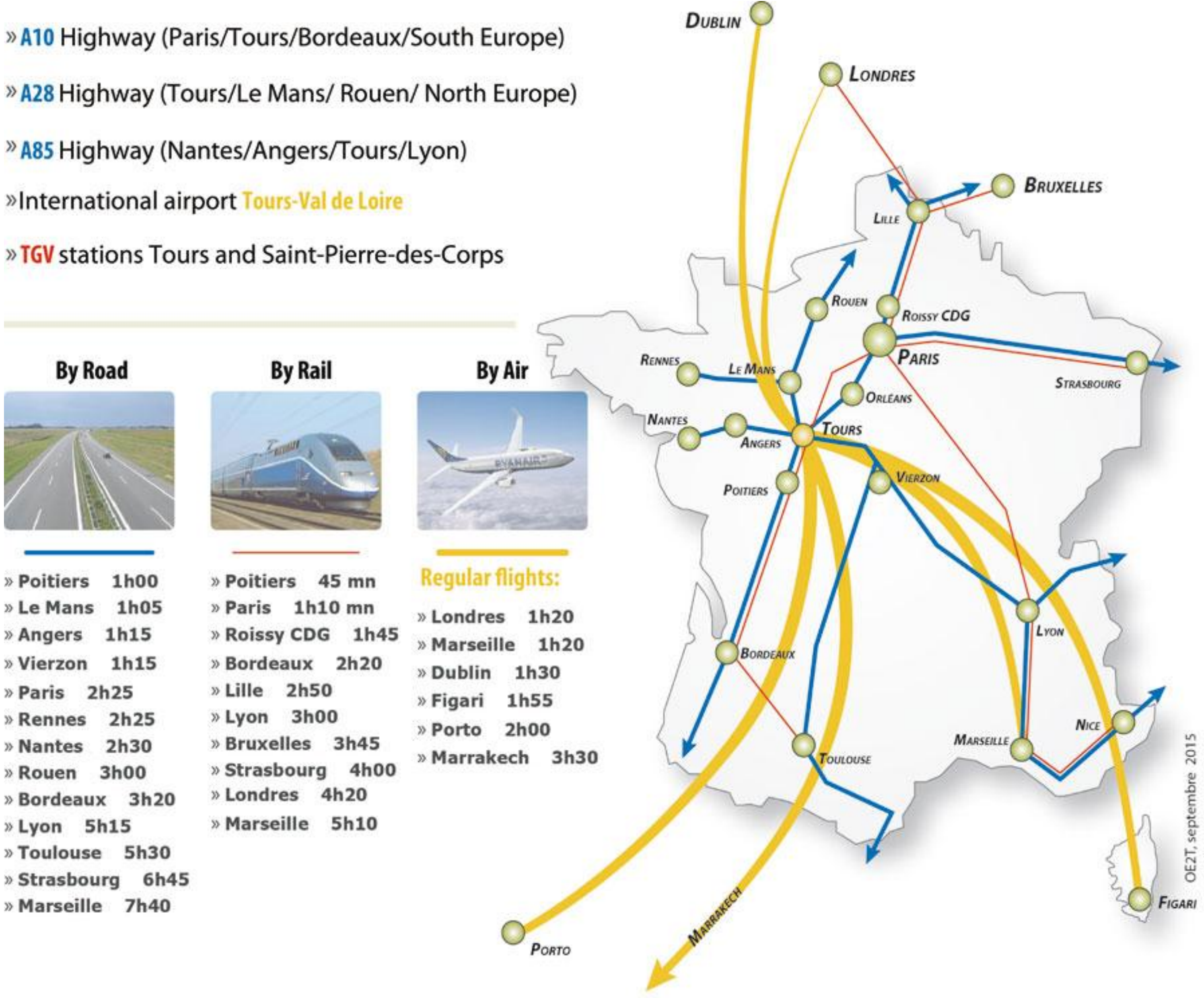
David Giron*, Franck Dedeine*, Géraldine Dubreuil*, Elisabeth Huguet*, Sylvain Pincebourde*, Nathalie Duchesne, Marjorie Tholmont and Wilfried Kaiser* - Université François-Rabelais/Centre National de la Recherche Scientifique, France.

Carlos Lopez-Vaamonde - Institut National de la Recherche Agronomique, France.

Aurélien Sallé - Université d'Orléans, France.

Jean-Christophe Simon* and Akiko Sugio* - Institut National de la Recherche Agronomique/Université de Rennes 1/Agrocampus Ouest, France.

**** COST FA1405 participants***



- » **A10** Highway (Paris/Tours/Bordeaux/South Europe)
- » **A28** Highway (Tours/Le Mans/ Rouen/ North Europe)
- » **A85** Highway (Nantes/Angers/Tours/Lyon)
- » International airport **Tours-Val de Loire**
- » **TGV** stations Tours and Saint-Pierre-des-Corps

By Road

» Poitiers	1h00
» Le Mans	1h05
» Angers	1h15
» Vierzon	1h15
» Paris	2h25
» Rennes	2h25
» Nantes	2h30
» Rouen	3h00
» Bordeaux	3h20
» Lyon	5h15
» Toulouse	5h30
» Strasbourg	6h45
» Marseille	7h40

By Rail

» Poitiers	45 mn
» Paris	1h10 mn
» Roissy CDG	1h45
» Bordeaux	2h20
» Lille	2h50
» Lyon	3h00
» Bruxelles	3h45
» Strasbourg	4h00
» Londres	4h20
» Marseille	5h10

By Air

Regular flights:

» Londres	1h20
» Marseille	1h20
» Dublin	1h30
» Figari	1h55
» Porto	2h00
» Marrakech	3h30

Source : Observatoire de l'Économie et des Territoires de Touraine (OE2T).
http://www.economie-touraine.com.

Located 240 km from Paris, the city of Tours is easily accessible by air, rail or road infrastructure. Tours is accessible from Paris (55 min), Roissy international airport (1h35 min), London (4h20 min), Brussels (3h30 min) and Geneva by high-speed train (TGV), as well as by motorways from Northern Europe, North-Eastern Europe, Spain, Italy and Switzerland. The Tours airport has direct flights to and from London (Ryanair), and is connected with most European capitals through Lyon (Airlinair).

Travelling from outside Europe by air and high speed train (TGV)

To come to Tours, the easiest way is to fly to Paris and then take the high speed TGV train to Tours. The two international Parisian airports (http://www.aeroportsdeparis.fr/en/homepage), Paris-Charles de Gaulle (CDG) and Paris-Orly, are connected to nearly 300 destinations worldwide via about 150 airlines. If flying to Paris-Charles de Gaulle (CDG), there is a direct high speed train connection to Tours through the Saint Pierre-des-Corps station, from which a shuttle train provides easy connection to the city center (http://en.voyages-sncf.com/en/). Public transports (RER https://www.transilien.com/ line B, or le bus direct: http://www.lebusdirect.com/en/ line 1 form Orly and 4 from CDG) also provide easy connection to the center of Paris, from which it is then possible to take a direct train to Tours Centre from Paris Montparnasse train station.

For train reservations from outside of Europe: www.raileurope.com.

Travelling from within Europe

Low cost flights direct to the international airport Tours-Loire Valley (http://www.tours.aeroport.fr/home) provide direct links (https://www.ryanair.com/gb/en/) to London-Stansted, Dublin, Figari, Porto, Marrakech and Marseille. Tours-Loire Valley airport is located only 15-30 minutes from Tours downtown (by car or 15 min walk to Vaucanson Tram station and bus line #2 Tempo to Gare Vinci),

By rail

Tours has two TGV stations: Tours-Centre in the heart of the city and Saint-Pierre-des-Corps, located 5-20 minutes from downtown Tours, accessible via a shuttle train or bus (Fil bleu, line #5 to Parc Grandmont stop at Gare Vinci). Tours is directly connected by high speed train (TGV) to Paris (Montparnasse station; 1h10), Paris Charles de Gaulle Airport (1h45), Lyon, Lille, Strasbourg and Marseille (SNCF), but also Brussels (Thalys) and London (Eurostar). From Paris you can also choose a slower way to discover French landscapes by taking the regional express train (TER) from Austerlitz station (about 2h-2h30). Tours train stations:
-Tours Centre Train Station
Place du Général Leclerc (Square of the Général Leclerc), 37000 Tours
-Saint-Pierre-des-Corps Train Station
67 rue Fabienne Landy (67 Fabienne Landy street), 37700 Saint-Pierre-des-Corps
http://en.voyages-sncf.com/en/
https://www.thalys.com/fr/en
http://www.eurostar.com/uk-en

Tips. There is a shuttle train from Saint-Pierre-des-Corps to Tours after almost every TGV train. The shuttle usually departs from the next platform (you may have to go down the stairs and up again – look for information on screens). When buying a ticket you will be assigned a car and a seat number. If you don't have an electronic ticket don't forget to validate your train ticket before entering the train using yellow boxes available throughout the station.

By road

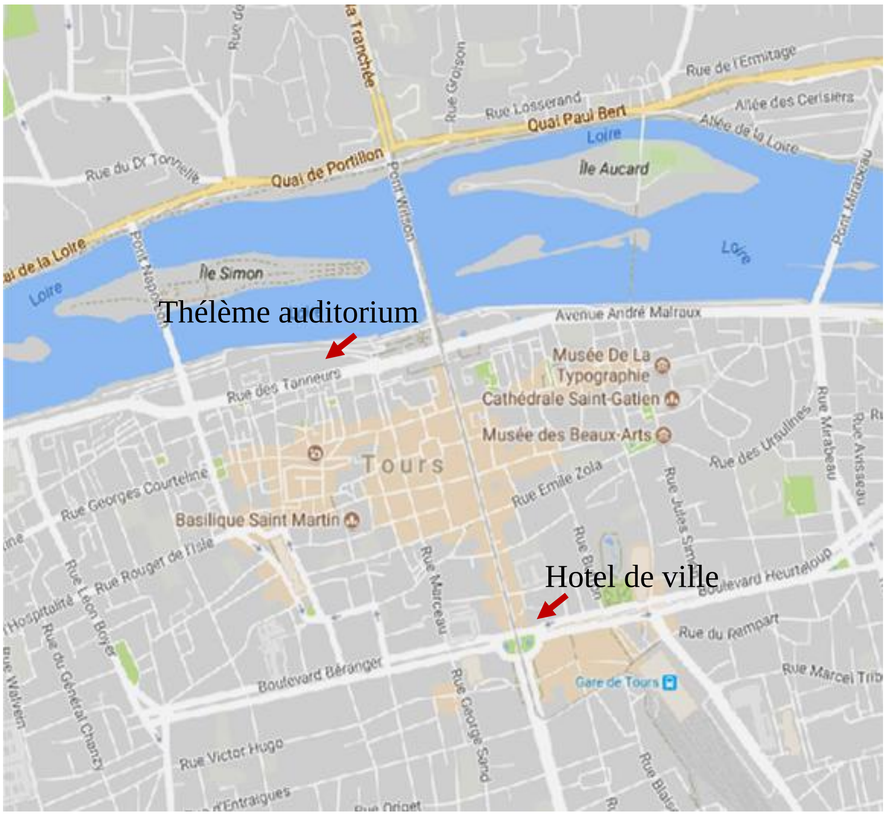
Tours city is at the heart of a motorway junction with the A10 (Paris-Spain), the A28 (Calais-Bayonne) and the A85 (Nantes-Lyon) connecting with the main cities of France. Bus companies (Eurolines, OUIBUS) make the connection between the bus station of Tours and many cities in France and Europe. Other bus companies:
-Eurolines
http://www.eurolines.fr/en/
-OUIBUS
http://www.ouibus.com/
-FLIXBUS
https://www.flixbus.com/

For more details on the Tours bus system:
https://www.filbleu.fr/en/

Tips: Free parking will not be available at the conference site. Public parking with limited parking-time is available throughout the city. Conference hall and opening ceremony are located in the city center at a walking distance from most hotels and the train station. Bus and tramway tickets need to be purchased on platforms before entering any public transport. Don't forget to validate your ticket once you have entered the bus/tramway. Transport to the gala dinner will be provided.

The welcome cocktail, plenary lecture and opening ceremony on Sunday will be held at the **Hotel de ville** (or mairie de Tours). The building is localized in the North-East corner of the place Jean Jaurès.

All conferences and poster sessions will take place at the **Thélème** auditorium, 3 rue des Tanneurs, 37000 Tours. This is located within the university building (site des tanneurs).


Thélème auditorium

Hotel de ville

The two sites are localized in the old center of Tours (or historic center). They are only 10-15 min walk from each other, but the TRAM is also an option in case you don't want to walk. The Hotel de Ville is near the Tours train station (Gare de Tours - 5 min walking distance).

Visit Touraine

For more details on excursions or trips to visit the castles of the Loire Valley :
http://www.tours-tourisme.fr/je-veux/visiter-les-chateaux-de-la-loire

The registration desk will open in the evening of July 2nd (Sunday), at the Hôtel de Ville. A welcome cocktail will be served upon arrival. The plenary lecture will be followed by an opening ceremony where food and drinks will be served in the salle des fêtes.

The registration desk will also be open throughout the conferences at the Thélème auditorium, starting on Monday morning. Please, once you arrive at the conference location, first thing is to register, so that we can give you the abstract book and other important information.

The registration desk will also guide those who will present a poster. Each poster will have a unique number which will be used to identify the place where you need to hang up your poster. This number will be provided at the registration desk. The format of posters is free but we recommend an A0 max (84,1 x 118,9 cm) in vertical orientation only. We do not accept digital posters. There are 2 posters sessions (on Monday and Tuesday). We recommend posters be put up at the morning coffee break or during the lunch break preceding your sessions. All posters from the Monday session will need to be put down before the morning coffee break on Tuesday.

Oral presentations will be 15 minutes long, including questions. All presentations (powerpoint or pdf) of a given session should be uploaded ahead of the session directly on stage. Oral presentations of Monday morning should be uploaded on Sunday evening upon arrival at the registration desk.

Due to recent events we are currently at a high level of security. Tours is a quiet place and there are no reasons to be concerned. However, it is strickly required that **each participant sign the attendance list each day** in case of an emergency.

WIFI will be available for each participant with a personal access code. Each participant should have received login information and code by email. The network is university of Tours (or eduspot). EDUROAM is also available. Please note that the WIFI access is limited to the Theleme auditorium.
A free wifi is also available at different hotspots in the city including the train station, the tourist office, the tramway stations place Jean Jaures and on the Loire riverside next to the Theleme auditorium. Name of the network: WITM

Welcome cocktail, opening ceremony, "wine & cheese" poster session, “saveurs de Loire” poster session, all lunches, and coffee breaks are included in the registration fees and will be served at the venue.

An excursion, followed by the gala dinner, is organized at the Montbazon forteresse on July 5th. A bus will take you around 16:00 in front of the Thélème auditorium, and it will also drive you back to city center. Come to discover a full medieval experience, including an animated dinner that will bring you back at the time of French kings! An entire village is brought to life at day and night, with introduction workshops and staged visits. The potter, the basket maker, the weaver, the dyer, the tailor, the calligrapher, the illuminator, the coin engraver, the candle maker, the blacksmith, the saddler, the stone carver, the herbalist, the shingler, the baker and the crossbowman will welcome you in their workshops.

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The fortress of Montbazon was built in 991 AD at the top of a rocky spur overlooking the river Indre. The Cormery monks complained to the King of France of Foulque Nerra's behaviour, as he had seized their land. He first built a motte-and-bailey-castle – a wooden donjon on a mound – and later replaced it by a stone donjon. This fortified place forms one of the oldest feudal castles in France. The donjon consisted of a 120 feet-high massive tower, 65 feet long and 50 feet wide. Nowadays, the tower is only 90 feet high. The walls are 9 feet-thick at the ground, and 6 feet-thick at the top of the tower. The south and east frontages are supported by buttresses. The edifice was composed of a cellar and three floors, build in wood and organised according to the class system – the nobles living of the upper floor. The last floor was topped by a hip roof. The entrance of the donjon was located on the north side, at 21 feet from the ground, and was reached thanks to a wooden ladder or a handrail.

As Montbazon is incorporated to the kingdom of France, the fortress becomes the property of a number of famous families such as the Mirabeau, Savary, Craon, La Rochefoucauld, and finally passing to the Rohan family, the earls of Montbazon at the eve of the French Revolution. Towards the end of the 16th century, the place has yet experienced deep changes. It was in theses times that Montbazon became one of the twelve duchy-peerages of the kingdom, and the second richest duchy after Orléans. A second castle was built in 1425, facing the 10th century donjon. The kings of France Charles VII and Louis XI regularly sojourned there. However, in 1746, the castle was demolished and its stones were used to divert the bed of the river Indre (the city council square was edified on the remains of the castle).

Excursion and Gala dinner

Montbazon fortress + Banquet: 50 € (http://www.forteressedufauconnoir.com/)
Important: Accompanying persons are welcome to "Excursion + Banquet" but don't forget to pay for them during your registration.

Restaurants & drinks

If you want to eat, take a coffee or a drink, you will find everything you need in the center, near the Loire. Tours's main street (rue Nationale), with its shops, is oriented north/south. The two main areas dedicated to restaurants and bars are located roughly on both sides near the Loire. In the west, Tours's most famous square, with its houses from the Middle Ages, is "la place Plumerau" or "place Plum" as we say here. In this square, you will find some diners but mostly pubs and bars. Do not hesitate to explore the little streets that spread around and choose the mood that best suits you. In the east, the other area where you can eat and drink is the street called "rue Colbert". The mood here is quieter and you essentially come here for small restaurants.

Each summer, we are fortunate to have **"la guinguette",** a place where you can go at any moment of the day to hit the dance floor (in the evening), play chess, enjoy a relaxing read, have a drink, go for a boat ride, or enjoy a film or concert or simply let yourself be surprised. It is easy to find: at the end of the main street (rue Nationale), on the banks of the river Loire, below the bridge "pont Wilson". It is possible with reservation to eat in the restaurant but there are also BBQ sandwiches or boards with meat and cheese and everything you want to drink...

Tips: La guinguette is located next to the Thélème auditorium. Don't forget to attend talks and posters between two drinks at la guinguette ;-)

As restaurants are small, it is better to reserve...
In the area of "place Plumereau", we recommend:
Le Bistrot N'Home (bistro), 11 rue de la Serpe, 37000 Tours, +33 9 81 00 62 21
Le Marché Gourmand (french cuisine), 27 rue du Grand Marché, 37000 Tours, +33 2 74 64 50 38
L'atelier Gourmand (gastronomic cuisine), 37 rue Etienne Marcel, 37000 Tours, +33 2 47 38 59 87La Deuvalière (french cuisine), 18 rue Monnaie, 37000, Tours, +33 2 47 64 01 57
L'Embellie (french cuisine), 21 rue de la Monnaie, 37000, Tours, +33 9 54 61 64 43
Mamie Bigoude (pancake house), 22 Rue de Châteauneuf, 37000 Tours, +33 2 47 64 53 85
Les trois écritoires (bistro), 53 Place du Grand Marche, 37000 Tours, +33 2 47 36 97 35
La maison des halles (authentic french cuisine), 19 Place des Halles, 37000, Tours, +33 2 47 39 96 90

In the area of "rue Colbert", we recommend:
Le Petit Patrimoine (gastronomic cuisine), 58 Rue Colbert, 37000 Tours, +33 2 47 66 05 81
Au lapin qui fume (french cuisine), 90 Rue Colbert, 37000 Tours, + 33 2 47 66 95 49
L'Evidence (gastronomic cuisine), 33 rue Colbert, 37000 Tours, +33 2 47 66 33 08
La souris gourmande (cheese plates), 100 Rue Colbert, 37000 Tours, +33 2 47 47 04 80
Beyrouth (Lebanese restaurant), 60 Rue Colbert, 37000, Tours, +33 2 47 31 94 43
L'escapade (french cuisine), 88 rue Colbert, 37000, Tours, +33 2 47 05 24 81
La réserve (wine bar), 84 Rue Colbert, 37000 Tours, +33 9 84 45 93 09

Outside of town, for an unforgettable experience:
L'auberge du 12ème siècle (tavern from the 12th century – Gastronomic restaurant), 1 rue du Château, 37190 Saché, +33 2 47 26 88 77

Tips: Feel free to ask the organizing committee for good suggestions

Currency

As in most countries of the European Union, the currency in France is the Euro (the “Euro” sign is €- here denoted as EUR). Major credit cards are accepted in most stores, restaurants and hotels.

Tipping

In France you normally "round up" the amount of restaurant bills, by leaving some change on the table.

Weather

Tours enjoys a temperate oceanic climate. In July visitors can expect average temperatures of 24-28 °C during daytime and 13 °C at night. July is generally above average for sunshine and storms are not unusual. Weather Forecast is available here.
(http://www.meteofrance.com/previsions-meteo-france/tours/37000)

Tips: Please note that air conditioning is not usual in most hotels, bars and restaurants.

Electricity

The electrical power supply in France is 220v, 50 Hz, AC.
You may use type E or C plugs

Security measures

Tourists are warmly welcomed in the city of Tours and the Loire Valley, which is considered as quiet and very safe. However usual personal safety should be applied. Bags should not be left unattended in public places. Remember to carry an ID with you.

In case of emergency

Firefighters and Ambulance: 112
Police: 17

	Sunday 2	**Monday 3**	**Tuesday 4**	**Wednesday 5**	**Thursday 6**
08h15-08h30		**Introduction**	**Introduction**	**Introduction**	**Introduction**
		Insect-plant-microbe interactions in forests and agrosystems	**Plant-insect-microorganisms interactions**	**Insect Effectors and plant response**	**Evolutionary genomics**
		Chairs M. Harris A. Sallé	**Chairs** A. Bennett F. Dedeine	**Chairs** G. Dubreuil M. Erb	**Chairs** JC. Simon N. Whiteman
08h30-08h45		**Keynote** D. Thierry	**Keynote** E. Zchori-Fein	**Keynote** I. Kaloshian	**Keynote** N. Whiteman
08h45-09h00					
09h00-09h15					
09h15-09h30		G. Aradottir	A. Bennett	M. Dicke	P. Abbot
09h30-09h45		S. Behmer	A. Biere	G. Felton	*H. Boulain (PhD)*
09h45-10h00		D. Bouchon	*L. Chrétien (PhD)*	*A. Guiguet (PhD)*	M. Karageorgi
10h00-10h15		*A. Cusumano (PhD)*	A. Martinez-Medina	M. Harris	N. Van Dam
10h15-11h15		**Coffee Break** ***sponsored by COST***	**Coffee Break** ***sponsored by COST***	**Coffee Break** ***sponsored by Féri***	**Coffee Break** **sponsored by INRA**
11h15-11h30		P. Fernandez-Conradi	*K. Moisan (PhD)*	R. Kirsch	**Keynote** M. Poulsen
11h30-11h45		J. Garnas	S. Pichon	R. Machado	
11h45-12h00		H. Lingfei	A. Pineda	*M. Stefanov (PhD)*	
12h00-12h15		A. Sallé	A. Smilanich	*C. Stolpe (PhD)*	**Business meeting & Concluding remarks**
12h15-12h30		D. Santos-Garcia	T. Vaello	B. Schimmel	
12h30-14h00		**Lunch** **Sponsored by University of Orléans**	**Lunch** **Sponsored by IRBI**	**Lunch** **Sponsored by Région Centre VL**	**Lunch bags** **Sponsored by University of Tours**
		Community ecology and phylogenetics	**Multitrophic interactions and ecological networks**	**Global change and thermal ecology**	
		Chairs C. Lopez A. Kawakita	**Chairs** M. Dicke E. Huguet	**Chairs** S. Pincebourde A. Woods	
14h00-14h15		**Keynote** A. Kawakita	**Keynote** T. Petanidou	**Keynote** J. Terblanche	
14h15-14h30					
14h30-14h45					
14:45-15:00		E. Frago	*Y. Aartsma (PhD)*	*M. Javal (PhD)*	
15:00-15:15		C. Lopez-Vaamonde	M. Baude	T. Li	
15:15-15:30		E. Poelman	C. Becker	M. Macel	
15h30-15h45		S. Rasmann	N. Borowiec	S. Morin	
15h45-16h00		G. Stone	*M. Cuny (PhD)*	Pincebourde & Woods	
16h00-16h30	**Registration and Welcome cocktail** **sponsored by the city of Tours**	**Coffee Break** **sponsored by CNRS**	**Coffee Break** **sponsored by IRBI**	**Departure for gala dinner**	
16h30-16h45		**Keynote** T. Palmer	*G. Delpon (PhD)*	**Excursion and Gala dinner** **(end ~23h30)**	
16h45-17h00			A. Kergunteuil		
17h00-17h15			D. Lucas-Barbosa		
17h15-17h30	**Opening** - Maire	T. Zuest	*G. Martinez (PhD)*		
17h30-17h45	**Opening** D. Giron	S. Zytynska	*Q. Rusman (PhD)*		
17h45-18h00					
18h00-18h15	**Plenary** L. Dyer	**Poster session 1** **“Wine and Cheese”** ***sponsored by Wiley***	**Poster session 2** **“Saveurs de Loire”** ***sponsored by BES and MIDI network*** **Functional Ecology Podcast**		
18h15-18h30					
18h30-18h45					
18h45-19h00					
19h00-19h15	**Opening ceremony** **sponsored by Tours +**				
19h15-19h30					
19h30-19h45					
19h45-20h00					

Sunday 2nd of July 2017 Hôtel de Ville Tours

16h00	**Welcome and registration** **Welcome cocktail** (sponsored by the city of TOURS)	
17h15	**Maire of Tours**	Opening
17h30	**David Giron** **Arjen Biere**	Opening The COST action FA1405: Using three-way interactions between plants, microbes and arthropods to enhance crop protection and production
18h00	**L. Dyer** ***Plenary Speaker***	Predators, herbivores, and phytochemicals: putting together the scales, nodes, and edges for appropriate hypothesis testing and theory development
19h00-20h00	**Opening ceremony** (sponsored by Tours +)	

Monday 3rd of July 2017 Salle Thélème Tanneurs

08h15 Introduction

Insect-plant-microbe interactions in forests and agrosystems - *COST action FA1405

Chairs M. Harris and A. Sallé

08h30	**Denis Thiery** ***Keynote Speaker***	How to improve grape moth pests control in viticulture. Which research fields should be promoted?
09h15	**Gudbjorg Aradottir**	Cereal aphid feeding behaviour – commonalities and differences depending on aphid species and wheat susceptibility
09h30	**Spencer Behmer**	Insect sterol requirements: a novel target for controlling insect herbivore pests
09h45	**Didier Bouchon**	Phytophagous insects' gut microbiome as facilitator of invasiveness?
10h00	**Antonino Cusumano**	Insect-associated symbionts impact plant-mediated interactions in brassicaceous plants
10h15	Coffee break (sponsored by the COST action FA 1405)	
11h15	**Pilar Fernandez-Conradi**	Fungi reduce preference and performance of insect herbivores on infected plants
11h30	**Jeff Garnas**	Understanding the ecology and evolution of forest insects in an interconnected world
11h45	**Hu Lingfei**	A root herbivore uses a siderophore to locate the most nutritious roots
12h00	**Aurélien Sallé**	Tree-killing aphid dramatically affects bark contents in carbohydrates and nitrogen compounds
12h15	**Diego Santos-Garcia**	Inside out: Are gut bacteria involved in whiteflies' plant adaptation?

12h30 Lunch (sponsored by the University of Orléans)

Community ecology and phylogenetics

Chairs A. Kawakita and C. Lopez-Vaamonde

14h00	**Atsushi Kawakita** ***Keynote Speaker***	Evolution of obligate pollination mutualism in Phyllanthaceae
14h45	**Enric Frago**	Signals of plant phylogeny and plant invasions on thrips diversity along elevational gradients
15h00	**Carlos Lopez-Vaamonde**	Have host plant shifts caused adaptive radiations in leaf-mining moths?

15h15	**Erik Poelman**	Keystone herbivores and the evolution of plant defense
15h30	**Sergio Rasmann**	The unfolding plant growth-defense syndromes along elevation gradients
15h45	**Graham Stone**	Sweet tetra-trophic interactions: multiple evolution of nectar secretion, a defensive extended phenotype in cynipid gallwasps
16h00	Coffee break (sponsored by the CNRS)	
16h30	**Todd Palmer** ***Keynote Speaker***	Costs, benefits and the community ecology of mutualism
17h15	**Tobias Zuest**	Mechanisms and consequences of phytochemical diversification in a rapidly evolving plant clade
17h30	**Sharon Zytynska**	Genetic interactions drive metacommunity species associations in a plant-aphid system
17h45	**Poster session 1 – "Wine and Cheese"** (sponsored by Wiley)	
19h30	Free evening	

Tuesday 4th of July 2017 Salle Thélème Tanneurs

08h15 Introduction

Plant-insect-microorganisms interactions - *COST action FA1405

Chairs A. Bennett and F. Dedeine

08h30	**Einat Zchori-Fein** ***Keynote Speaker*** **(Sponsored by COST)**	Insect symbionts as bio-control agents against phloem-restricted plant pathogens
09h15	**Alison Bennett**	Indirect influences of a belowground microbe on aboveground parasitism of plant herbivores
09h30	**Arjen Biere**	Can beneficial microbes help mitigate plant growth-defense trade-offs under shading?
09h45	***Lucille Chrétien PhD***	Can flowering plants resist insect and pathogen attack? Induction of phytohormones and resistance of plants under multiple attack
10h00	**Samuel Pichon**	Evolutionary stability of beneficial gut microbial communities in wood-feeding termites
10h15	Coffee break (sponsored by the COST action FA1405)	
11h15	**Ainhoa Martinez-Medina**	An integrative 'omics' approach to unravel the mechanisms driving the impact of root symbionts on plant multitrophic interactions
11h30	***Kay Moisan PhD***	Warning or blessing? Volatiles emitted by pathogenic and non-pathogenic fungi affect plant development and resistance to insects
11h45	**Ana Pineda**	Steering soil microbiomes through plant-soil feedbacks to enhance resistance to herbivores
12h00	**Angela Smilanich**	Host range expansion and the insect immune response
12h15	**Teresa Vaello**	Facilitation between aphids and thrips is modulated by parasitization but not by plant-soil feedbacks
12h30	Lunch (sponsored by the Insect Biology Research Institute)	

Multitrophic interactions and ecological networks

Chairs M. Dicke and E. Huguet

14h00	**Theodora Petanidou** ***Keynote Speaker*** **(Sponsored by COST)**	The Aegean revisited: unravelling the Archipelago's "small, great world" through ecological network analysis

14h45	***Yavanna Aartsma PhD***	Parasitoid attraction to herbivore-induced plant volatiles across spatial scales
15h00	**Mathilde Baude**	Quantifying nectar resources for pollinators in Great Britain across the last century
15h15	**Christine Becker**	Plant mediated bottom-up effects of nitrogen and water supply on leafminers and aphids as well as their parasitoids
15h30	**Nicolas Borowiec**	Comparative dynamics of introduced and native parasitoids: the case-study of classical biological control against the chestnut gall wasp in France
15h45	***Maximilien Cuny PhD***	The interactive effects of seed beetles and parasitoids on seed germination and plant performance in wild Lima bean

16h00 Coffee break (sponsored by the Insect Biology Research Institute)

16h30	***Gaël Delpon PhD***	Dynamics of plant-butterfly interaction networks along secondary successions
16h45	**Alan Kergunteuil**	Indirect plant defences do not get high: adaptive differentiation of phytochemistry along elevation gradients drives variations in the strength of plant-mediated trophic cascades
17h00	**Dani Lucas-Barbosa**	Plant life-style determines defensive strategies against insect herbivores, and consequences for plant fitness
17h15	***Gonzalo Martinez PhD***	Preference and performance of an herbivorous true bug: Feeding or laying eggs ?
17h30	***Quint Rusman PhD***	Flowering plants under attack: The generality and specificity of plant-mediated interactions between insect herbivores and flower visitors

17h45 **Poster session 2 – "Saveurs de Loire"** (sponsored by The British Ecological Society and the MIDI network)
Functional Ecology Podcast

19h30 Free evening

Wednesday 5th of July 2017 Salle Thélème Tanneurs

08h15 Introduction

Insect effectors and plant responses

Chairs G. Dubreuil and M. Erb

08h30	**Isgouhi Kaloshian** ***Keynote Speaker***	Aphid-plant interactions: unraveling arsenals used in this arms race
09h15	**Marcel Dicke**	Natural variation in plant responses to combinations of biotic and abiotic stresses
09h30	**Gary Felton**	Multitrophic Manipulation of Herbivore Perception by Plants
09h45	***Antoine Guiguet PhD***	Insights into mechanisms of gall morphogenesis and the origin of gall induction
10h00	**Marion Harris**	Plant Galls Induced by Insects: Lessons from Plant Galls Induced by Bacteria

10h15 Coffee break (sponsored by the Féri)

11h15	**Roy Kirsch**	Biological relevance of pectolytic enzymes in herbivorous beetles
11h30	**Ricardo Machado**	Herbivory-induced jasmonates impact carbon acquisition and thereby constrain plant resistance and defoliation tolerance
11h45	***Martin Stefanov PhD***	Inference of plant-mediated interactions in herbivorous insect communities from time series count data

12h00	***Clemens Stolpe PhD***	Aphids suck their own grave – induced elevated concentrations of cadmium and zinc in phloem exudates of a hyperaccumulator plant lead to negative potentiation effect on *Myzus persicae*
12h15	**Bernardus Schimmel**	Overcompensation of herbivore reproduction through hyper-suppression of plant defenses in response to competition

12h30 Lunch (sponsored by the Région Centre Val de Loire)

Global change and thermal ecology

Chairs S. Pincebourde and A. Woods

14h00	**John Terblanche** ***Keynote Speaker***	Mechanisms and responses of insects to climate stress
14h45	***Marion Javal PhD***	Respiration-based monitoring of metabolic rate following cold-exposure in two invasive Anoplophora species (Cerambycidae) depending on acclimation regime
15h00	**Tao Li**	Long-term effects of elevated CO2, warming and droughts on VOC emission and phenolics production of *Calluna vulgaris* in a temperate heath ecosystem
15h15	**Mirka Macel**	Rapid evolution of a range expanding plant
15h30	**Shai Morin**	Projecting pest population dynamics under global warming: the combined effect of inter- and intra- annual variations
15h45	**Pincebourde/Woods**	Extended phenotypes and global change biology

16h00 Departure for excursion and gala dinner

16h30 Montbazon Forteresse

23h30 Departure from gala dinner

Thursday 6th of July 2017 Salle Thélème Tanneurs

08h15 Introduction

Evolutionary genomics

Chairs JC Simon and N. Whiteman

08h30	**Noah Whiteman** ***Keynote Speaker***	Breaking bad: The evolution of herbivory in Drosophilidae
09h15	**Patrick Abbot**	Transcriptional profile and differential fitness across a cardenolide gradient in a specialist milkweed insect reveal the costs of response
09h30	***Hélène Boulain PhD***	Evolutionary analyses of a new quantitative catalogue of candidate secreted salivary effectors in *Acyrthosiphon pisum*
09h45	**Marianthi Karageorgi**	Olfactory specialization contributes in the making of the fruit pest *Drosophila suzukii*
10h00	**Nicole Van Dam**	Ecogenomics analysis of *Solanum dulcamara* reveals chemical diversity in glycoalkaloids related to slug resistance

10h15 Coffee break (sponsored by the INRA)

11h15	**Michael Thomas-Poulsen** ***Keynote Speaker***	Novel insights into symbiotic paths to sustainable agriculture

12h00 Business meeting and Concluding remarks

12h30 Lunch bags (sponsored by the University of Tours)

14h00 End of the meeting

Welcome and Plenary Session

Sunday 2nd of July 18h Hôtel de Ville

16h00	**Welcome and registration** **Welcome cocktail** (sponsored by the city of TOURS)	
17h15	**Maire of Tours**	Opening
17h30	**David Giron** **Arjen Biere**	Opening The COST action FA1405: Using three-way interactions between plants, microbes and arthropods to enhance crop protection and production
18h00	**L. Dyer** ***Plenary Speaker***	Predators, herbivores, and phytochemicals: putting together the scales, nodes, and edges for appropriate hypothesis testing and theory development
19h00-20h00	**Opening ceremony** (sponsored by Tours +)	

Plenary

Predators, herbivores, and phytochemicals: putting together the scales, nodes, and edges for appropriate hypothesis testing and theory development.

Lee Dyer[1]*

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Thousands of important chemically mediated trophic interactions have been described in great detail since thoughtful papers from Brower (1958); Fraenkel (1959); Hairston, Smith and Slobodkin (1960); Ehrlich and Raven (1964); Berenbaum (1978); and Price (1980) provided elegant theoretical frameworks for elucidating simple food webs that are tied together by chemistry. The empirical byproducts of these theoretical advances produced a wealth of good science and yielded benefits such as a better understanding of the diversification of plants and insects, guiding principles for pest control in agriculture, insight into synergistic interactions between molecules in mixtures, wonderful natural history stories, and productive collaborations between chemists and ecologists. This literature is lacking a few important components and I will discuss three of these gaps in knowledge. First, there has been confusion and disagreement about local and regional consumer diet breadth in these tritrophic webs. Second, there are no consistent methods for documenting the richness and abundance of these interactions in local communities and specific habitats, thus we are left with messy collections of data that we call food webs. Third, there has been an unjustified focus on individual plant metabolites or on crude measures of broad classes of compounds as the most important mediators of multitrophic interactions. I will discuss new methods for documenting chemically mediated interaction diversity at different scales and will show results from models, observational data, and experiments, demonstrating that local and regional interaction diversity is affected by consumer diet breadth and by diverse phytochemical mixtures.

Keywords: interaction diversity, phytochemical diversity, specialization, networks, scale

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Insect-plant-microbe interactions in forests and agrosystems
*COST action FA1405

Monday 3rd of July 2017 Salle Thélème Tanneurs

08h15 Introduction

Insect-plant-microbe interactions in forests and agrosystems
Chairs M. Harris and A. Sallé

08h30	**Denis Thiery** ***Keynote Speaker***	How to improve grape moth pests control in viticulture. Which research fields should be promoted?
09h15	**Gudbjorg Aradottir**	Cereal aphid feeding behaviour – commonalities and differences depending on aphid species and wheat susceptibility
09h30	**Spencer Behmer**	Insect sterol requirements: a novel target for controlling insect herbivore pests
09h45	**Didier Bouchon**	Phytophagous insects' gut microbiome as facilitator of invasiveness?
10h00	**Antonino Cusumano**	Insect-associated symbionts impact plant-mediated interactions in brassicaceous plants
10h15	Coffee break (sponsored by the COST action FA 1405)	
11h15	**Pilar Fernandez-Conradi**	Fungi reduce preference and performance of insect herbivores on infected plants
11h30	**Jeff Garnas**	Understanding the ecology and evolution of forest insects in an interconnected world
11h45	**Hu Lingfei**	A root herbivore uses a siderophore to locate the most nutritious roots
12h00	**Aurélien Sallé**	Tree-killing aphid dramatically affects bark contents in carbohydrates and nitrogen compounds
12h15	**Diego Santos-Garcia**	Inside out: Are gut bacteria involved in whiteflies' plant adaptation?

12h30 Lunch (sponsored by the University of Orléans)

Keynote

How to improve grape moth pests control in viticulture. Which research fields should be promoted?

Denis Thiéry[1*], Fanny Vogelweith[2] and Jérôme Moreau[3]

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2- Abteilung Evolutionsbiologie, Johannes Gutenberg-Universität Mainz, Institut für Zoologie, 55128 Mainz, Germany
3- Université de Bourgogne, Equipe Ecologie-Evolution, UMR 6282 Biogéosciences, 6 Bd Gabriel, 21000 Dijon, France

Lepidopterans larvae are most exclusively phytophagous and several tortricid moth species cause severe damages to fruit production such as orchards and grapes. In viticulture, the two moths *Eupoecilia ambiguella* and *Lobesia botrana* are considered major pests in European viticulture and *L. botrana* recently invaded the American vineyards.

The larvae of these species attack the grape bunch from spring to autumn, cause direct losses and also qualitative deviation to wines, but they can also favour the development of fungi responsible of the well-known rots and may produce harmful toxins to humans like ochratotoxins. These tortricids moths have existed for a long time in viticulture, *E. ambiguella* being described as early as in the bible and roman viticulture. The other species *L.botrana* is currently the species, which is colonizing new viticulture areas. It for example invaded American viticulture a few years ago.

To drastically reduce insecticide use in viticulture, several Integrated Pest Management control methods have been developed against these pests, involving mating control, parasitoids/predators release and environmental control based on practices and landscape management. In this present talk we attempted to review the different interactions between the grape cultivars and these two pests.

In these species, the different cultivars of grapes affect life history traits, such as reproduction and immune defence, but also the parasitism success of parasitoids. Recent data also show how the landscape architecture and the grape training practices influences the activity of natural enemies. Research on trophic networks around grapes and these pests are now investigated in more detail. The effect of global warming on the immune systems and reproductive output are now investigated on these species with the perspective of future application in the biological control of these pests.

Many factors influence the biological control of *L. botrana*, depending on coevolution mechanisms between plant-pest and pest-parasitoids in the context of tritrophic interactions. Understanding factors that cause varying host/prey quality is crucial to avoid unexpected failures in biological control.

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Cereal aphid feeding behaviour –commonalities and differences depending on aphid species and wheat susceptibility.

Gudbjorg Aradottir *† 1, Amma Simon 1, Beant Singh 1, 2, Emmanuel Ziramba 3, Lucas Bruguier 1, Alexander Greenslade 1, Suzanne Clark 1, Janet Martin 1, Lesley Smart 1

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Cereal aphids can cause significant problems for farmers, affecting yield directly by feeding and indirectly by spreading viruses, such as the barley yellow dwarf virus. For some aphid species, such as the Russian wheat aphid (*Diuraphis noxia*) resistant varieties are commercially available, whereas for other aphid species in cereals, control is mainly via insecticide applications. We have studied the development and feeding behaviour of three cereal aphid species, *Rhopalosiphum padi*, *Sitobion avenae* and *D. noxia* on wheat lines ranging from modern elite varieties, landraces and wild relatives. This has been done using laboratory bioassays and the Electrical Penetration Graph. The main focus has been on studying the difference in feeding behaviour on lines differing in susceptibility or resistance to cereal aphids as well as how other factors, such as mycorrhizal fungi can affect how aphids feed. Here we present results showing how aphid feeding behaviour differs depending on aphid species, host-plant susceptibility and mycorrhizal association. We discuss possible explanations for these differences and implications for aphid control and management in agro-ecosystems.

Keywords: Aphid, wheat, *Rhopalosiphum padi*, *Sitobion avenae*, *Diuraphis noxia*, insect, plant interactions, feeding behaviour

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Insect sterol requirements: a novel target for controlling insect herbivore pests

Ivy Chen [1], Keyan Zhu-Salzman [1], Robert Grebenok [2], Spencer Behmer *† [1]

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[2] Canisius College – United States

All insects require a dietary source of sterol, which is used primarily in cell membranes and as a precursor to molting hormone. Cholesterol is the most abundant sterol found in insects, but it is rare in plants, so plant-feeding insects generate cholesterol by metabolizing ingested plant sterols. However, plant-feeding insects are often limited in terms of which sterols can be converted to cholesterol. Exploiting sterol metabolic constraints in insects represents a novel way to potentially control insect herbivores that feed on economically important agricultural plants. One way to attack insect sterol metabolic constraints is to modify the sterol profile of plants, to increase the expression of sterols that insect herbivores cannot readily convert to cholesterol. Here we use an RNAi approach to silence an enzyme in the plant sterol biosynthetic pathway in Arabidopsis and report its effects on the green peach aphid.

Keywords: nutrition, sterol, aphid, Arabidopsis

*Speaker, †Corresponding author: s-behmer@tamu.edu

Phytophagous insects' gut microbiome as facilitator of invasiveness?

Marie-Caroline Lefort [1,2], Travis Glare [2], Didier Bouchon [3*], Stéphane Boyer † [1,2]

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In phytophagous insects, dispersal ability, environmental tolerance, phenotypic plasticity and their associated epigenetic drivers are critical determinants of invasion success. These attributes can potentially be modified through the action of gut bacteria and yet the role of the gut microbiome in invasion success remains largely unexplored. As part of our new international research project MADII (Microbiome As Driver of Insect Invasiveness), we used Next Generation Sequencing (NGS) technologies to interrogate the role of gut microbial communities in driving invasiveness in phytophagous insects. We analysed the diet and the gut microbiome composition of two closely related scarab beetles from New Zealand, the invasive *Costelytra zealandica* (White) and the non-invasive *C. brunneum* (Broun). Significant differences were observed in the gut microbial composition between the two species. In addition, intraspecific differences were also observed within the invasive species. Specimens from different ecotypes (from native grassland, vineyard and exotic pastures) and which correspond to putative host-races based on feeding preferences, displayed significant differences in their diet and in their gut microbiome. Our results suggest that gut microbiome in Costelytra beetles is influenced by diet and phylogeny. In this presentation we will discuss the mode of transmission of the different group of bacteria discriminating the model species and ecotypes studied and discuss their possible role driving these insects' invasiveness. We will discuss the role of the gut microbiome in insect invasiveness as well as its potential implications for pest control and biosecurity.

Keywords: Biological control, phytophagous insects, invasive species, high throughput DNA sequencing, genomics

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Insect-associated symbionts impact plant-mediated interactions in brassicaceous plants

Antonino Cusumano *† 1, Marcel Dicke 1, Erik Poelman 1

1 Wageningen University and Research – Netherlands

The importance of mutualistic symbioses is increasingly recognized in plant responses to herbivory as well as in plant-mediated interactions. It is well established that beneficial microbes such as mycorrhizal fungi and plant growth-promoting bacteria can play a role in plant responses to herbivory. Symbionts associated with herbivorous insects are also known to affect the way the herbivore interacts with its food plant by manipulating plant-physiology for the benefits of their herbivore hosts. However the role of insect-associated symbionts has received less attention in a multi-trophic perspective. Here, we will address the effects of symbionts associated with insects at different positions in the community structure. Using as model system a cabbage-based food-web network, we show that insect-associated symbionts induce phenotypic changes in the plant, with consequences for other insect community members. We argue that insect-associated symbionts can play an important role in plant-mediated interactions highlighting a fascinating complexity of terrestrial-ecological networks.

Keywords: insect, associated symbionts, plant, mediated interactions, multitrophic perspective

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Fungi reduce preference and performance of insect herbivores on infected plants

Pilar Fernandez-Conradi *[1], **Hervé Jactel** [1], **Cécile Robin** [1], **Ayco Tack** [2], **Bastien Castagneyrol** [1]

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Although insect herbivores and fungal pathogens frequently share the same individual host plant, we lack general insights in how fungal infection affects insect preference and performance. We addressed this question in a meta-analysis of 1,113 case studies gathered from 101 primary papers that compared preference or performance of insect herbivores on control vs. fungus infected plants. Generally, insects preferred, and performed better on, non-infected plants, regardless of experimental conditions. Insect response to fungus infection significantly differed according to fungus lifestyle, insect feeding guild and the spatial scale of the interaction (local/distant). Insect performance was reduced on plants infected by biotrophic pathogens or endophytes but not by necrotrophic pathogens. For both chewing and piercing-sucking insects, performance was reduced on infected plants when interactions occurred locally but not distantly. In plants infected by biotrophic pathogens, both preference and performance of herbivores were negatively impacted, whereas infection by necrotrophic pathogens reduced herbivore preference more than performance and endophyte infection reduced only herbivore performance. Our study unequivocally demonstrates that fungi are key drivers of plant-herbivore interactions, suggesting both direct and plant-mediated effects of fungi on insect's behavior and development.

Keywords: biotrophic pathogens, endophytes, necrotrophic pathogens, plant defense, plant, mediated indirect interactions, tripartite interactions

*Speaker: pilar.fernandez-conradi@inra.fr

Understanding the ecology and evolution of forest insects in an interconnected world

Jeff Garnas * [1,2], **Michael Wingfield** [2], **Bernard Slippers** [2,3]

[1] University of New Hampshire (UNH) – Durham, New Hampshire, United States
[2] Forestry and Agricultural Biotechnology Institute (FABI) – Hatfield, Pretoria, South Africa
[3] University of Pretoria Department of Genetics (UP Genetics) – Pretoria 0002, South Africa

The widespread application of simple and affordable tools for molecular reconstruction of invasion patterns has brought with it an emerging understanding that the biogeography, introduction history and subsequent movement and spread of many invasive insect species is far more complex than previously understood. For a number of invasive alien insects, there is strong accumulating evidence that multiple introductions, complex global movement, and population admixture within the invasive range are common. This is particularly true in forested ecosystems where regionally dominant tree species (i.e., Pinus, Eucalyptus and Acacia) are increasingly cultivated and/or adventive worldwide, where these trees encounter novel biotic communities and stressful abiotic conditions. This forms a backdrop characterized by diverse evolutionary contexts and high global connectivity that strongly impacts both propagule pressure, as well as the ecology and evolution of associated insect pests in both the native and exotic ranges of host trees. We highlight key aspects of this phenomenon with respect to insects as drivers of forest pestilence, including 1) the role of admixture and frequent interchange of genetic material among discrete parts of the exotic range, and 2) the acquisition and exchange of novel symbionts. We use examples from across the recent and historical literature together with primary research on a number of plantation pests, particularly the globally invasive European woodwasp (*Sirex noctilio*), to highlight the consequences of elevated global connectivity for the ecology and evolution of invasive insect pests. We argue that invasive dynamics and impacts must increasingly be understood in the context of the global network rather than as isolated regional phenomena.

Keywords: *Sirex noctilio*, invasion biology, global change, invasion genetics, insect, fungal interactions, novel associates

*Speaker: jeff.garnas@unh.edu

A root herbivore uses a siderophore to locate the most nutritious roots

Hu Lingfei [*] [1], **Robert Christelle** [1], **Bühler Bettina** [1], **Ye Meng** [1], **Erb Matthias**[†] [1]

[1] Institute of Plant Sciences, University of Bern – Switzerland

Benzoxazinoids (BXs) are the predominant class of defensive metabolites in cereals. Our previous work revealed that the specialist root herbivore, *Diabrotica virgifera* (the western corn rootworm, WCR) can tolerate BXs and use them to locate nutritious tissues. However, it remained unknown, which BXs are used as signposts by the larvae. Screening BX-deficient mutants suggested that DIMBOA or DIMBOA-Glc may be responsible for the observed foraging behavior. However, both compounds were inactive when tested *in vitro*. As DIMBOA is known to chelate with iron, we investigated the possibility that WCR may use this siderophore for orientation. In choice experiments, WCR larvae were attracted to DIMBOA-Fe, and DIMBOA-Fe was sufficient to restore the attractiveness of BX-deficient plants. Furthermore, DIMBOA-Fe application was sufficient to misdirect WCR larvae to non-preferred primary roots. Our results show that WCR uses a siderophore to locate the most nutritious tissues. The direct and indirect benefits of foraging for roots, which produce high amounts of DIMBOA-Fe are currently under investigation.

Keywords: maize, benzoxazinoids, western corn rootworm, foraging behavior, siderophore

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Tree-killing aphid dramatically affects bark contents in carbohydrates and nitrogen compounds

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Aphids can affect the growth or architecture of their host-trees, but rarely challenge their survival. Nonetheless, the woolly poplar aphid, *Phloeomyzus passerinii*, can kill healthy, mature poplars during outbreaks. Trees fail to budbreak and flush their leaves in the spring following a severe infestation. This insect develops on poplar trunks, where it induces galls, which accumulate amino acids and deplete starch content in the bark tissues. Here, we hypothesized that an infestation may then affect carbohydrates and nitrogen compounds allocations and consequently compromise the spring reactivation of trees. The bark contents of non-structural carbohydrate (NSC) and non-structural nitrogen compounds (NSNC) were quantified in autumn for poplars exhibiting different levels of infestation and located in two distant stands. In one stand, NSC and NSNC contents in the bark were also quantified in spring and the damage level in the crowns were evaluated. In both stands, the infestation dramatically reduced the NSC and NSNC contents in autumn, especially starch and protein contents. While the drop in protein content was not related to infestation duration, the starch content gradually decreased when infestation duration increased. The infestation effect on starch content was still detectible in spring, after reserves had been mobilized for the spring reactivation. Starch content in autumn and spring was strongly positively correlated with crown damage level. These results suggest that poplars infested by *P. passerinii* may die from carbon reserves deficiency, which would be an unprecedented situation for tree-aphid and tree-gall inducing insects interactions. Further experiments monitoring seasonal dynamics of NSC and NSNC reserves in different organs of infested trees should be conducted to validate this hypothesis. The results also suggest that the starch content in the bark of infested trees, in autumn, might be used as a predictor of tree survival.

Keywords: gall, inducing insect, *Phloeomyzus passerinii*, Populus, reserves allocation, resources mobilization

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Inside out: Are gut bacteria involved in whiteflies' plant adaptation?

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Polyphagous insects require an ability to overcome different sets of host plant defense compounds. In general, during host-plant switching, there is a quick response of the insect, which shows a reduced performance that only rebounds few generations later. Natural selection (a slow process) seems not to be the main force driving this relatively short-term adaptation. Indeed, phenotypic plasticity and host-gut bacteria interactions are fast processes that could be involved in the host switching process. Gut-associated bacteria can help the host by processing the food and/or degrading the plant's defense compounds. In addition, bacteria can acquire new genetic material to deal with new environmental conditions.

The whitefly *Bemisia tabaci*, a tiny phloem-feeder, is considered an important polyphagous pest species. Reported microbiomes of *B. tabaci* are dominated by bacterial endosymbionts. However, because insects' gut microbiota can play a major role in host-plant adaptation and are mainly acquired from the diet/environment, we hypothesized that *B. tabaci* might acquire environmental bacteria that can provide different benefits/costs related to host adaptation. Accordingly, our goal was to explore the putative role of gut bacteria in the plant-adaptation process of *B. tabaci* under field conditions.

We conducted a field-like assay by following the adaptation process of a *B. tabaci* population switching from watermelon (suitable host) to pepper (unsuitable) along four generations. Each generation, we collected samples for gut dissections (cDNA 16S rRNA amplicons) and performance assays (offspring survival). Amplicons were generated using a blocking strategy to decrease the endosymbionts' load and analyzed with USEARH and phyloseq.

Our results show that *B. tabaci* adaptation to pepper took 2-3 generations but also some microbiome differences between watermelon/pepper populations. Genera significantly associated with watermelon or pepper diets and with generational time were identified. These data suggest that gut bacteria might help *B. tabaci* to adapt to new host plants.

Keywords: *Bemisia tabaci*, Insect, plant interaction, Gut microbiota, Adaptation process, Amplicon sequencing

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Community ecology and phylogenetics

Monday 3rd of July 2017 Salle Thélème Tanneurs

Community ecology and phylogenetics Chairs A. Kawakita and C. Lopez-Vaamonde		
14h00	**Atsushi Kawakita** ***Keynote Speaker***	Evolution of obligate pollination mutualism in Phyllanthaceae
14h45	**Enric Frago**	Signals of plant phylogeny and plant invasions on thrips diversity along elevational gradients
15h00	**Carlos Lopez-Vaamonde**	Have host plant shifts caused adaptive radiations in leaf-mining moths?
15h15	**Erik Poelman**	Keystone herbivores and the evolution of plant defense
15h30	**Sergio Rasmann**	The unfolding plant growth-defense syndromes along elevation gradients
15h45	**Graham Stone**	Sweet tetra-trophic interactions: multiple evolution of nectar secretion, a defensive extended phenotype in cynipid gallwasps
16h00	Coffee break (sponsored by the CNRS)	
16h30	**Todd Palmer** ***Keynote Speaker***	Costs, benefits and the community ecology of mutualism
17h15	**Tobias Zuest**	Mechanisms and consequences of phytochemical diversification in a rapidly evolving plant clade
17h30	**Sharon Zytynska**	Genetic interactions drive metacommunity species associations in a plant-aphid system

Keynote

Evolution of obligate pollination mutualism in Phyllanthaceae

Atsushi Kawakita [1]*

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The myriad of ways by which angiosperms accomplish outcrossing demonstrate the intensity of the struggle they face to secure reliable pollinators. We recently discovered a novel example of highly coevolved mutualism between trees/shrubs of Phyllanthaceae and nocturnal moths of the genus Epicephala (Gracillariidae). In the Old World tropics, roughly 500 species of Phyllanthaceae are pollinated by specialized Epicephala seed parasites that lay eggs in flowers and whose larvae feed on the developing seeds. Remarkably, the pollinating moths actively collect pollen on male flowers with their proboscises and use it to pollinate female flowers to secure food for their seed-feeding larvae. In most cases, each Phyllanthaceae species has its own pollinator Epicephala species, and this high specificity is mediated by floral scent, which the pollinators use to locate host flowers in the dark. Phylogenetic analysis of plants and moths suggest that Epicephala pollination evolved at least five times independently in Phyllanthaceae, after the origin of pollination behavior in Epicephala 25 million years ago. This mutualism is maintained because a single moth larva only destroys a fraction of the seeds produced in each fruit, but why do moths not evolve to eat more seeds, driving the mutualism to collapse? We found that plants selectively abort flowers with heavy egg load, thereby limiting the evolution of 'cheaters' that overexploit plant resources. Such a 'sanction' mechanism by hosts may provide a general explanation for the long-term persistence of potentially disruptive mutualisms such as the Phyllanthaceae–Epicephala mutualism.

Keywords: mutualism, pollination, floral scent, seed parasite, host specificity, Phyllanthaceae, Gracillariidae

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Signals of plant phylogeny and plant invasions on thrips diversity along elevational gradients

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Abiotic factors and interactions with host plants can determine the diversity and composition of herbivorous insect communities. To explore these questions, elevational gradients are increasingly used to assess the effect of abiotic factors on insect communities because several variables such as temperature covary with elevation. The phylogenetic composition at the plant layer is also important in these communities because herbivorous insects tend to feed on a few, and often related, host plant species. In this study we sampled thrips (Thysanoptera) on different plant species along replicated elevational gradients in Reunion island, a French overseas territory in the Indian Ocean. Although this island is a diversity hotspot considered as a UNESCO world heritage, its diversity is greatly threatened by invasive plant species, which mostly colonise low altitude areas. We hypothesise that thrips diversity and community composition will (i) vary with elevation, and will depend (ii) on whether the host plant is exotic or native, and (iii) on the phylogenetic structure of the plant community. We have found that invasive plant species harbour an important diversity of thrips, and that particular thrips species may find refuges in native plants that colonise high elevations. Despite these evidences, plant phylogenetic signals and elevation were weak predictors of community structure and diversity in this group. Our results reveal intricate interactions between herbivores, the distribution of their host plants, and abiotic conditions, and emphasise the need of experimental work to better understand the mechanisms underlying the patterns observed.

Keywords: community ecology, trophic, web, elevational gradient, invasive plant, thrips

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Have host plant shifts caused adaptive radiations in leaf-mining moths?

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Flowering plants and their associated herbivorous insects comprise a large proportion of terrestrial biodiversity. Therefore, insights into the mechanisms of diversification of those groups would increase our understanding of the evolution of big chunks of this terrestrial biodiversity. An attractive explanation for the enormous diversity of phytophagous insects and plants is ecological speciation, a process by which a shift in host plant within an ancestral species causes the divergence into two new sister species, each adapted to feed on different host plants. However, the relative importance of host plant shifts in the speciation process of herbivorous insects is an area of debate. Here we test the hypothesis that host plant families constitute new adaptive zones, so shifting to them would lead to adaptive radiation (including increased rates of diversification). To test this hypothesis, we studied the diversification of two groups of leaf-mining moths: pygmy leaf-mining moths (Nepticulidae) and leaf-blotch mining moths (Gracillariidae: Lithocolletinae). We inferred phylogenies based on eight genes for 335 species of Lithocolletinae and 645 species of Nepticulidae, which encompasses approximately 50% of their known diversity. Using state-speciation-extinction analyses next to a Bayesian approach we found that as the climate cooled since the Cretaceous, overall diversification rates decreased. Additionally, we found that in both groups there have been two significant shifts in diversification with very similar timing. The diversification rates of the leaf-miners are significantly higher for groups that feed on Fagaceae or Rosaceae, but not for those feeding on Fabaceae, even though they also constitute an important host family. Our findings indicate that global temperatures influence 'baseline' diversification rates but also that evolutionary events such as the Miocene diversification of plants in temperate climate have led to the present diversity of leaf-miners.

Keywords: Adaptive radiation, leaf, miners, angiosperms, Diversification rate shifts, Multi state, speciation, extinction model

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Keystone herbivores and the evolution of plant defense

Erik H. Poelman *† 1, **André Kessler** 2

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Plants need to defend themselves against a diverse and dynamic herbivore community. Such communities may be shaped by keystone herbivores that through their feeding alter the plant phenotype as well as the likelihood of attack by other herbivores. Not only may these herbivores have a large effect on the interaction network structure and insect assembly on individual plants, these effects of keystone herbivores may have associated fitness consequences for the plant. In a field study on *Brassica nigra* and its insect community, we identified that caterpillars of *Pieris rapae* may qualify as keystone herbivores. Induced responses to feeding by *P. rapae*, but not to the aphid *Brevicoryne brassicae*, caused plants to be colonized earlier and more frequently by other insect herbivores and the indirect effect of *P. rapae* herbivory on community assembly negatively affected plant fitness. Thereby, *P. rapae* may be considered a dominant agent of selection on plant defense traits by its large indirect effect on plant fitness that overarches its direct effect on plant fitness. Merging the keystone herbivore concept with plant fitness and trait selection frameworks will provide an approach to identify which herbivores drive selection in complex multispecies interactions.

Keywords: plant mediated interactions, insect community, induced plant defense, diffuse evolution

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The unfolding plant growth-defense syndromes along elevation gradients

Sergio Rasmann *† [1], **Emmanuel Defossez** [1], **Loic Pellissier** [2], **Holger Danner** [3], **Martha Serrano** [4], **Nicole Van Dam** [5]

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The full understanding of leaf economics that drives plant investment of carbon and nutrients requires including variation in abiotic, but also biotic interactions such as herbivory. We analysed leaf functional traits related to growth, as well as constitutive and inducible direct and indirect defences against herbivores across 15 species of Cardamine (Brassicaeae), that together have colonized the whole elevation gradient of the Alps. In a phylogenetic comparative framework, we explored the variation of the geometrical shape of plant strategies (i.e. the functional space of growth and defence) across the full abiotic and biotic variation of the elevation gradient. We found that Cardamine species set themselves along; 1) a high elevation syndrome of slow growth- high constitutive defences where climatic conditions are cold and wet and herbivory is rare, 2) a mid-elevation syndrome of high biomass (high competitive abilities) - high nitrogen-low levels of defences in resource-rich forested habitats, and 3) a low elevation syndrome of fast-growth and high inducibility of defences in hot and dry habitats and high herbivore pressure. We thus argue that ecological gradients shape variation in both biotic and abiotic factors, in turn shaping plant functional spaces to converge into stable plant-growth defence syndromes within each elevation zone.

Keywords: habitat filtering, glucosinolates, volatile organic compounds, ecological gradients, climate

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Sweet tetra-trophic interactions: multiple evolution of nectar secretion, a defensive extended phenotype in cynipid gallwasps

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Many herbivores employ reward-based mutualisms with ants to gain protection from natural enemies. We examine the evolutionary dynamics of a tetra-trophic interaction in which gallwasp herbivores induce their host oaks to produce nectar-secreting galls, which attract ants that provide protection from parasitoids. We show that, consistent with other gall defensive traits, nectar secretion has evolved repeatedly across the oak gallwasp tribe and also within a single genus (Disholcaspis) that includes many nectar-inducing species. Once evolved, nectar secretion is never lost in Disholcaspis, consistent with high defensive value of this trait. We also show that evolution of nectar secretion is correlated with a transition from solitary to aggregated oviposition, resulting in clustered nectar-secreting galls, which produce a resource that ants can more easily monopolize. Such clustering is commonly seen in ant guard mutualisms. We suggest that correlated evolution between maternal oviposition and larval nectar-induction traits has enhanced the effectiveness of this gall defense strategy.

Keywords: cynipid, gall, nectar, ant, multitrophic, mutualism

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Keynote

Costs, benefits and the community ecology of mutualism

Todd Palmer [1]*

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Mutualisms are species interactions of reciprocal benefit, and are often studied from the perspective of these benefits. Yet many mutualisms also involve costs, which are much less well-understood. In this talk I present results from recent field work exploring these costs in a widespread ant-plant mutualism in East Africa, and argue that a more explicit accounting of costs can help us to better understand these interactions and their role in the broader communities that surround them.

Keywords: ant, plant, myrmecophyte, mutualism, costs and benefits, East Africa, invasive species, Crematogaster

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Mechanisms and consequences of phytochemical diversification in a rapidly evolving plant clade

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Plants often express a diverse array of defensive chemicals to fight off enemies. Phytochemical diversity may be advantageous for a plant, as complex chemical mixtures can interact with more target sites in herbivores, or can harbor more potential for facilitation among compounds to increase toxicity. Yet in contrast to the large number of different compounds produced by any one plant, the number of chemical classes these compounds belong to is often much reduced and highly phylogenetically constrained. For example, the vast majority of defensive compounds produced by plants of the Brassicaceae belong to a single compound class, the glucosinolates. Such phylogenetic conservatism in chemical defense likely facilitates specialization of herbivores, as a gain of tolerance to one compound will increase the likelihood of tolerance to related compounds as well. As a strategy to lose co-adapted herbivores, plants have occasionally gained the ability to produce completely novel defense classes in addition to the phylogenetically basal defense. Plants of the genus Erysimum (Brassicaceae) have gained the ability to synthesize toxic cardenolides in addition to glucosinolates, making them resistant to several specialist herbivores of the Brassicaceae. Such events of gain-of-function provide unique opportunities for the study of the selective forces that drive phytochemical diversification, as they involve mostly non-adapted herbivores and thus allow us a peek at co-evolutionary processes while they are out of balance. Here I show how generalist and Brassicaceae-specialist herbivores are coping with phytochemical diversity at the levels of chemical classes as well as compounds. I highlight patterns of diversification in both the basal and novel defense following the gain of the novel trait, and finally I identify a potential molecular mechanism involved in phytochemical diversification.

Keywords: cardenolides, glucosinolates, coevolution, phytochemical defense

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Genetic interactions drive metacommunity species associations in a plant-aphid system

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Metapopulations, groups of spatially separated populations of the same species, will rarely exist without interactions linking them to a wider ecological community, and thus must be considered in this metacommunity context, even though not all species within this community will have the same home-range size or dispersal ability. Specialized insect herbivores feeding on a host plant are examples for such systems, whereby even a single plant may host a local population of the target species. Under the framework of community genetics, within-species genetic variation drives variation in the outcome of interactions between species and, in turn, community dynamics, but examples from metacommunities are rare. We used a natural patch-forming chemically-diverse plant (tansy; *Tanacetum vulgare*), its specialised aphids, their mutualistic ants, and aphid natural enemies, to test our hypothesis that plant intraspecific chemical variation in volatile terpenoids drives aphid metapopulation genetic structuring and metacommunity dynamics at the small-spatial scale of a single field of ~200 individual plants. Neither the different plant chemotypes nor aphid genotypes were spatially clustered, but we found consistent effects of plant chemotypes on aphid genetic clustering. Overall, it was the full profile of volatile terpenoids stored in the glands on the plant's surface that influenced aphid population genetic structuring rather than individual compounds. This was further mediated by the presence of mutualistic ants and parasitoid wasps, leading to local community dynamics occurring at the level of individual plants. We show that by approaching metacommunity ecology from the community genetics viewpoint (i.e. the importance of genetic interactions) we can begin to explain the co-existence of multiple species, and genotypes within a species, across spatially separated habitats.

Keywords: *Metopeurum fuscoviride*, *Lasius niger*, ecological genetics, microsatellites, monoterpenes

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Plant-insect-microorganisms interactions
*COST action FA1405

Tuesday 4th of July 2017 Salle Thélème Tanneurs

08h15 Introduction

Plant-insect-microorganisms interactions - *COST FA1405
Chairs A. Bennett and F. Dedeine

08h30	**Einat Zchori-Fein** **Keynote Speaker** ***(Sponsored by COST)***	Insect symbionts as bio-control agents against phloem-restricted plant pathogens
09h15	**Alison Bennett**	Indirect influences of a belowground microbe on aboveground parasitism of plant herbivores
09h30	**Arjen Biere**	Can beneficial microbes help mitigate plant growth-defense trade-offs under shading?
09h45	***Lucille Chrétien PhD***	Can flowering plants resist insect and pathogen attack? Induction of phytohormones and resistance of plants under multiple attack
10h00	**Samuel Pichon**	Evolutionary stability of beneficial gut microbial communities in wood-feeding termites
10h15	Coffee break (sponsored by the COST action FA 1405)	
11h15	**Ainhoa Martinez-Medina**	An integrative ‘omics’ approach to unravel the mechanisms driving the impact of root symbionts on plant multitrophic interactions
11h30	***Kay Moisan PhD***	Warning or blessing? Volatiles emitted by pathogenic and non-pathogenic fungi affect plant development and resistance to insects
11h45	**Ana Pineda**	Steering soil microbiomes through plant-soil feedbacks to enhance resistance to herbivores
12h00	**Angela Smilanich**	Host range expansion and the insect immune response
12h15	**Teresa Vaello**	Facilitation between aphids and thrips is modulated by parasitization but not by plant-soil feedbacks
12h30	Lunch (sponsored by the Insect Biology Research Institute)	

Keynote

Insect symbionts as bio-control agents against phloem-restricted plant pathogens

Einat Zchori-Fein *[1], **Lilach Iasur Kruh** [2], **Ofir Bahar** [3], **Ofir Lidor** [4], **Tirza Zahavi** [5], **Vered Naor** [6]

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Phloem restricted bacterial pathogens pose a major threat in many agricultural crops. Because the conventional application of chemical sprays is inefficient, endophytes have been suggested as a potential reservoir for innovative control approaches. We hypothesized that insects that are involved in the transmission of plant pathogens may harbor microbes that affect disease agents. The study reported is focused on a bacterium that was isolated from the planthopper *Hyalesthes obsoletus* (Hemiptera: Cixiidae), the insect vector of Bois noir disease. The isolate belongs to the bacterial family Xanthomonadaceae, and its full genome suggests it is a new genus. This isolate could be introduced into a number of healthy and infected crop plants, and its presence in plant tissues was confirmed up to four weeks post inoculation. In the presence of the isolate symptoms of disease-causing agents such as Phytoplasma were markedly reduced in both laboratory and field experiments. Taken together, the results demonstrate that insects that serve as vectors for plant pathogens may be a useful source for potentially beneficial bacteria.

Keywords: DLB, endophytes, grapevines, Hyalesthes obsoletus, phytoplasma

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Indirect influences of a belowground microbe on aboveground parasitism of plant herbivores

Alison Bennett [1]*

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Soil microbial communities are known to indirectly impact insect herbivores, but in this talk I will demonstrate that soil microbial communities can also indirectly impact insect herbivore enemies via multiple mechanisms. In this talk we focus on a community of the soil organism arbuscular mycorrhizal (AM) fungi, which can change host plant quality for insect herbivores altering plant nutritional quality and/or by priming effects that lead to enhanced inducible and constitutive plant defences. Thus there are two mechanisms of AM fungal influence: First, plant quality effects (due to altered nutrition or direct defenses) on herbivores could cascade to higher trophic levels influencing natural enemy control of insect pests. Second, via their priming influence, AM fungi could alter indirect defences by altering volatiles used to attract parasitoids. Building on previous work, we addressed the relative importance of these two pathways in a series of experiments in which we manipulated the presence of a natural AM fungal community, Solanum species and genotype, potato aphid genotype, and parasitism of potato aphids. We measured aphid growth rates, and conducted parasitism assays with aphids in a neutral environment and involving host plants (and host plant volatiles). We found that AM fungi altered parasitism via both mechanisms: AM fungi increased parasitism success of aphids in a neutral environment without cues from the host plant, and parasitoid attraction to plants hosting AM fungi was much greater than attraction to plants that did not host AM fungi. However, in both cases, the influence of these pathways was dependent upon Solanum species and genotype. As a result, AM fungi influenced parasitism via multiple mechanisms, but this influence was dependent on host plant. The redundancy in parasitoid influence may allow AM fungi to alter parasitism regardless of individual host plant responses to AM fungi.

Keywords: aphid, parasitoid, arbuscular mycorrhizal fungi, herbivore quality, defense priming

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Can beneficial microbes help mitigate plant growth-defense trade-offs under shading ?

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The outcome of interactions between plants and insect herbivores can be strongly modulated by plant-associated microbes such as arbuscular mycorrhizal (AM) fungi. AM fungi have been shown to enhance plant growth and to induce or prime plants for jasmonic acid (JA)-signalled defences against necrotrophic pathogens and generalist chewing insect herbivores. We tested whether the AM fungus *Funneliformis mosseae* enhances resistance of *Plantago lanceolata* against the necrotrophic pathogen *Botrytis cinerea* and the generalist leaf chewing insect herbivore *Mamestra brassicae* when plants are under simulated competition from neighbours.

Shading by neighbours reduces the ratio of red to far-red light perceived by plants, leading to activation of the so-called shade avoidance syndrome (SAS) characterized by elongation growth. Recent studies have shown that activating SAS comes at a cost of the plant's ability to activate JA signalled defences. We studied whether mycorrhizae can mitigate such trade-offs under simulated shading (low red to far-red ratio).

Simulated shading enhanced susceptibility to the pathogen, but only in older plants, and mycorrhiza did not mitigate this effect. By contrast, mycorrhizae enhanced resistance of older plants to *Mamestra brassicae*, largely independent of light treatment. The mycorrhiza-enhanced resistance was associated with a reduced leaf digestibility due to a higher leaf C/N and C/P ratio, induction of the defense metabolite aucubin, and a higher leaf dry matter content. Interestingly, in young plants mycorrhiza had opposite, positive, effects on leaf digestibility, associated with reduced leaf C/N ratio and leaf dry matter content.

We conclude that AM fungi can strongly enhance plant resistance to insect herbivores, but that their effect is highly dynamic during plant ontogeny, with opposite effects on young vs. old plants. AM fungi do not appear to play a significant role in mitigating trade-offs between resistance and elongation growth under shading.

Keywords: plant herbivore microbe interaction, resistance, C/N ratio, *Mamestra brassicae*, light quality, mycorrhizae

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Can flowering plants resist insect and pathogen attack? Induction of phytohormones and resistance of plants under multiple attack

Lucille Chrétien * [1,2,3], Anja David [4], Eirini Daikou [1], Wilhelm Boland [4],
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In nature, the period where insects are most abundant generally coincides with the flowering peak. Thus, plants face a multitude of attackers during their reproductive phase. Plant responses to one attacker can interfere with responses to a second attacker, and phytohormones that regulate reproduction in plants are also involved in resistance to insect and pathogen attack. In this study, we quantified phytohormonal responses of flowering plants to single and dual attack, and the consequences of dual attack for plant resistance against the insect attackers. Plants were exposed to single and dual attack by a chewing caterpillar, a sap-sucking aphid, and a pathogen. We quantified phytohormonal concentrations in leaves and inflorescences during the development of the plant and of the attackers, and determined consequences of phytohormonal changes for plant direct and indirect resistance. Interestingly, caterpillars highly induced the upregulation of jasmonic-acid-related phytohormones in inflorescences, but not in the leaves. Upregulation of jasmonic-acid-related phytohormones was particularly high on dually attacked plants, and dual attack increased plant resistance to caterpillars, but compromised plant resistance to aphids. Parasitoid performance was negatively correlated with the performance of their hosts. In this presentation, we will discuss that chewing herbivores are the main drivers of responses in flowering plants despite the identity of the second attacker, and that plants prioritize resistance of reproductive tissues over vegetative tissues.

Keywords: Phytohormones, inflorescences, plant resistance, multiple attack, phytopathogens, florivorous insects, parasitoids

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Evolutionary stability of beneficial gut microbial communities in wood-feeding termites

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Many herbivorous insects rely on beneficial microbial symbionts to exploit their plant resources, but yet the stability mechanisms of such mutualistic associations remain poorly understood. Here we present recent results obtained in the associations between wood-feeding termites (genus Reticulitermes) and their gut microbial communities that are essential to degrade and supplement lignocellulose. Using both metabarcoding (16S and 18S for prokaryotic and eukaryotic symbionts) and more conventional cloning / sequencing approaches, we estimated the level of host-symbiont specificity and inferred the evolutionary history of these complex symbiotic systems. Together, our results revealed that the evolutionary diversification of termite – symbiont associations is not only characterized by co-speciation events, but also exhibits multiple host switching. Implications of these results in the understanding of the stability mechanisms of host-microbiota mutualisms are discussed.

Keywords: Symbiosis, mutualism, microbiota, metabarcoding, termites

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An integrative ‘omics’ approach to unravel the mechanisms driving the impact of root symbionts on plant multitrophic interactions

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Plants nurture a vast community of symbiotic microbes, which in analogy to microbial communities in the human gut, provides their host with essential functions related to nutrient acquisition and protection against infections. Among them, arbuscular mycorrhizal (AM) and Trichoderma fungi are widespread soil inhabitants that establish symbiosis with a vast majority of terrestrial plants, conferring positive effects on growth and fitness. Root microbial symbionts represent thus a promising contribution to sustainable pest management strategies. However, the mechanisms underlying the impact of root symbionts on plant-insect interactions remain largely unknown, and mostly based on targeted analysis of a limited set of defense-related traits. Moreover, besides improving plant growth and inducing defenses against herbivorous insects, root-colonizing microbes may affect plant-insect performance via interactions at higher trophic levels. In our study, we take an ‘integrative multi-omics approach’, combining untargeted transcriptomics and metabolomics, with performance and behavioral studies to uncover key processes driving the impact of the AMF fungus *Rhizophagus irregularis* and *Trichoderma harzianum* on the interaction of tomato plants with the specialist and generalist herbivores *Manduca sexta* and *Spodoptera exigua*, respectively. We found that root interactions with both fungal symbionts influence the shoot metabolome and transcriptome, priming the plant for strong accumulation of different defense-related compounds. As consequence, root inoculation with the fungal symbionts strongly altered the dynamics of the plant-herbivore interaction by negatively affecting insect’s growth and survival rates, pupation success, sex ratio, and even host selection by ovipositing moths, which eventually translated in an improved plant fitness. Moreover, fungal symbionts strongly affected the blend of volatiles released by the plants after herbivory, indicating that the effect of root symbionts on herbivores can escalate up to further trophic levels.

Keywords: Metabolomics, Mycorrhiza, Plant Defenses, Plant, Microbe, Herbivore Interactions, Priming, Transcriptomics, Trichoderma, Volatile Organic Compounds

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Warning or blessing? Volatiles emitted by pathogenic and non-pathogenic fungi affect plant development and resistance to insects

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Plants are exposed to a manifold of interactions both below- and aboveground, and can be simultaneously or sequentially exposed to beneficial and antagonistic macro- and microorganisms. We, therefore, expect plants to have developed strategies to distinguish friends from foes, which would be especially advantageous to anticipate enemies. In fact, prior to a direct physical contact, plants can perceive and respond to odours (i.e. volatiles) emitted by various organisms, including other plants, herbivorous insects and microorganisms. Various volatiles emitted by beneficial microorganisms, such as soil bacteria and fungi, have shown to positively affect plant development, and to enhance plant resistance to pathogens, hence acting as a blessing. Whether plants distinguish and perceive volatiles from pathogenic fungi as a warning remains unknown. Additionally, how these volatile-mediated belowground interactions affect aboveground interactions are still elusive. In this study, we aimed to elucidate if plants perceive fungal volatiles as a warning or a blessing by investigating (1) whether plants can discriminate volatiles emitted by pathogenic and non-pathogenic soil-borne fungi, (2) what the effects are on plant development, and (3) what the ecological consequences are for plant resistance against a generalist insect herbivore. During this presentation, I will discuss how plant development, including flowering time, and plant resistance to an insect herbivore are affected upon exposure to volatiles emitted by fungi with different lifestyle.

Keywords: volatiles, soil fungi, *Arabidopsis thaliana*, growth, development, resistance, herbivory, pathogenicity, saprophyte

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Steering soil microbiomes through plant-soil feedbacks to enhance resistance to herbivores

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The rhizosphere is colonized by an astonishing diversity of microbes, the so-called microbiome, and the soil is the major source of these plant-associated microbes. A current challenge is how we can manipulate the plant-associated microbiome to enhance plant growth and resistance to their attackers. Plants shape soil microbiomes in a species-specific manner, with consequences for the performance of future plants. This is the main mechanism of plant-soil feedbacks, a long-standing concept in succession ecology. Here, by conditioning the soil with wild plant species from two functional groups (i.e. grasses and forbs), we applied the plant-soil feedback concept to create healthy soils. Then we assessed in the cut-flower crop Chrysanthemum, plant growth, phenolics and resistance against aphids and thrips, as well as performance of an aphid parasitoid. Understanding how microbiomes affect plant-insect interactions in natural ecological systems may give us new insights on how to apply microbiomes in ecologically intensive agroecosystems.

Keywords: Plant, soil feedbacks, induced resistance, microbiome, greenhouse crop

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Host range expansion and the insect immune response

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Introduction: Investigating the factors that influence herbivore host range expansion can provide insight into the process of diet shifts. In addition to plant chemistry and natural enemies, we are interested in the role that the immune response plays in the incorporation of a new host plant, and whether the degree of its importance varies depending on the diet breadth and sequestration ability of the herbivore.

Methods: Herbivores were reared on either their native host or a naturalized exotic host (*Plantago lanceolata*) that has been incorporated into the diet of the focal species. Each native-exotic pairing differed in the presence or amount of iridoid glycosides. In addition, each herbivore had a range of sequestration ability from high to low. Herbivores were challenged with viral or bacterial pathogen, then assayed for immune strength, survival, and development.

Results/Discussion: The importance of the immune response will be discussed in terms of the diet breadth and sequestration abilities of the individual. At least in one case, it appears that the immune response is not as important for survival against pathogenic enemies as plant chemistry. This is most likely a result of the high sequestration ability of the herbivore. Moreover, regardless of the immune response, survival was highest of the exotic host suggesting a beneficial effect of incorporating the host into the diet of the herbivore. It appears that the importance of the immune response in host range expansion is context dependent with diet breadth, sequestration, and plant chemistry having important interactive effects.

Keywords: ecological immunology, caterpillar, immune response, diet breadth, specialization, pathogen, virus, bacterium, sequestration, chemistry

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Facilitation between aphids and thrips is modulated by parasitization but not by plant-soil feedbacks

Teresa Vaello *† [1], **Martine Kos** [2], **Saandep Sarde** [3], **Martijn Bezemer** [2],
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Plant-soil interactions can influence the performance of plants that grow later in the soil, termed known as ‘plant–soil feedbacks’, these interactions can be caused by soil microorganisms, such as bacteria, mycorrhizal or pathogenic fungi. Soil microbial communities changes can influence primary and secondary plant metabolite concentration and consequently affect the performance of above-ground insects feeding. However, little is known about the potential effect of plant-soil feedbacks in enhancing the defensive response in plants, where salicylic and jasmonic acid signalling pathways play a major role. Moreover, no much information exists about plant resistance in plants that are attacked by parasitized and unparasitized insects or how this can affect the performance of future herbivory. The objective of this study was to investigate the plant-soil feedback effects on the induction of salicylic and jasmonic acid signalling at transcriptional level in the plant *Capsicum annuum*, after attack by the aphid *Myzus persicae* (comparing aphid vs. parasitized aphid by *Aphidius colemani*) and the consequences for a secondary attack by the thrips *Frankliniella occidentalis*. Our results show how plant defence respond differently when aphids were parasitized or not, independently of plant-soil feedbacks. Moreover, the effect of sequentially herbivory on the *Frankliniella occidentalis* performance will be discussed.

This work was funded by the CGL2016-79054-R (Ministerio de Economia, Industria y Competitividad, Spain), STW 13848 and the STSM Cost Action FA1405 funded by the European Union.

Keywords: Plant, soil feedbacks, induced systemic resistance, multitrophic interactions, insect, plant, microbe interactions, sweet pepper.

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Multitrophic interactions and ecological networks

Tuesday 4th of July 2017 Salle Thélème Tanneurs

Multitrophic interactions and ecological networks Chairs M. Dicke and E. Huguet		
14h00	**Theodora Petanidou** **Keynote Speaker** **(sponsored by COST)**	The Aegean revisited: unravelling the Archipelago's "small, great world" through ecological network analysis
14h45	***Yavanna Aartsma PhD***	Parasitoid attraction to herbivore-induced plant volatiles across spatial scales
15h00	**Mathilde Baude**	Quantifying nectar resources for pollinators in Great Britain across the last century
15h15	**Christine Becker**	Plant mediated bottom-up effects of nitrogen and water supply on leafminers and aphids as well as their parasitoids
15h30	**Nicolas Borowiec**	Comparative dynamics of introduced and native parasitoids: the case-study of classical biological control against the chestnut gall wasp in France
15h45	***Maximilien Cuny PhD***	The interactive effects of seed beetles and parasitoids on seed germination and plant performance in wild Lima bean
16h00	Coffee break (sponsored by the Insect Biology Research Institute)	
16h30	***Gaël Delpon PhD***	Dynamics of plant-butterfly interaction networks along secondary successions
16h45	**Alan Kergunteuil**	Indirect plant defences do not get high: adaptive differentiation of phytochemistry along elevation gradients drives variations in the strength of plant-mediated trophic cascades
17h00	**Dani Lucas-Barbosa**	Plant life-style determines defensive strategies against insect herbivores, and consequences for plant fitness
17h15	***Gonzalo Martinez PhD***	Preference and performance of an herbivorous true bug: Feeding or laying eggs ?
17h30	***Quint Rusman PhD***	Flowering plants under attack: The generality and specificity of plant-mediated interactions between insect herbivores and flower visitors

Keynote

The Aegean revisited: unravelling the Archipelago's ”small, great world” through ecological network analysis

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The ”small, great world” is a poetic narrative swinging between the microcosm and the macrocosm of O. Elytis' (poet, Nobel Prize in Literature 1979) valued world, the Aegean. This popular poetic account has been the inspiring ground for the current scientific approach that is based simply on species relationships (viz. plant–pollinator interactions) expressed as network links. Despite its apparent simplicity, the Aegean is very complex, and I predict that investigating this world using ecological network analysis tools provides an alternative, more holistic and, thus, better understanding of its essence.

My talk is based on data from plant–pollinator interaction networks collected in > 100 sites with phrygana (Mediterranean low scrub), on 24 islands in the Aegean. My approach covers ecological, biogeographical, and conservation/restoration aspects, organized in the following three umbrella-sections:

Networks represent functional aspects of the real world addresses the subjects/questions: networks of small vs. large islands, also exploring the effect of bee-sizes and specialization/generalization issues; the role of floral color, odor, and nectar secretion in network structure; and year-to-year network variability.

The three worlds addresses the issue of geographical scale at the level of site, island, and the entire archipelago, including the issue of specialization/generalization of either partners (plants, pollinators).

Threats and conservation/restoration explores the role of traditional management in the area (e.g. grazing, bee-keeping) and the threat of global warming from a conservational perspective of the Aegean world; it also pinpoints the importance of super-generalist plants constituting network hubs for wild bee conservation and the eventual creation of wild bee sanctuaries in the area.

Keywords: plant–pollinator interactions, pollination networks, network analysis, Aegean Archipelago, islands, phrygana, Mediterranean srublands

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Parasitoid attraction to herbivore-induced plant volatiles across spatial scales

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Herbivore-induced plant volatiles (HIPVs) mediate host-seeking behaviour of carnivorous insects, such as parasitoids and predators, and are considered a part of a plant's indirect defence against herbivores. Plants show both intra- and interspecific variation in the quality and quantity of HIPVs, affecting the attraction of carnivorous insects. Studies on HIPV variation and parasitoid behaviour are often conducted in small-scale choice assays. However, the relevance of HIPVs on larger spatial scales is not well understood. This is especially true for the effects of plant variation in HIPV emissions on parasitoid behaviour in the field. The distance from which HIPVs influence parasitoid behaviour may influence parasitoid movement and consequently their population distribution. In addition, the relevance of HIPVs may be affected by the landscape context in which the plant is embedded, including background odours and the physical structure of the vegetation. Therefore, parasitoids have to find their hosts in a chemically and structurally complex environment. Understanding how parasitoids are influenced by this complexity is important for our understanding of tritrophic interactions in realistic field settings. We will discuss field experiments with cabbage cultivars that differ in attractiveness to parasitoids, in combination with the spatial context of parasitoid foraging behaviour. We discuss these findings in both an ecological and applied context.

Keywords: herbivore induced plant volatiles, host location by parasitoids, landscape ecology, spatial scales, tritrophic interactions

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Quantifying nectar resources for pollinators in Great Britain across the last century

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The lack of floral resources is suspected to be one of the main factors involved in pollinator decline. However, floral resources are rarely quantified at large scale making difficult 1- to assess the value of habitats in feeding pollinators and 2- to study the changes in the availability of floral resources across time. We estimated the nectar sugar values for 260 common plant species from the flower to the landscape scale through empirical nectar sampling, flower density counting and statistical modeling based on plant traits. We then combined this nectar database with vegetation data from the Countryside Survey, a national-scale representative survey of British plant communities. We found that a few productive species and habitats increasingly dominate national nectar supplies and that the total nectar production of Great Britain showed a marked decline in floral resources from 1930s to 1970s, followed by a period of stable low production and then increased post-2000. These results will be discussed in the context of opportunities for conservation and restoration efforts dedicated to pollinators and we will present how this database could be used to improve our understanding of the role of floral resources in plant-pollinator networks.

Reference: Baude, M; Kunin, WE; Boatman, ND; Conyers, S; Davies, N; Gillespie, MAK; Morton, RD; Smart, SM; Memmott, J; Historical nectar assessment reveals the fall and rise of floral resources in Britain, Nature, 530, 7588, 85-88, 2016

Keywords: plant pollinator interactions, nectar resources, pollinator declines

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Plant mediated bottom-up effects of nitrogen and water supply on leafminers and aphids as well as their parasitoids

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In the context of global change, resource input into agricultural systems has to be optimized but crop production must stay feasible. Dry regions like the Mediterranean face water limitation and nitrogen (N) leaching risks eutrophication. Yet, water and N are necessary for basic processes in plants, like photosynthesis and growth, and linked to defense compound production. Plant-feeding insects obtain their N from plant tissue but can be impacted by toxins. Water availability can influence this interaction depending on their dietary specialization. Nutritional value and/or toxin concentration of insect hosts can affect parasitoids. We studied how moderately reduced amounts of N and/or water impact tomato plants (*Solanum lycopersicum*) while monitoring bottom-up effects on two specialist herbivores, feeding on leaf-tissue (*Tuta absoluta*) or plant sap (*Macrosiphum euphorbiae*), and on their respective parasitoids (*Necremnus tutae*, *Aphelinus abdominalis*).

On the first and second trophic levels, we detected several clear effects. Plant development and photosynthesis decreased with reduced N but were hardly affected by water supply. Importantly, the number of fruits was not reduced by lower N supply. *M. euphorbiae* population size increased with reduced N supply on ”low water”-plants. Regarding *T. absoluta*, neither growth rate nor consumed leaf area were significantly affected. The nutritional value of both species was reduced on ”low N”-plants. On the third trophic level, we detected no significant effect – only a trend towards higher emergence rates of *A. abdominalis* on ”high N high water”-plants. Our results indicate that reducing N input in tomato production is feasible without significant yield loss. However, water supply should not be reduced simultaneously, to avoid increased herbivore pressure by aphids. While some stressed plants offer more readily available nutrients to herbivores, defense compounds may also be influential. Analyses of alkaloid and phenolics concentrations are in progress and will be discussed.

Keywords: bottom up effect, nitrogen, water, plant ecophysiology, plant defense, *Tuta absoluta*, *Macrosiphum euphorbiae*, *Necremnus tutae*, *Aphelinus abdominalis*

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Comparative dynamics of introduced and native parasitoids: the case-study of classical biological control against the chestnut gall wasp in France

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Based on the introduction of an exotic species for its permanent establishment and the long-term control of an agricultural pest, classical biological control can be used as an experimental frame to study the biology of introduced populations in real-life ecosystems. Following the arrival in France in 2008 of *Dryocosmus kuriphilus* (CGW, Cynipidae), a major pest of Castanea worldwide, a classical biological control program using the exotic parasitoid *Torymus sinensis* (Torymidae) was implemented in 2011. The first aim of this project was to allow the long-term control of CGW populations, both in commercial orchards and in forests. This project was also a good opportunity to assess ecological mechanisms linked with biological invasions, in particular (i) the role of propagule pressure on the dynamics of *T. sinensis* and (ii) the ecological changes in communities of native parasitoids induced by the arrival of both exotic species. Between 2011 and 2015, a total of almost 15000 *T. sinensis* were released on 58 sites, covering a large geographic area. All of these releases were proven to be highly successful with a rate of establishment of 100%. Dynamics of *T. sinensis* is characterized by a 4-years exponential increase of population size. The number of individuals introduced did not significantly influenced population's size or dynamics of *T. sinensis*. Interestingly, dynamics were similar on sites naturally colonized by *T. sinensis* but with higher population size, suggesting high propagule pressure from natural populations. Analysis of the dynamics of native parasitoids belonging to the Eupelmus genus showed influence of some ecological factors like habitat connectivity or invasive status of CGW (i.e. core versus front of invasion) but no sign of either positive (e.g. facilitation) or negative (e.g. competition) interaction with *T. sinensis*. This apparent neutral state may nevertheless change over time when host population size will start decreasing.

Keywords: biological control, dynamics, parasitoids

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The interactive effects of seed beetles and parasitoids on seed germination and plant performance in wild Lima bean

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For natural plant populations, pre-dispersal seed predation can have devastating effects on subsequent seedling recruitment and plant fitness. However, if insect damage does not completely deplete seed reserves, seeds may still be able to germinate and produce healthy seedlings. In this context, the action of natural enemies such as parasitic wasps that kill or halt the development of seed predators may reduce the negative effects of seed predation on plant fitness. We examined the interactive effects of seed predation by Bruchinae beetles and parasitoids of these beetles on seed germination and plant performance in wild lima bean *Phaseolus lunatus*. Seeds with varying degrees of beetle and parasitoid infestation were collected from natural populations in Mexico. These were then used to conduct field and laboratory experiments to determine the relationship between seed damage, germination success, and plant performance.

In the lab, seed predation had a positive effect on seed germination at low infestation levels compared to undamaged seeds, and a negative effect at high infestation level. Parasitism mitigated the negative effects of high levels of infestation. Moreover, seedling performance (growth rate and shoot mass) was higher for plants grown from seeds with parasitoids than seeds infested by beetles only.

In the field, low levels of seed damage did not improve germination success, but did enhance germination speed. In parallel, the negative effects of seed damage on plant performance were stronger. Plants from damaged seeds were more attacked by leaf-chewing herbivores and flowered later than plants from undamaged seeds.

Our results demonstrate that seed beetles can negatively affect seedling recruitment depending on the severity of damage and that natural enemies can lessen these effects. These results highlight the importance of seed predators and their parasitoids on plant population dynamics and seed bank persistence in *P. lunatus*.

Keywords: tritrophic interactions, pre-dispersal seed predation, *Phaseolus lunatus*, plant perfor- mance, germination, natural populations

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Dynamics of plant-butterfly interaction networks along secondary successions

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In the current context of changes in land uses, the consequences of secondary successions on plant-insect interactions remains poorly investigated. Butterflies are widely recognized as relevant integrators of landscape dynamics since they are involved in obligatory interactions with one or several plant species at larval stage. Distribution and abundance of host plants are thus one of the key factors driving the distribution patterns and temporal dynamics of butterfly communities. We performed an analysis of a caterpillars-host plants bipartite network, assembling 2230 interactions among 250 butterfly species and 830 plant species in France. Based on this large dataset, we investigated how the structure of the interaction network varies during secondary succession linked to changes in plant communities. Our analysis revealed independent modules of plant-butterfly interactions. Large modules show close interactions between some butterfly genera and their specifically associated plant families. Other modules show that plant traits (herbs, bushes, trees) differentiate available resource for several groups of butterflies. Last, few small modules link monophageous butterflies to their specific hosts. We also investigated how life history traits of butterfly species underlie these modules to identify those to be considered as determinant in such structuration. In the light of plant ecological requirements, such interaction network was then used to simulate the potential response of the host plant pool (in terms of species composition) to natural dynamics of habitat closure from open grassland to forest. We assessed the dynamics of both butterfly species richness and network structure along these stages, and showed that these changes contribute to understand the impacts of secondary successions on the composition of butterfly communities. Our results show that network analyses may be used as predictive tools to describe changes in local butterfly communities and identify the most threatened species during changes in land uses.

Keywords: Butterflies, host plants, herbivory, host, specificity, bipartite network, ecological successions

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Indirect plant defences do not get high: adaptive differentiation of phytochemistry along elevation gradients drives variations in the strength of plant-mediated trophic cascades

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Despite a relatively well-resolved picture of ecological mechanisms governing indirect plant defences, their evolution has received very little consideration to date. From micro-evolutionary perspectives, exploring the distribution of indirect plant defences across different environments provides a valuable framework to shed light on the assemblage of tri-trophic systems and, thereby, unravel the drivers influencing the strength of trophic cascades. Based on surveys of soil-dwelling natural enemies along mountain slopes, we predicted an adaptive decrease in indirect root defences with elevation. Olfactometer bioassays confirm a relaxation of plant-regulated trophic strength for subalpine and alpine plants. While linear discriminant analyses of root volatiles enable to discriminate chemotypes between altitudinal plant populations, variations in natural enemies' recruitment along elevation gradients are more particularly correlated to the emissions of oxylipins. We completed the study by a reciprocal transplant experiment to test whether variations in top-down forces mediated by indirect plant defences rely on versatile plasticity at the phenotype level or local adaptations based on genetic differentiation between altitudi- nal populations. In a global warming context and colonization of alpine habitats by herbivore insects, the ability of mountain vegetation to rapidly overcome future biotic stresses likely depends on these two opposite hypotheses. More generally, this study brings additional brick to the still-debated question of whether or not indirect plant defences confer fitness benefit for plants. Finally, our results also challenges the principle of allocation cost of indirect plant defences and raises a pending issue about individual and combined selective agents responsible for their local adaptations along ecological gradients.

Keywords: tritrophic interactions, trophic strength, plant fitness, local adaptation, micro, evolution

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Plant life-style determines defensive strategies against insect herbivores, and consequences for plant fitness

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This study addresses insect-plant interactions when regarding defences of plants against insects, and reproduction, as a result of insect-pollination. We investigated whether plant life-style determines plant defensive strategies across Brassicaceae. We designed greenhouse and field experiments to study tolerance and plant resistance traits against herbivorous-insects, in 21 brassicaceous species, including annual and perennial plant-species. In the field, we investigated the effects of plant exposure to insect-herbivores, on insect-pollinator behavior and plant fitness. We found that perennial plants species invest more in direct resistance to insect-herbivores, whereas annual species can best attract parasitoids. All plants can to some extent tolerate herbivory, however, inducible plant responses by a chewer herbivore led to negative consequences for plant fitness in perennial plants, but did not affect the reproductive output of annual plant species. During this talk, I will discuss to what extent the impact on plant reproduction can be explained by changes in behavior of insect-pollinators.

Keywords: resistance, tolerance, herbivory, pollinators, plant fitness

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Preference and performance of an herbivorous true bug: Feeding or laying eggs?

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Optimal foraging and optimal oviposition may be major selective forces during plant selection by female herbivorous insects. However, their contribution to the host-selection process in sucking herbivores has been little investigated. Understanding the behavioral patterns involved in host-plant selection is particularly relevant in species of economic importance as it may be used in the development of sustainable management strategies. We studied feeding and oviposition behavior of an invasive forestry pest, the bronze bug *Thaumastocoris peregrinus*, which attacks Eucalyptus plantations worldwide. We used dual-choice bioassays to evaluate the preference of females between host species, developmental leaf stages, or prior plant exposure to potential competitors, either conspecifics or the lerp psyllid *Glycaspis brimblecombei*. We assessed the link between these preferences and offspring performance, by comparing survival and developmental rates of nymphs reared on the different treatments. Using healthy adult leaves of *Eucalyptus tereticornis* as a reference host, we found that female bugs discriminated among plant species and developmental leaf stages. In addition, infestation with either the bronze bug or the lerp psyllid stimulated oviposition. Nymphal performance varied among treatments, suggesting a correlation with oviposition preference. Thus, *T. peregrinus* females seem to use different criteria when selecting sites for feeding or oviposition. Oviposition choice may generally be linked with nymphal performance. We discuss these findings in the context of management alternatives for this pest.

Keywords: Host selection, mother, knows, best hypothesis, forestry pest, dual, choice assay, *Thaumastocoris peregrinus*, *Glycaspis brimblecombei*, Eucalyptus

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Flowering plants under attack: The generality and specificity of plant-mediated interactions between insect herbivores and flower visitors

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To optimize reproductive output, plants need to maintain interactions with mutualists, such as pollinators, and at the same time deal with antagonists, such as herbivorous insects. Although many plant species rely on inducible defences to save metabolic costs in absence of herbivores, plant responses induced by herbivore attack can lead to important ecological costs. For example, herbivore-induced responses can affect flower traits and alter interactions with flower visitors, and the effects can vary depending on the herbivore species or feeding guild of the plant attacker. The current knowledge on the generality and specificity of plant-mediated herbivore-flower-visitor interactions and its consequences for plant fitness is limited. Using a common-garden set-up, we found that herbivore induction by 10 different herbivores resulted in changes in pollinator community composition of the annual *Brassica nigra*. Aboveground chewing and belowground herbivory resulted in changes in pollinator community composition when compared with uninfested or plants exposed to phloem-feeding herbivores. In addition, plants exposed to belowground herbivory overcompensated in seed set, setting more seeds compared with uninfested or plants exposed to aboveground herbivores. In the greenhouse, we found that herbivory by five herbivore species resulted in species-specific changes in the pollinator behaviour of a syrphid fly and a butterfly, with increased or decreased visitation, or no response. To explain our results, we investigated which flower traits are changed upon herbivory. We found herbivore species-specific changes in the volatile emission of flowering *B. nigra* plants. There were also specific changes depending on the feeding guild of the herbivores; the volatile blend of plants induced by chewing and phloem-feeding herbivores was different. Thus, we show that plant-mediated interactions between herbivores and flower visitor are common, may be specific for the herbivore and pollinator involved, are mediated by herbivore-induced changes in flower traits, and might come with consequences for plant reproduction.

Keywords: plant mediated interactions, flower visitors, pollinators, herbivores, plant reproduction, herbivore induced plant responses

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Insect effectors and plant responses

Wednesday 5th of July 2017 Salle Thélème Tanneurs

Insect effectors and plant responses Chairs G. Dubreuil and M. Erb		
08h30	**Isgouhi Kaloshian** **Keynote Speaker**	Aphid-plant interactions: unraveling arsenals used in this arms race
09h15	**Marcel Dicke**	Natural variation in plant responses to combinations of biotic and abiotic stresses
09h30	**Gary Felton**	Multitrophic Manipulation of Herbivore Perception by Plants
09h45	***Antoine Guiguet PhD***	Insights into mechanisms of gall morphogenesis and the origin of gall induction
10h00	**Marion Harris**	Plant Galls Induced by Insects: Lessons from Plant Galls Induced by Bacteria
10h15	Coffee break (sponsored by the Féri)	
11h15	**Roy Kirsch**	Biological relevance of pectolytic enzymes in herbivorous beetles
11h30	**Ricardo Machado**	Herbivory-induced jasmonates impact carbon acquisition and thereby constrain plant resistance and defoliation tolerance
11h45	***Martin Stefanov PhD***	Inference of plant-mediated interactions in herbivorous insect communities from time series count data
12h00	***Clemens Stolpe PhD***	Aphids suck their own grave – induced elevated concentrations of cadmium and zinc in phloem exudates of a hyperaccumulator plant lead to negative potentiation effect on *Myzus persicae*
12h15	**Bernardus Schimmel**	Overcompensation of herbivore reproduction through hyper-suppression of plant defenses in response to competition
12h30	Lunch (sponsored by the Région Centre Val de Loire)	

Keynote

Aphid-plant interactions: unraveling arsenals used in this arms race

Isgouhi Kaloshian [1]

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We study the interactions of tomato (*Solanum lycopersicum*) with its aphid pest, the potato aphid (*Macrosiphum euphorbiae*), to understand the evolutionary arms race between plants and aphids for survival. To identify the repertoire of the potato aphid salivary arsenals, *in vitro* collected aphid saliva was subjected to mass spectrometry. The majority of the identified proteins were of unknown function. Using functional analyses, we identified roles for several of the aphid effectors in altering plant immunity. In addition, we identified a host target for one of these immunomodulating effectors suggesting a mechanism how aphids overcome plant immunity. Remarkably, among the salivary proteome were proteins of microbial origin including the obligate endosymbiont *Buchnera aphidicola*, a bacterium essential for aphid survival. In addition, peptides of known and novel insect viruses were also present in the aphid saliva. For plant immune responses against aphids, we identified a potato aphid early immune recognition receptor, the Somatic Embryogenesis Receptor Kinase 1 (SERK1), associated with the resistance protein Mi-1.2. M-1.2 encodes a coiled-coil nucleotide-binding leucine-rich repeats protein and confers resistance to three species of piercing-sucking insects and root-knot nematodes, respectively. The tomato SERK1 belongs to a gene family of three transmembrane receptor kinases known for their roles in pattern-triggered immunity. In this presentation, I will describe the aphid arsenals and counter defense by the plant host and present a model for their race for survival.

Keywords: Effectors, plant immunity, Hemiptera, aphids, microbes

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Natural variation in plant responses to combinations of biotic and abiotic stresses

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Plants are exposed to a plethora of biotic and abiotic stresses in their local habitat. As a result, different populations of a species are subject to different selection pressures leading to adaptation to local conditions and intraspecific divergence. Yet, plant stress responses are usually investigated for individual stresses only. The annual brassicaceous plant *Arabidopsis thaliana* is an attractive model for ecologists and evolutionary biologists due to the availability of a large collection of re-sequenced natural accessions. This rich resource can be used to investigate how Arabidopsis responds to single stresses as well as combinations of biotic and abiotic stresses, including caterpillars, aphids, thrips, pathogens, salt stress and drought. Here, we will address global transcriptional responses to single stresses and combinations of stresses, genetic architecture underlying responses to various single stresses and stress combinations as well as the effects of plant life-history on resistance against herbivorous insects as single and double stresses.

When two stresses were applied in sequence, plants displayed transcriptome profiles that were very similar to the second stress, irrespective of the nature of the first stress. Nevertheless, significant first-stress signatures could be identified in the sequential stress profiles. The transcriptional profiles strengthened the notion that phytohormones are global modulators of interactions between different types of stresses. Genome-wide association analyses identified QTLs with contrasting and with similar responses to biotic vs abiotic stresses, and below-ground vs above-ground stresses. A newly developed multi-trait GWA analysis revealed novel candidate genes associated with multiple stress responses, where specific contrasts were identified with some genes positively associated with the resistance to one set of stresses while being negatively associated with another set of stresses. Finally, plant life-history strategy was shown to be an important determinant of stress responses.

Keywords: Pieris, Frankliniella, Myzus, Botrytis, Arabidopsis, biotic stress, abiotic stress, transcriptome, phenome, multiple stress, ecology, evolution

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Multitrophic Manipulation of Herbivore Perception by Plants

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Herbivore oral secretions may contain elicitors or herbivore-associated molecular patterns (=HAMPs) that are perceived by plants and then trigger an array of induced defenses. Much of this research has been conducted without considering that, in some instances, herbivores in the field harbor rich microbial communities, may be parasitized or infected with pathogens. Consequently, our research shows plant perception of herbivores and their HAMPs may be manipulated by these higher trophic levels. Suppression of direct plant defenses may allow the herbivore to grow faster and thus serve as a better host for the third trophic level. Manipulating herbivore perception could also benefit the third trophic level by reducing the sustained release of volatiles that would attract competitors including predators that may consume parasitized hosts.

Keywords: saliva, oral secretions, parasitoids, polydnaviruses, bacteria, baculoviruses

Insights into mechanisms of gall morphogenesis and the origin of gall induction

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Galls induced by arthropods constitute one of the most spectacular examples of hijacking plant development by a parasite. During the evolution of insects, this ability evolved several times in diverse orders. Price (1987) proposes the hypothesis that the galligenous lifestyle evolved from the leaf-miner lifestyle. The old origin of the capacity to induce galls in major galligenous families like the Cynipidae (Hymenoptera) and the Cecidomyidae (Diptera) makes it difficult to validate this hypothesis within these groups. For this reason, we decided to study the Gracillariidae (Lepidoptera), the majority of which are leaf miners. This family contains around 2000 species but includes only three galligenous species. Among them, *Caloptilia cecidophora* induce a gall on leaves of *Glochidion obovatum* (Phyllanthaceae). Other species in the Caloptilia genus are characterized by a leaf-miner/endophyte lifestyle at early instars followed by a leaf-roller/ectophyte lifestyle at late instars. To understand which of these lifestyles is ancestral to the galligenous lifestyle of *C.cecidophora*, we conducted a complete histological study of the development of *C.cecidophora* galls and compared it with a closely related species, *C.ryukyuensis*, at same larval stages. It appears that first and second instars of *C.cecidophora* dig a mine with no alteration of cell development of leaves as *C.ryukyuensis*. On the contrary, the third instar of *C.cecidophora* activates cell growth and cell divisions at the mine edges, leading to a closure of leaf tissues around the larvae, whereas in *C.ryukyuensis* simply making tentiform mines at the same stage. Then, later stages induce the development of two new tissues absent from the normal leaf but found in complex galls like those made by Cynipidae. By confirming the Price hypothesis and showing a convergence in complex gall structures, these results light on the origin of gall induction by insects and help to understand the mechanisms of gall morphogenesis.

Keywords: gall, Gracillariidae, histology, salivary effectors, evolution

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Plant Galls Induced by Insects: Lessons from Plant Galls Induced by Bacteria

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Galls are the end point of a deviation in plant growth caused by a foreign organism. The foreign organisms are diverse. Among Prokaryotes, the Kingdom Bacteria has three Phyla with well-known gall inducers: Proteobacteria, Actinobacteria, and Tenericutes (phytoplasmas). Among Eukaryotes, three Kingdoms have well-known gall inducers: Fungi, Plantae and Animalia. Animal gall inducers are found in three phyla: Nematoda, Rotifera, and Arthropoda (insects and mites). Across these phylogenetically and ecologically diverse foreign organisms, insects stand out for sheer numbers of gall-inducing species. Nevertheless, within the field of plant-insect interactions, the study of gall-inducing species has been isolated from the mainstream. In spite of this, insect-induced galls have attracted devotees among both scientists and naturalists. Paleobiologists have appreciated the clear-cut and long-lasting imprint that galls make on host plants, which persist long after the gall inducer has departed. Ecologists similarly appreciate this feature, which enables comparisons of the incidence of the gall-inducing strategy compared to other strategies across plant species and the world's ecosystems. Our interest in plant galls is on the mechanistic side, both how the gall inducer succeeds in manipulating the plant to do its bidding and how plants fight off or limit the harm from such manipulations. Currently, the deepest mechanistic understanding of plant galls comes from plant-bacteria interactions. We focus on lessons from these systems for the study of insect-induced galls. We propose several benefits of deeper mechanistic understanding of insect-induced plant galls. First, it will bring insect-plant gall interactions into the mainstream of insect-plant interactions. Second, it will create beneficial links with other disciplines that study plant biotic interactions. Finally, by refining our sense of what plant galls truly represent for plant biotic interactions, it will contribute to the ecological and evolutionary interpretation of patterns of galling across plant species and ecosystems.

Keywords: Plant Galls, biotrophs, effectors, induced susceptibility

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Biological relevance of pectolytic enzymes in herbivorous beetles

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Pectin is the most complex polysaccharide in nature and a highly abundant component of the plant cell wall contributing to the wall's protective function by balancing its flexibility and stiffness. It forms the matrix where cellulose and hemicelluloses are embedded in, and is the first cell wall polysaccharide degraded by phyto-pathogenic microbes during infestation. The best studied pectolytic enzymes secreted by microbes are polygalacturonases (PGs) that hydrolyze the pectin backbone, and it has been shown that PG-deficient mutants are less or non-pathogenic. This illustrates the importance of PGs for pathogens regarding plant colonization and nutrient acquisition. Genes encoding PG family members were also identified in several herbivorous insects including mirid bugs, stick insects and the Phytophaga beetle lineages of weevils, longhorned beetles and leaf beetles. Although it is believed that PGs enable these insects to digest plant cell walls, thus promoting herbivory, and their activity has been characterized *in vitro*, the biological relevance of PG enzymes in the context of insect-plant interaction has not been experimentally tested so far. To address this point, we silenced the three active endo-PGs of the mustard leaf beetle *Phaedon cochleariae* by RNA interference and recorded larval development. Successful knockdown of the three PGs at once in 2nd instar larvae resulted in an 80% reduction of total PG activity in their guts compared to both gfp-injection and non-injection controls. PG-silenced larvae showed a slower development with a delay in molting from 2nd to 3rd instar, and a significantly lower weight gain and food intake. These findings clearly show the benefit of expressing PG genes as an adaptation to feed on plants and indicate that PG activity in insects helps to get access to the plant cell wall encased protein-rich cytoplasm and/or to directly utilize the pectin breakdown products as carbon source.

Keywords: plant cell wall degrading enzymes, Phytophaga, leaf beetles, polygalacturonases, RNA interference

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Herbivory-induced jasmonates impact carbon acquisition and thereby constrain plant resistance and defoliation tolerance

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Jasmonates regulate a vast array of plant processes as secondary metabolism and plant development. Whether and how they influence plant primary metabolism and in turn plant resistance to herbivores and defoliation tolerance is unclear. I will present our work in this context, which covers four major topics: i) the impact of herbivory-induced jasmonates on leaf and root carbohydrate pools[1,2]; ii) the mechanisms through which jasmonates regulate carbohydrate accumulation[3,4] iii) the effect of herbivory-induced, jasmonate-dependent changes in carbohydrate accumulation on herbivory performance[3] and iv) on plant tolerance to herbivory[5]. Our research illustrates that herbivory-induced jasmonates reduce carbohydrate accumulation by regulating gibberellin signaling, and that carbon depletion constrains plant resistance to herbivory by increasing herbivore growth, and reduces defoliation tolerance. Our findings provide novel insights on the mechanisms that may contribute to natural variation in jasmonate-signaling and to the evolution of plant defense syndromes in nature.

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Keywords: Herbivory, Jasmonates, Gibberellins, Primary Metabolites, Defoliation Tolerance, Plant Resistance

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Inference of plant-mediated interactions in herbivorous insect communities from time series count data

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Plant–mediated interactions shape the insect herbivore community on plants. Attack by one herbivore species induces a plant response that in turn affects the preference and performance of other herbivores interacting with the induced plant. The number and type of herbivorous insects determine the defence response of plants. Thus, each herbivore species may differentially affect the composition of the herbivorous community at subsequent times. So far, these plant-mediated interactions have been studied with multivariate techniques applied to count time-series data. However, such techniques offer limited insight into the structural and quantitative wiring of plant-mediated interaction networks. Thus, we propose a data-based generalized time-series model that establishes a probabilistic relationship between present and past herbivore infestations. To achieve this we use time-series count data while accounting for interactions, space, time, growth rate of insects, and random plant variation. We built a new framework of unprecedented complexity, adopting common elements from well-accepted models. A new experiment was carried out in which insect populations on cabbage plants were monitored on a daily basis for one growth season. With this high-resolution time-series dataset and the new time-series model, we succeeded in 1) quantifying the sign, strength, and decay of insect-insect interactions; and 2) identifying which herbivore species have strong effects on the presence of others (so called keystone herbivores) and which species strongly respond to induced plants. We show that the species *Autographa gamma* has the highest instantaneous effect on all other species, but the species *Myzus persicae* has the highest season long effect. We link the discrepancy between strength and season-long effect of inducers to the abundance, spread, and order of arrival of insects which have been shown to be important to the community dynamics.

Keywords: plant mediated interactions, time series models, herbivores, *Brassica oleracea*

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Aphids suck their own grave – induced elevated concentrations of cadmium and zinc in phloem exudates of a hyperaccumulator plant lead to negative potentiation effect on *Myzus persicae*

Clemens Stolpe *[1], Franziska Giehren [1], Ute Krämer [2], Caroline Müller [1]

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Plants that are able to (hyper)accumulate heavy metals and metalloids store these in their aboveground tissues and can avoid self intoxication. However, it was unknown whether heavy metals also accumulate in the phloem of such plants and thus could act detrimental against phloem-sucking herbivores and whether they are inducible upon herbivore infestation. Therefore, we collected phloem exudates from leaves of the (hyper)accumulator species *Arabidopsis halleri* with and without aphid infestation and analyzed the ionome. Phloem exudates collected from plants that grew on heavy metal-amended soil contained indeed higher concentrations of Cd and Zn than exudates of plants grown on unamended soil. Moreover, these heavy metals were found in highest concentrations in phloem exudates of aphid-infested plants, indicating that inorganic defences may be similarly inducible as organic defences. To investigate long term effects of Cd and Zn on the performance of the aphid *Myzus persicae*, we added them in different combinations with and without their phloem-specific metal transport proteins in artificial diets. Diets amended with both heavy metals showed a potentiation effect leading to more negative influences on aphid survival and reproduction compared to diets amended with only one metal. The presence of phloem-specific metal transport proteins in the artificial diets had no effect on the aphids. Our results provide evidence that elevated concentrations of Cd and Zn, particularly in combination, can serve as an effective defence in metal-(hyper)accumulating plant species against phloem- sucking insects, supporting the elemental defence hypothesis.

Keywords: Brassicaceae, chemical ecology, environmental toxicity, heavy metals

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Overcompensation of herbivore reproduction through hyper-suppression of plant defenses in response to competition

Bernardus Schimmel *† [1], Livia Ataide [1,2], Rachid Chafi [1], Carlos Villarroel [3], Juan Alba [1], Robert Schuurink [3], Merijn Kant [1]

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Spider mites are destructive arthropod pests on a variety of crops. The generalist herbivorous mite *Tetranychus urticae* induces defenses in tomato (*Solanum lycopersicum*) when feeding on it and this constrains its fitness. In contrast, the Solanaceae-specialist *T. evansi* upholds a high reproductive performance by suppressing tomato defenses. When present on the same plant, *T. evansi* outcompetes *T. urticae* as was found in natural settings as well as in laboratory experiments, but it is not known to which extent this is facilitated by the defenses of the plant. Here we show that *T. evansi* switches to hyper-suppression of defenses after its tomato host is also invaded by its natural competitor *T. urticae*. Jasmonate (JA) and salicylate (SA) defenses were suppressed stronger, albeit only locally at *T. evansi*'s feeding site, once *T. urticae* was introduced to an adjacent area on the same leaflet. The hyper-suppression of JA and SA defenses coincided with increased expression of *T. evansi* genes coding for salivary defense-suppressing effector proteins and was paralleled by an increased reproductive performance of the mite. Together, these observations suggest that *T. evansi* overcompensates its reproduction through hyper-suppression of plant defenses in response to nearby competitors. We hypothesize that the competitor-induced overcompensation promotes *T. evansi*'s competitive population growth on tomato.

Keywords: competition, defense suppression, effectors, overcompensation, plant, mediated interactions, spider mites, tomato

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Global Change and Thermal Ecology

Wednesday 5th of July 2017 Salle Thélème Tanneurs

Global change and thermal ecology Chairs S. Pincebourde and A. Woods		
14h00	**John Terblanche** **Keynote Speaker**	Mechanisms and responses of insects to climate stress
14h45	**Marion Javal *PhD***	Respiration-based monitoring of metabolic rate following cold-exposure in two invasive Anoplophora species (Cerambycidae) depending on acclimation regime
15h	**Tao Li**	Long-term effects of elevated CO2, warming and droughts on VOC emission and phenolics production of *Calluna vulgaris* in a temperate heath ecosystem
15h15	**Mirka Macel**	Rapid evolution of a range expanding plant
15h30	**Shai Morin**	Projecting pest population dynamics under global warming: the combined effect of inter- and intra-annual variations
15h45	**Pincebourde/Woods**	Extended phenotypes and global change biology

16h00 Departure for excursion and gala dinner

16h30 Montbazon Forteresse

23h30 Departure from gala dinner

00h00 Return

Keynote

Mechanisms and responses of insects to climate stress

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Understanding terrestrial arthropod population dynamics is a critical component of forecasting for risk (invasions, agricultural or species vulnerability). Accurate forecasting of, for example, diurnal activity patterns, population fitness, niche shifts, environmental stress, or key phonological events allows timely, cost-effective interventions and management strategies. However, due to the diversity of physiological or behavioural strategies within (e.g. between life-stages) and among insect species in their sensitivity toward climate, insect pest population abundance models are often not easily interpreted for, or lack direct relevance to, management strategies in the field. Here we describe our efforts to better establish functional links between laboratory trait-based assays and insect field responses. Using diverse Lepidotera and Diptera in agro-ecosystems as model taxa, we further show how distinct species-specific trait-environment associations, and their plastic responses to environmental conditions, challenge any broad generalizations regarding climate change responses. We then discuss how a population's age-structure, especially in species with overlapping generations, partly determines the outcome of climate extremes experienced during a particular season on downstream fitness and the following season's population abundance. The application of biophysical, process-based or agent-based models at fine spatial or temporal grains to forecast field population abundance holds promise for understanding the ecologically-relevant microclimate of insects on their hosts plants. In consequence, the integration of these models with trait responses at diverse time scales should reveal important insights into the functional or adaptive evolutionary potential of key species, and ultimately, lead to better understanding of trait-environment associations and the evolution of plasticity in novel environments.

Keywords: phenotypic plasticity, thermal tolerance, physiological response, population dynamics, overwintering

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Respiration-based monitoring of metabolic rate following cold-exposure in two invasive Anoplophora species (Cerambycidae) depending on acclimation regime

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Asian and Citrus longhorned beetles *Anoplophora glabripennis* (ALB) and *A. chinensis* (CLB) respectively, are two closely related xylophagous invasive species whose native ranges overlap in Eastern Asia. Although both species are capable to develop in a wide range of hosts in their invaded areas, their invasion patterns differ. Introduction pathway is usually wood packaging for ALB but plants for planting for CLB. ALB shows numerous outbreaks remaining localized in urban areas in North-East America and Western Europe, whereas CLB is presently restricted to the Mediterranean area but spreading in natural areas. Temperature is pivotal in setting distribution limits of ectotherms, and limiting low temperatures may most likely be encountered by overwintering larvae of ALB and CLB. To investigate whether differential cold tolerance can contribute to setting the limits of both species' invaded ranges, we monitored larval metabolic rate before and after exposure to a one-week moderate cold stress assumed to be ecologically relevant in their European range (-2/+2 ◦C, 14/10 hours). We tested two distinctive fluctuating acclimation regimes before the cold exposure to check whether larval thermal experience prior to introduction events could alter the invasive success in new areas. Survival was high in all conditions for both species. While visual examination showed temporary locomotor and feeding inactivity during the stress, we found no clear evidence of altered respiration rate when comparing pre-stress and post-stress measurements, suggesting that larvae could immediately resume their initial metabolic activity after the stress, regardless of the acclimation regime. These results tend to indicate similar tolerances to the moderate stress considered for both species, but further studies on prolonged and more acute stresses are mandatory to address whether putative differential cold tolerance contribute to their distinctive spread patterns. Assessing respective propagule pressures through their introduction pathways is also required to understand their different invasion dynamics.

Keywords: ALB, CLB, Anoplophora, acclimation, invasive species, respirometry, cold stress

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Long-term effects of elevated CO2, warming and droughts on VOC emission and phenolics production of *Calluna vulgaris* in a temperate heath ecosystem

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Climate change is reshaping species interactions with ecosystem-level consequences. The mechanisms underlying the shift in species interactions are multifaceted, including climate-related changes in plant secondary metabolites that are potentially implicated in these interactions. Volatile organic compounds (VOCs) and phenolics are among those that have increasingly been shown to mediate myriad species interactions and be influenced by climate change. Components of climate change, including increasing CO2 levels, warming and droughts can drastically influence the production of plant secondary chemicals. Despite increasing studies addressing this issue, most of them have primarily focused on the effects of single climate change factors and employed relatively short exposure durations. Under natural conditions, however, plants are simultaneously confronting multiple abiotic and/or biotic factors. It is becoming increasingly apparent that plant responses to multiple environmental factors differ from and cannot be predicted by the effects of these factors acting alone. In addition, plant responses to long-term exposure to environmental stresses may differ from responses to short-term exposure because of their capability to acclimate and adapt successfully to novel environments. In order to more accurately characterize the trajectory of plant secondary metabolite responses and provide more realistic prediction of how projected climate change will restructure species interactions, long-term, multifactor experiments are in urgent need.

Here we aimed to investigate plant secondary metabolism response to elevated CO2, droughts and night-time warming using the dominant evergreen dwarf species, *Calluna vulgaris*, in a temperate heath. We measured VOC emissions at the branch level and quantitated the production of phenolics and tannins in different plant organs (leaves, stems and flowers) over two growing seasons after six years of exposure to these environmental factors. We will present these data and discuss the ecological consequences as well as the potential feedbacks on the local and regional climate.

Keywords: climate change, phenolics, volatile organic compounds

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Rapid evolution of a range expanding plant

Martine Huberty [1,2], Jennifer Cross [2], Klaas Vrieling [3], Nicole Van Dam [4,5], Mirka Macel *† [2,5]

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Due to climate change, some species are shifting their distribution ranges towards the poles. What happens with these species in their novel range? Do they quickly evolve and adapt to their new biotic and abiotic environments? Can we predict evolutionary changes in the novel range? We tested the genetic and phenotypic differentiation of the range expanding plant *Rorippa austriaca* (Brassicaceae). This species is native to south central-east Europe and has expanded its range to northwards with its current range limit in southern Scandinavia. Molecular genetic analyses showed that the genotypes from the novel range in North-West Europe were different from genotypes of the core distribution. Plants from the novel range showed increased vigor and differences in chemical defenses (glucosinolates) and insect herbivore resistance. In a common garden in the new range, there was a higher insect abundance and more herbivore damage on the plants originating from the core distribution compared to plants from the novel range. Our results suggest that range expanding plants may evolve increased vigor and altered herbivore resistance in their novel range, analogous to evolution of invasive plants. Theories on the evolution of invasive species could therefore (partly) be used to predict the evolution of species that are on the move due to global warming.

Keywords: climate change, insect communities, chemical defenses, latitudinal gradient

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Projecting pest population dynamics under global warming: the combined effect of inter- and intra-annual variations

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The typical short generation length of insects makes their population dynamics highly sensitive not only to mean annual temperatures but also to their intra-annual variations. To consider the combined effect of both thermal factors under global warming, we propose a modeling frame-work that links general circulation models with a stochastic weather generator and population dynamics models to predict species population responses to inter- and intra-annual temperature changes. This framework was utilized to explore future changes in populations of *Bemisia tabaci*, an invasive insect pest-species in the Mediterranean region. We considered three locations representing different pest status and climatic conditions: Montpellier (France), Seville (Spain) and Beit-Jamal (Israel). We produced ensembles of local daily temperature realizations representing current and future (mid 21-century) climatic conditions under two emission scenarios. Our simulations predicted a significant increase in the average number of annual generations and in population size, and a significant lengthening of the growing season in all three locations. A negative effect was found only in Seville for the summer season, where future temperatures lead to a reduction in population size. High variability in population size was observed between years with similar annual mean temperatures, suggesting a strong effect of intra-annual temperature variation. Critical periods were from late spring to late summer in Montpellier and from late winter to early summer in Seville and Beit-Jamal. Although our analysis suggested that earlier seasonal activity does not necessarily lead to increased populations load unless an additional generation is produced, it is likely that the insect will become a significant pest at Mediterranean latitudes above 40◦ during the next 50 years. Our simulations also implied that current predictions based on mean temperature anomalies are relatively conservative and it is better to apply stochastic tools to resolve complex responses to climate change while taking natural variability into account.

Keywords: climate change, population dynamics models, general circulation models, down scaling, weather generator, invasive species, intra, annual temperature variability, reproductive performance, *Bemisia tabaci*

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Extended phenotypes and global change biology

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Insects build shelters using an astonishing array of materials and techniques. The shelters are extended phenotypes of the insects and can fulfill diverse physiological and ecological functions: they may protect their inhabitants from predators, provide access to more or better food, and ameliorate poor abiotic conditions, particularly temperature and humidity. Here, we argue that insect-built shelters may also affect how insects respond to climate change, particularly change in abiotic factors. Climate change is causing monotonic shifts in conditions, such as long-term increases in atmospheric CO2 and mean surface temperature, and it is causing higher levels of variability, e.g., in temperature, rainfall, and frequency of extreme events. Insect-built shelters are effectively external integuments, made of living or non-living layers, that separate the insect from its proximate macro-environment and that alter exchanges of heat and water vapor. Using a set of case studies, we examine how strong this filtering can be, and we evaluate evidence about whether structures show developmental plasticity or phenotypic flexibility in their design. Finally, we integrate physiological and biophysical aspects of insect-built structures with anticipated patterns of change in temperature, solar irradiation, and hydrological cycles to predict the consequences of climate change for shelter-building insects.

Keywords: extended phenotype, plasticity, temperature, humidity, climate change

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Evolutionary genomics

Thursday 6th of July 2017 Salle Thélème Tanneurs

Evolutionary genomics Chairs JC Simon and N. Whiteman		
08h30	**Noah Whiteman** ***Keynote Speaker***	Breaking bad: The evolution of herbivory in Drosophilidae
09h15	**Patrick Abbot**	Transcriptional profile and differential fitness across a cardenolide gradient in a specialist milkweed insect reveal the costs of response
09h30	***Hélène Boulain (PhD)***	Evolutionary analyses of a new quantitative catalogue of candidate secreted salivary effectors in *Acyrthosiphon pisum*
09h45	**Marianthi Karageorgi**	Olfactory specialization contributes in the making of the fruit pest *Drosophila suzukii*
10h00	**Nicole Van Dam**	Ecogenomics analysis of *Solanum dulcamara* reveals chemical diversity in glycoalkaloids related to slug resistance
10h15	Coffee break (sponsored by the INRA)	
11h15	**Michael Thomas-Poulsen** ***Keynote Speaker***	Novel insights into symbiotic paths to sustainable agriculture
12h00	Business meeting and Concluding remarks	
12h30	Lunch bags (sponsored by the University of Tours)	
14h00	End of the meeting	

Keynote

Breaking bad: The evolution of herbivory in Drosophilidae

Noah Whiteman *† [1], **Andrew Gloss** [2], **Anna Nelson-Dittrich** [3], **Richard Lapoint** [3]

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Southwood proposed that the paucity of insect orders with herbivorous members was due to effective hurdles that herbivorous insects must overcome when colonizing plants: nutritional, attachment, desiccation and host finding. Once overcome, evolutionary transitions to herbivory drive species radiations and herbivory explains 30% of the variation in diversification rates across insect orders. The ancient origin of herbivory in most lineages renders identifying the genomic architecture associated with overcoming the hurdles difficult, such as Cuculionoidea and Lepidoptera. We leveraged a recent transition to herbivory within the Drosophiliae to study the genomic architecture of traits linked to overcoming hurdles to herbivory. We sequenced and annotated the genome of *Scaptomyza flava*, a drosophilid fly that feeds on living leaves of mustards and that of *S. pallida*, a non-herbivorous relative that feeds on decaying leaves. The close relatedness between *S. flava* and *Drosophila melanogaster*, the genetic model insect, enabled the discovery of evolutionary innovations in Scaptomyza using comparative genomics. Genes playing key roles in metabolism of plant-derived dietary compounds evolved at an accelerated rate following the transition to herbivory in *S. flava*, consistent with the hypothesis that plant chemicals are major drivers of herbivore evolution. Notably, an expanded set of rapidly evolving glutathione S-transferases confer unprecedented capacity to detoxify insecticidal mustard oils produced by host plants. An altered sterol profile in *S. flava* relative to microbe-feeders was coupled with rapid evolution of sterol transporters that are orthologous to a gene essential for cholesterol homeostasis in humans. Genome-wide association mapping revealed the neural developmental pathway is involved in the formation of dense, plant-cutting pegs on the *S. flava* ovipositor, a key morphological innovation in *S. flava*. Overall, these analyses highlight how targeted modification of pre-existing genes-rather than dramatic genome-wide changes-plays a key role in overcoming barriers to the evolution of herbivory.

Keywords: Evolution, herbivory, adaptation, mustard oils, Arabidopsis, Drosophilidae

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Transcriptional profile and differential fitness across a cardenolide gradient in a specialist milkweed insect reveal the costs of response.

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Interactions between plants and herbivorous insects have been models for theories of specialization and coevolution for over at century, and it is well-established that phytochemistry governs many aspects of these interactions. Despite this, the mechanisms insect specialists employ to sequester or otherwise tolerate plant secondary metabolites, and the costs of these responses, remain poorly characterized. Using a milkweed-specialist aphid model, the *Aphis nerii* system, we test the effects of increased plant secondary metabolites on aphid life history traits and whole transcriptome gene expression. We show that increased secondary metabolites have a negative effect on aphid development and lifetime fecundity. When feeding on host plants with higher levels of secondary metabolites, aphids differentially express a narrow, targeted set of genes including those involved in canonical detoxification processes including P450s, esterases, hydrolases, and UDP-glucuronosyltransferases. These results indicate that *A. nerii* marshal a variety of metabolic detoxification mechanisms in host plant specialization and circumvention of milkweed secondary compounds, but not without deleterious effects on fitness.

Keywords: specialist, insect, secondary metabolite, sequestration, tolerance

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Evolutionary analyses of a new quantitative catalogue of candidate secreted salivary effectors in *Acyrthosiphon pisum*

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The pea aphid, *Acyrthosiphon pisum*, is a sap-feeding phytophagous insect that forms a complex of 15 biotypes, each of which is specialized to one or a few species of Fabaceae. Successful establishment of aphid phloem feeding depends on the functions of salivary proteins injected into the host plant. Most of the proteins secreted with aphid saliva are thought to be produced in salivary glands (SG) of the aphid, and some are shown to suppress or trigger plant defence reactions like effectors of microbial pathogens. Transcriptomics and proteomics studies of SG or isolated saliva have created catalogues of candidate salivary proteins in the past; however, those catalogues often lack quantitative data of expression and tissue specificity. To create more informative catalogue of salivary proteins with quantitative expression data, and to analyse their evolutionary histories in *A. pisum*, we conducted SG and guts transcriptome by RNAseq. The data revealed around 2000 genes that were up-regulated in SG compared to gut. Among these SG induced genes, more than 600 genes are predicted to encode secreted proteins. Orthologous gene search conducted with 16 arthropod whole genomes (1 arachnid, and 15 insects including 5 aphid species) revealed that more than 50 % of our salivary gene candidates were aphid or *A. pisum* specific. By analysing the evolutionary rates of well-characterized salivary genes and their orthologues, we observed contrasting evolutionary patterns possibly influenced by their different roles in aphid feeding. The orthology analysis also revealed expansions of some gene families in *A. pisum* compared to other aphid species. Moreover, the positive selection acting on some salivary gene copies among these families suggests an important role of gene duplication in the evolution of *A. pisum* and may indicate the involvement of these genes in host adaptation.

Keywords: Salivary genes, evolutionary patterns, pea aphid

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Olfactory specialization contributes in the making of the fruit pest *Drosophila suzukii*

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Behavioral innovations can facilitate animal invasions into new ecological niches, with the potential of turning species into pests. However, currently little is known about the underlying genetic basis of such events. Here, we study how the agricultural fruit pest *Drosophila suzukii* has evolved its egg-laying preference for ripening fruit. Most closely related Drosophila species, including *D.melanogaster*, lay their eggs in decaying plant substrates. In our study, we combined behavioral experiments in multiple species with neurogenetics and mutant analysis using the CrispR/Cas9 technology in *D. suzukii*. Our results establish that *D. suzukii* has evolved a specific egg-laying preference for ripening fruit, but most likely it has retained the ancestral feeding preference for decaying fruit. Our results also show that changes in the olfactory system of *D. suzukii* have contributed to the evolution of its novel egg-laying behavior. In particular, we show that the odorant receptor subsystem is involved in its olfactory attraction to fresh fruit as well as the detection of odorant egg-laying stimulants present in fresh fruit. Interestingly, though a comparative transcriptomic analysis, we find that the several orthologs of odorant receptors that detect odors of fresh fruit in *D. melanogaster* are upregulated in the antennae of *D. suzukii*. In overall, our study shows that olfactory specialization, likely through remodelling of the odorant receptor repertoire, has contributed in the novel egg-laying preference of *D. suzukii*.

Keywords: *D. suzukii*, agricultural pest, egg, laying, evolution, olfaction, CrispR/Cas9, neuroge- netics

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Ecogenomics analysis of *Solanum dulcamara* reveals chemical diversity in glycoalkaloids related to slug resistance

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Chemical diversity among individuals within a single plant species is commonly found in natural populations. This diversity is thought to originate from and maintained by (local) co-evolution between plants and herbivores. Metabolomic analyses are extremely valuable to study such natural polymorphisms. Because of their untargeted nature, they provide a comprehensive overview of the plant’s metabolome. These individual metabolomic profiles can be correlated to measures of herbivore resistance. Here we present an example of how resistance to slugs in natural populations of *Solanum dulcamara* (Bittersweet nightshade) concurs with metabolomic differences. A high throughput resistance screening performed on a total of 96 accessions from eight natural populations in the Netherlands identified a sub-set of accessions covering a consistent range of resistance to slug feeding, ranging from highly preferred to fully rejected. Metabolomic analyses on Liquid Chromatography-Time of Flight-Mass Spectrometry (LC-qToF-MS) revealed a high diversity in glycoalkaloid (GA) concentrations and profiles among the selected accessions. Whereas slugs overall preferred plants with low GA concentrations, it was also found that most susceptible accession showed a completely different GA profile than the more resistant accessions. Molecular studies showed that plant chemical diversity may readily arise from mutations, gene-duplications and neo-functionalization of specific enzymes within a biosynthetic pathway. Because of their toxicity to humans and presence in closely related crops, such as tomato (*S. lycopersicum*) and potato (*S. tuberosum*) many of the genes and enzymes involved in GA biosynthesis are known. Therefore, we combined our metabolomic studies with a comprehensive RNAseq analysis of five of the genotypes with the most divergent GA profiles and slug resistance scores. Combined with additional data on natural herbivore damage in a common garden experiment, these ecogenomics analyses will show the ecological consequences of this natural chemical and genetic diversity.

Keywords: chemical ecology, chemodiversity, glycoalkaloids, Liquid Chromatography, Time of Flight, Mass Spectrometry, metabolomics, slugs, Solanum, transcriptomics

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Keynote

Novel insights into symbiotic paths to sustainable agriculture

Michael Thomas-Poulsen * 1

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Thirty million years ago, the ancestors of the termite sub-family Macrotermitinae and the basidiomycete Termitomyces joined forces in what became one of the most sophisticated plant biomass decomposition symbioses on Earth. Through an intricate and efficient decomposition process that involves plant biomass passing termite guts before decomposition in external fungal gardens, these termites fully utilize a range of plant substrates and have become major decomposers in the Old World, while having no apparent problems with infectious diseases. Here I review how recent applications of state-of-the-art sequencing and chemical analyses tools have provided novel insights to our understanding of complementary symbiont biomass decomposition, division of labour in termite hosts, and how obligate gut passage of the plant substrate may be key to efficient suppression of antagonists of the symbiosis.

Keywords: Macrotermitinae, symbiosis, gut microbiota, 16S rRNA, metagenomics, CAZymes, LC, MS

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Session 1 Monday evening

Insect-plant-microbe interactions in forests and agrosystems - *COST action		**Poster Session 1**
P1	**Fatma Acheuk**	Insecticidal and developmental inhibitory properties of extracts of the saharian plant *Haplophyllum tuberculatum* (Rutaceae) on *Locusta migratoria* five instar larvae (Acrididae : Oedipodinae)
P2	**Niccolò Bassetti**	Towards the genetic basis of the hypersensitive response induced by *Pieris* spp. eggs in *Brassica rapa*
P3	**Moe Bakhtiari**	Root Induced Defense specificity in Above & Belowground tri-trophic Interaction in *Cardamine* Spp.
P4	**Emilie Bosquée**	*Myzus persicae* dispersion and Potato virus Y transmission under elevated CO2 atmosphere
P5	**Agnès Brosset**	Belowground and aboveground damage can impact the conifer growth and feeding behavior of the weevil *Hylobius abietis* (Coleoptera: Curculionidae)
P6	**Yayuan Chen**	Variation in induced resistance among tree genotypes: how does it influence the interaction between bark-feeding insects and conifer seedlings?
P7	**Xavier Chiriboga**	Root-colonizing bacteria enhance the levels of (E)-β-caryophyllene produced by maize roots in response to rootworm feeding
P8	**Michael Eisenring**	Reduced Caterpillar Damage Benefits *Lygus hesperus* on Bt Cotton
P9	**Maria Faticov**	Geographical variation of endosymbionts in the insect food web on oak
P10	**Ludovico Formenti**	Interactive effects of mycorrhizal inoculation and jasmonic acid endogenous production on plant resistance against herbivores
P11	**Tae Woong Jang**	Effect of ground-fogging of thiacloprid on target and non-target insects in Korean pine forests
P12	**Giacomo Santoiemma**	Distribution and development of *Drosophila suzukii* along elevation gradients
P13	**Jeltje Stam**	Herbivory and florivory at different strawberry plant resistance levels
P14	**Meng Ye**	A conserved priming signal: Volatile indole activates early defense signaling in Rice
P15	**Wei Huang**	Neighborhood effects determine plant-herbivore interactions below ground
P16	**Sihem Ziouche**	Interactions plantes-insectes dans un écosystème forestier : le cas de la chenille processionnaire du pin *Thaumetopoea pityocampa* en région de l’Est Algérien

Community ecology and phylogenetics	**Poster Session 1**	
P17	**Ayman Elsayed**	Life history of two leaf bud gallers associated with the deciduous tree *Schoepfia jasminodora (Schoepfiaceae)* in Japan
P18	**Rieta Gols**	Herbivore-mediated fitness effects of increasing chemical variation among neighbouring Plants
P19	**Kotaro Konno**	Why are terrestrial ecosystems generally green with small herbivores biomass? Why are anti-nutritive and inducible defenses effective? The realities that a novel fully-parameterized food web model tells
P20	**Antonino Cusumano**	Canola/cabbage aphid food web – underestimated top-down pressure in invaded range
P21	**Veronika Mayer**	Evolutionary and functional ecology of ant-plant-fungus symbioses
P22	**Daan Mertens**	Plastic plant defence strategies as an optimal response to unpredictable multiherbivore Communities
P23	**Yu Okamura**	Pieris butterflies regulate two genes differently for adapting to wide range of Brassicaceae host plants
P24	**Daniel Potter**	Teaching Insect-Plant Relationships - Template for a Successful Graduate Course
P25	**Lora Richards**	Diverse phytochemical profiles and ecological interactions
P26	**Diego Santos-Garcia**	Portiera as a phylogenetic tool on whiteflies
P27	**Bernardus Schimmel**	Overcompensation of herbivore reproduction through hyper-suppression of plant defenses in response to competition
P28	**Jiri Skuhrovec**	Morphological adaptations of coccinellid species determined by host-plant architecture
P29	**Johan Stenberg**	Plant resistance ecology: what happens to insect communities when host plants evolve more resistant?
P30	**Klaas Vrieling**	Paralell evolutionary changes in resource allocation to anti-herbivore traits in an invasive plant species.

Plant-insect-microorganisms interactions - *COST action		**Poster Session 1**
P31	**Sandra Baksay**	Pollination network analyzis by environmental metagenomics
P32	**Junior Corneille Fingu Mabola**	Impact of endophytic entomopathogenic fungus on plant attractiveness in aphid virus-plant interaction
P33	**Gabriella Caballero Vidal**	Are aphid vectors manipulated by plant virus?
P34	**Fryni Drizou**	Insect-pathogen interaction in oilseed rape (OSR): *Myzus persicae* increases susceptibility of *Brassica napus* to *Rhizoctonia solani* AG 2-1.
P35	**Galit Eakteiman**	Using dsRNA of the BtGST2 Detoxification Gene to Develop *Bemisia tabaci* Resistant Plants
P36	**Luis R Paniagua Voirol**	Antibiotic treatment of *Pieris brassicae* attenuates egg-mediated anti-herbivore defenses in two brassicaceous species
P37	**Hyeok Jun Kwon**	Dispersal capacity of *Monochmus saltuarius* (Gebler) (Coleoptera: Cerambycidae) on fight mills
P38	**Ian Kaplan**	Phylogenetic farming: Can evolutionary history inform crop and insect management?
P39	**Miika Laihonen**	Fungal grass endophytes can influence host plant preference and fitness of a satyrine butterfly
P40	**Kirsten Leiss**	Induced resistance to thrips by bacterial infection
P41	**Valeria Mereghetti**	Strength in cooperation: bacterial symbionts help the insect host overcome plant defences
P42	**Luis R Paniagua Voirol**	The role of the *Pieris brassicae* microbiome during a host-plant shift
P43	**Bruna De Càssia Ramos**	Learning in two butterfly species when using flowers of the tropical milkweed *Asclepias curassavica*: no benefits for pollination
P44	**Sandeep Sarde**	Sweet Pepper-Thrips Interaction: Uncovering dynamics of the plant defense-signaling network to identify novel leads for maximizing crop protection
P45	**Osariyekemwen Uyi**	Developmental and reproductive performance of a specialist herbivore depend on seasonality of, and light conditions experienced by, the host plant
P46	**Zhenggao Xiao**	Earthworms indirectly mediate plant-herbivore interaction via changes in soil nutrient composition and plant chemical traits

Session 2 Tuesday evening

Multitrophic interactions and ecological networks Poster Session 2		
P47	**Christine Becker**	Herbivore-induced plant volatile blends are influenced by plant nutrition
P48	**Mascha Bischoff**	Disease in bloom - exploring the link between pollination and phytopathology
P49	**Zoe Bont**	A herbivore tag-and-trace system reveals contact and density-dependent repellence of a root toxin
P50	**Sandrine Mariella Bayendi Loudit**	Can we use semiochemicals to control *Aphis craccivora* Koch?
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Evolutionary genomics Poster Session 2

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Poster abstracts

Poster 1

Insecticidal and developmental inhibitory properties of extracts of the saharian plant *Haplophyllum tuberculatum* (Rutaceae) on *Locusta migratoria* five instar larvae (Acrididae : Oedipodinae)

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Many plant bio-synthesized compounds with toxic and defensive action of the plant against phytophagous insects have been identified. These compounds from the secondary metabolism of plants belong to different chemical groups: phenols, terpenoids, alkaloids, steroids and others. To assess the bioinsecticidal effects of compounds produced by *Haplophyllum tuberculatum* (Rutaceae) on *Locusta migratoria migratoria*, a crude ethanolic extract and alkaloids were obtained by maceration of leaves and stems of the plant. Newly emerged fifth instar larvae were treated by forced ingestion. The test extracts (ethanolic extract and alkaloids extract) exhibited a potent larvicidal effect, with dose-dependent mortality. At higher concentrations (> 1000 g/larvae), the two extracts induced a strong neurobehavioral toxicity and a significant inhibition of acethylcholinesterase activity for alkaloids. At a sub-lethal dose of 300 g/larvae, the extract had anti-feedant effects and caused severe developmental disruption, manifested by a delay in adult emergence and a high level of morphological deformities in larvae. In addition, protease activity was strongly reduced in treated larvae. In contrast, we observed an induction of glutathione S-transferase and esterase activities. Phytochemical analysis of the test extract revealed the presence of several active compounds, which may act as larvicides.

Keywords: *Haplophyllum tuberculatum*, *Locusta migratoria*, alkaloids, methanolic extract, toxicity, sublethal effect

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Poster 2

Towards the genetic basis of the hypersensitive response induced by *Pieris* spp. eggs in *Brassica rapa*

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Pests and pathogens are responsible on average for about a third of yearly crop losses. Identification of resistance (R) genes in crops has been successful for pathogens and partly for phloem-feeding insects such as aphids, whiteflies and planthoppers. However, R-gene-mediated resistance mechanisms against caterpillars (butterflies and moths) are less explored. An alternative may be preventing the caterpillar attack by investigating plant defence mechanisms that target the insect egg-laying phase. Eggs of *Pieris spp.* (cabbage white butterflies) induce a necrotic lesion in different brassicaceous plant species, including crops like *Brassica rapa*. This lesion resembles the hypersensitive response (HR) usually triggered by pathogens. It determines egg mortality through egg desiccation and dropping off. In a preliminary screening, different *B. rapa* accessions showed phenotypic variation for egg-induced lesions. This opens the possibility to study plant direct response against insect eggs through genetic approaches.

This project aims at unravelling the genetic and molecular mechanisms of the HR-like necrosis induced by *Pieris* spp. eggs in *B. rapa* through a combination of genetic mapping, transcriptomics and phenotyping of TILLING populations. This research will result in improved knowledge on egg-targeting plant defences as first line of resistance against lepidopteran pest insects.

Poster 3

Root Induced Defense specificity in Above and Belowground tri-trophic Interaction in *Cardamine* Spp.

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Herbivore induced plant volatiles (HIPVs) are part of indirect defensive arsenal of many plant species against herbivores and have been shown to aid plants against herbivores by attracting natural enemies of herbivores. However, the extent in which such defensive strategies are employed by plants against belowground herbivores, and how the presence of different aboveground herbivores modifies the nature of these interactions remains largely untested. We examined the effect of AG herbivory by *Pieris brassicae* and *Brevicoryne brassicae* on BG herbivory by *Delia radicum* and its natural enemy's recruitment, nematode *Heterorhabditis megidis* to test for the specificity of root indirect defense among five different *Cardamine* plant species, originating from different elevation gradients. We used a custom-made four-arms BG olfactometer to test the attraction of entomopathogenic nematodes toward 4 different odour sources: 1) control plants without herbivory, 2) plants infested with the specialist root-chewers *D. radicum*, 3) plants co-infested with *D. radicum* and *P. brassicae*, and 4) plant co-infested with *D. radicum* and *B. brassicae*. Overall, we observed consistent patterns in the BG attraction of natural enemies toward each treatment among the species originating from low elevation habitats. Although the presence of root herbivores strongly enhanced the attraction of natural enemies, this pattern was negatively affected by AG herbivores, indicating that AG herbivores, independent of their feeding guilds, reduce the ability of roots to signal distress when damaged by root herbivores. On the other hand, mid-elevation plant species attracted more nematodes when co-infested by phloem-feeding *B. brassicae* and *D. radicum*. Our results indicates the specificity in induction of root defenses by different AG herbivores in different *Cardamine* species belonging to different elevation gradients which can be explained by variation in emission of HIPVs from damaged roots and root biomass

Poster 4

Myzus persicae dispersion and Potato virus Y transmission under elevated CO2 atmosphere

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Most phytoviruses are dependent on insect vectors to spread and infect the surrounding crop plants. To increase their chances of dissemination, viruses are able to indirectly modify the behavior of insects through changes in plant physiology. However, changes in abiotic factors such as atmospheric gas concentrations could also alter plant physiology and metabolism, influence vector's biology and therefore, modify virus spread strategy. The present study compared the impact of two carbon dioxide (CO2) concentrations (aCO2 and eCO2) on the ability of a phytovirus (Potato Virus Y, PVY) to spread from a central infected tobacco plant to surrounding healthy ones, thank to the dispersion of aphid vectors (*Myzus persicae* (Sulzer)). We found that aphid dispersal, as well as the associated spread of viruses, were not affected by an increased CO2 concentration. In addition, the ability for aphids to transmit efficiently the virus was also determined. Here we highlighted the better capacity of aphids grown under eCO2 to transmit viruses to healthy plants, compared to aphids reared under aCO2 conditions. The results of the experimental trials undertook herein indicate that CO2 level could significantly modify the feeding behaviour of insect herbivores and thus alter the viral transmission ability, but not sufficiently to increase PVY spread.

Keywords: Green peach aphid, PVY, carbon dioxide, dispersal, transmission, non persistent virus

Speaker*

Poster 5

Belowground and aboveground damage can impact the conifer growth and feeding behavior of the weevil *Hylobius abietis* (Coleoptera: Curculionidae).

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Regeneration plantations of conifer seedlings are subject to feeding by bark beetles (Hylastes sp.) and pine weevils (*Hylobius abietis*). Both species are severe pests of young conifers and limit the forest regeneration at clear-cuttings in Europe. To protect seedlings from damage, a novel method utilizing the plant hormone Methyl Jasmonate (MeJA) has shown promising results by inducing resistance and decreasing the amount of damage received. However, the efficacy of MeJA has not been compared to other methods that can also be used to induce defences in plants (e.g. mechanical damage). In this study, we investigated how equal amount of mechanical damage either on stem or roots and previous feeding damage by the pine weevil on Scots pine seedlings can: 1) affect successive pine weevil feeding behavior, measured in terms of area debarked and 2) impact the plant growth measured by comparing the size of damaged and undamaged seedlings each week during two months. The experiment showed that previous herbivore and mechanical damage on stem and root altered the pine weevil feeding by limiting the area debarked on seedlings with a tendency for less feeding found for the root damage treatment. These results may suggest that the root damage disturbed seedling physiology by inducing defenses in responses to the damage and could impact the aboveground feeding behavior of pine weevils. It was also indicated that the root damage treatment reduced the seedling growth, suggesting that damage to belowground part, essential for the extraction and transport of the nutrients, may have a strong cost for the plant. To develop plant protection methods to reduce damage caused by the bark beetles and pine weevils, the sensitivity of the root should be taken into account.

Keywords: *Pinus sylvestris*, *Hylobius abietis*, feeding behavior, seedling damage, above, below-ground interaction, plant growth.
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Poster 6

Variation in induced resistance among tree genotypes: how does it influence the interaction between bark-feeding insects and conifer seedlings?

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Plants are food resources to many organisms and to fight attacks from herbivores they possess constitutive and induced defences. Constitutive defences are continuously expressed regardless of herbivore attack, while induced defences are activated when plants receive signals that they are being damaged. Methyl jasmonate (MeJA), a plant signalling hormone, has been proven to trigger induced defences when exogenously applied to plants. In Swedish managed conifer forests, feeding damage by the pine weevil *Hylobius abietis* and the black spruce beetle *Hylastes cunicularius* constitutes a severe threat to newly-planted seedlings in regeneration areas, causing high levels of seedling mortality and growth loss. Efforts to reduce damage have recently generated studies investigating if MeJA-induced defence can protect seedlings, and so far results are promising. However, responses to MeJA have been examined in only a few families/genotypes and we lack knowledge on genetic variation in induced responses to MeJA treatment and their effectiveness in deterring herbivores. To investigate variation in induced defence among genotypes, different families/genotypes of Norway spruce *Picea abies* and Scots pine *Pinus sylvestris* will be treated with MeJA. After MeJA treatment, the feeding extent and behaviour of bark-feeding insects, the defence traits induced and the growth of seedlings will be investigated. This will provide insight on how induced defences can influence the interaction between bark-feeding insects and conifer seedlings.

Keywords: methyl jasmonate, Norway spruce, Scots pine, induced defence
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Poster 7

Root-colonizing bacteria enhance the levels of (E) - β- caryophyllene produced by maize roots in response to rootworm feeding

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When larvae of rootworms feed on maize roots they induce the emission of the sesquiterpene (*E*)-β-caryophyllene (*E*βc) in most maize genotypes. *E*βc is attractive to entomopathogenic nematodes, which parasitize and rapidly kill WCR larvae, thereby protecting roots from further damage. Certain root-colonizing bacteria of the genus Pseudomonas benefit plants, by promoting growth, suppressing pathogens or inducing systemic resistance (ISR). In addition, some strains also have insecticidal activity. Effects of root-associated bacteria on direct and indirect plant defenses against insect herbivores have been studied aboveground. But, how beneficial soil bacteria may influence the emission of herbivore-induced plant volatiles (HIPV's) below-ground is not yet understood. In this study, we measured production of *E*βc in roots colonized by the growth-promoting-insecticidal bacteria *Pseudomonas protegens* CHA0 and *Pseudomonas chloraphis* PCL-1391 upon feeding by larvae of the banded cucumber beetle, *Diabrotica balteata* Le Conte (Coleoptera: Chrysomelidae). We used a combination of chemical analysis and gene expression measurements to evaluate *E*βc production and release, and assessed weight gain and mortality of *D. balteata* larvae to determine the effects of Pseudomonas spp. root-colonization. We found that *E*βc emission and expression of the *E*βc synthase gene-TPS23 was enhanced in Pseudomonas-colonized roots after 72 hours of *D. balteata* feeding. Undamaged roots colonized by Pseudomonas spp. showed no measurable increase in *E*βc production, but a slight increase in TPS23 expression. Root biomass was not affected by Pseudomonas colonization. Larvae that fed on roots colonized by *P. protegens* CHA0 tended to gain more weight than larvae that fed on roots colonized by *P. chloraphis* PCL-1391. Larvae mortality on Pseudomonas spp.-colonized roots was slightly, but not significantly higher. Observed enhanced production of *E*βc upon Pseudomonas spp. colonization may have consequences for interactions with root herbivores and other soil organisms such as entomopathogenic nematodes.

Keywords: Root, colonizing bacteria, *Diabrotica balteata*, (*E)*-β-caryophyllene, terpene synthase, maize

Speaker*

Poster 8

Reduced Caterpillar Damage Benefits *Lygus hesperus* on Bt Cotton

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The wide scale adoption of genetically modified cotton producing insecticidal Cry proteins from *Bacillus thuringiensis* (Bt), has led to area-wide suppression of major lepidopteran pests and a reduction of insecticide application. However, non-target pests not susceptible to the produced Cry proteins, such as the plant bug *Lygus hesperus*, have increased in Bt cotton fields in some parts of the world. In addition to the reduced application of insecticides, *L. hesperus* might also benefit from reduced caterpillar damage on Bt cotton. The latter was found to reduce the induction of insecticidal terpenoids enhancing the crops' susceptibility to other herbivores. The effects of plant induction on *L. hesperus* development was studied by caging nymphs on Bt and non-Bt cotton plants growing in a greenhouse. Plants were either non-damaged, previously damaged by Bt tolerant caterpillars (*Spodoptera exigua*), or treated with jasmonic acid (JA), a plant hormone known to induce cotton defense. Caterpillar induction, and to a lesser extent, JA induction of plant defenses negatively affected *L. hesperus* survival compared to non-damaged plants. This result was consistent for Bt and non-Bt plants. Induced plants showed increased levels of several terpenoids (incl. gossypol) compared to non-induced plants. Artificial diet feeding assays using purified terpenoids and molecular analyses of potential *L. hesperus* stress gene upregulation are being conducted to better understand mechanisms behind the greenhouse results. This study underpins the importance of plant-mediated, indirect interactions between herbivores for explaining agro-ecological processes and indicates how insect-resistance plant traits can indirectly impact herbivore communities.

Keywords: *Lygus hesperus*, plant mediated indirect interaction, cotton, terpenoid, defense induction

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Poster 9

Geographical variation of endosymbionts in the insect food web on oak

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The majority of insects harbor symbiotic bacteria (endosymbionts). Studies show that endosymbionts have diverse effects on their insect host, ranging from protection from natural enemies to manipulating the host's reproduction. Thus, endosymbionts may directly or indirectly affect insect ecology and shape insect food web structure. To elucidate the effect of endosymbionts on the structure and dynamics of insect communities, we need to know their spatial distribution and community structure, which is currently quite limited. The main aim of this project is to investigate the spatial distributions of endosymbionts within the insect food web on the oak tree *Quercus robur*.

For this, we are currently rearing thousands of leaf mining, galling and parasitoid insects from five different geographical locations: Finland (Wattkast), Sweden (Link'oping, Skane), the Netherlands (Loenermark) and France (Bordeaux). We will use molecular tools to identify endosymbiont species, including Wolbachia strains, to answer the following questions: 1) Is there geographical variation in endosymbionts associated with individual species of plant-feeding and parasitoid insects? 2) Do more closely related insect species share more similar endosymbiont communities? 3) Are some insect species simultaneously infected with more than one endosymbiont? 4) Can one plant-feeding insect species be infected with several strains of Wolbachia spp.?

Keywords: herbivore insects, endosymbionts, geographical variation

Speaker*

Poster 10

Interactive effects of mycorrhizal inoculation and jasmonic acid endogenous production on plant resistance against herbivores

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Mycorrhizal fungi, in addition to improve plant performance via increased food acquisition, they have also been shown to increase plant resistance against herbivores, but little is known how endogenous plant defences and mycorrhizal defence enhancement interact with each other in the presence of herbivores. With this study, we asked whether the increased plant resistance conferred by the mycorrhizal symbiosis can synergistically interact with the jasmonic acid (JA) phytohormonal pathway of the plant responsible for orchestrating plant defence strategy against chewing herbivores. To measure the interactive effects of mycorrhizal inoculation and JA-mediated defences, we measured resistance against *S.littoralis* larvae and plant defensive traits of wild-type tomato plants and two mutants lines; a JA-knockout mutant, and a mutant which overexpresses JA, in the presence or absence of mycorrhizal fungi. According to predictions, we observed that plant defensive traits such as the number of trichomes and specific leaf area were higher in WT plants and plants that overexpress JA, compared to plants impaired in JA production. Additionally, both wild-type plants, enhanced JA-producing plants, and mycorrhizal inoculation reduced *S.littoralis* survival and biomass, but their effects were not additive. Instead, the positive effects of mycorrhizal inoculation on plant resistance weakened with increasing JA production. In sum, both JA production and mycorrhizal inoculation increase plant resistance, but do not synergistically interact for multiplying resistance. Instead, we suggest that the magnitude of resistance conferred by mycorrhizal fungi can substitute the lack of defences in plants impaired in the JA phytohormonal pathway.

Keywords: Jasmonic Acid, Tomato, Mutant, Spodoptera littoralis, Arbuscular Mycorrhizal Fungi, Plant resistance

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Poster 11

Effect of ground-fogging of thiacloprid on target and non-target insects in Korean pine forests

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This study was conducted to assess effect of thiacloprid fogging on mortality of *Monochamus saltuarius* as one of vector insects of pine wood nematodes, and *Apis mellifera* as a non-target species. We compared mortality of two insects among four treatment groups (control and thiacloprid-fogged groups with 3 different doses) in *Pinus koraiensis* forests located in the Kangwon National University Forest. Area of each study plot was about 0.5 ha, and a total of 12 study plots were selected. Before ground-fogging, *M. saltuarius* and *A. mellifera* were put into each meshed cage which installed at 7 m and 15 m heights in center of each study plot. Thiacloprid was sprayed only once (middle May) in each plot using a fogging machine. Overall, thiacloprid fogging was appeared to be low toxicity to the mortality of *A. mellifera*, while it seems effectively impact on the mortality of *M. saltuarius*. However, thiacloprid fogging seems more influenced by microclimates in forests because the mortality of *M. saltuarius* in mesh cages was different according to heights and spatial locations. To control the population density and dispersal of *M. saltuarius* using by fogging techniques, therefore, it may be necessary to minimize the uncertainty about the effectiveness of thiacloprid fogging by improving the fogging techniques.

Keywords: Pine wood nematode, Pine wilt disease, Environmental risk assessment, *Monochamus saltuarius*, *Apis mellifera*
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Poster 12

Distribution and development of *Drosophila suzukii* along elevation gradients

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Drosophila suzukii (Matsumura, 1931), also known as Spotted Wing Drosophila (SWD), is a polyphagous invasive crop pest native of South-East Asia. The species is widely distributed on the Italian territory due to its large array of host plants and high tolerance to different climatic conditions. The goal of this work was to define the abundance and the distribution of SWD at different elevations in NE Italy. We selected 12 transect covering an overall elevation gradient of 2080 m: 8 transects in the Prealps, ranging between 120 and 1300 m a.s.l. and 4 in the Dolomites, ranging between 1030 and 2200 m a.s.l. Every 100 m ca. elevation gain we identified a sampling site (tot. 115), where we placed a trap lured with selective SWD attractant, monitored every 2 weeks from June to November 2015. Female fertility was determined by checking the development stage of the ovaries. Fruits of elderberry (*Sambucus nigra* L.), largely available in the region and suitable for SWD development, were collected along the Prealps transects to assess the emergence rate of the fly.

The pest shows its highest abundance around 1000 m a.s.l. in the Prealps and a significant positive relationship between emergence rate and increasing elevation. The most interesting results were found in Dolomites region where, despite a decrease of abundance with elevation, female ratio and female fertility seem to increase at high altitudes, leaving open the hypothesis of a summer partial migration towards higher elevations to better exploit food resources.

Keywords: *Drosophila suzukii*, elderberry, elevation gradient, transects, ovary development
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Poster 13

Herbivory and florivory at different strawberry plant resistance levels

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Herbivory can cause large damage to plants, leading to both ecological costs for the plant, and economic losses for agriculture. In addition to herbivory on leaves, also flowers can be damaged (florivory). This might reduce pollination and therefore plant fitness. Ideally, plant resistance against herbivory reduces negative effects of both herbivory and florivory, but this is not often studied in combination.

Here we use perennial woodland strawberry plants, *Fragaria vesca*, to address the question whether plants with a higher resistance to herbivory by the strawberry leaf beetle *Galerucella tenella*, have higher flower and fruit production than more susceptible plants. Second, strawberry plants can also reproduce vegetatively via runners. Therefore we investigated whether herbivore resistance poses a trade-off in vegetative versus sexual reproduction.

Wild strawberry plants were collected from Uppsala County, Sweden, and genotypes with either a higher or lower susceptibility to *G. tenella* herbivory were planted in a common garden field experiment. Half of these plots were exposed to *G. tenella* beetles, of which the adults and larvae feed on both leaves and flowers. During the summer, the occurrence of insects and the damage on leaves and flowers was recorded, as well as the sexual (berries) and vegetative (runners) plant fitness.

The results indicate that *G. tenella* caused losses of leaf tissue and strawberries, but this was variable for the resistance levels of the plant genotypes. Importantly, especially susceptible plant genotypes might allocate more to vegetative reproduction when under herbivore pressure. Susceptible plants had heavier runners when beetles were present and a negative runners-versus-berries correlation.

This asexual/sexual reproduction trade-off and the effects of florivory can have important consequences for plant fitness in perennial plants. Moreover, these are important components to take into account when wild plants are used for reverse breeding to increase herbivore resistance in crops.

Keywords: Herbivory, florivory, insect, plant interactions, pollination, resistance, strawberry, wild plants

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Poster 14

A conserved priming signal: Volatile indole activates early defense signaling in rice

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The capacity of plants to perceive and respond to herbivore-induced plant volatiles is well-known. However, the impact of volatile priming signals on early defense signaling events is not well understood. We studied the impact of indole on early defense signaling in rice (*Oryza sativa*). Indole is induced by herbivory and has been shown to be a strong priming signal in maize in an earlier study (Erb *et al*., 2015). We found that indole pre-treatment primed rice plants to produce higher levels of the defensive phytohormone jasmonic acid (JA) and the release of monoterpenes upon simulated herbivory. The JA precursor OPDA was directly induced by indole. Furthermore, the expression of the WRKY transcription factor WRKY70, which is involved in early defense signaling, was primed by indole. Our results suggest that indole boosts plant defenses by inducing the biosynthesis of hormonal precursors and priming upstream transcription factors such as WRKY70 (Li *et al*., 2015). Our results also show that indole can prime both rice and maize, which suggests that it may be a conserved priming signal within the Poaceae.

Keywords: plant volatiles, priming, indole, phytohormone, defense signaling, rice

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Poster 15

Neighborhood effects determine plant-herbivore interactions below ground

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Plant neighbors may strongly influence the interactions between below ground herbivores and focal plants, for instance by providing food of different quality (consumptive effects) or by changing the behavior and metabolism of the herbivore and the focal plant without being consumed (non-consumptive effects). Here, we quantified the impact of nine different grassland plant species on the interaction between *Taraxacum officinale* and the root-feeding insect *Melolontha melolontha* and investigated the contribution of consumptive and non-consumptive effects to the observed patterns. *Melolontha melolontha* growth was strongly affected by the presence of different neighboring species. The three grass species increased larval growth when growing with *T. officinale*, with *Poa pratensis* having a synergistic effect in the mixture compared to both monocultures. The forb *Centaurea stoebe* reduced larval growth when growing with *T. officinale* or alone. The other five species had no measurable impact on larval performance. Diet-mixing experiments showed that *P. pratensis* increased *M. melolontha* growth when offered together with *T. officinale*, while *C. stoebe* suppressed it. When feeding was restricted to artificial diet, larval growth was not changed by the presence of *P. pratensis* or *C. stoebe*. However, when feeding was restricted to *T. officinale*, larval growth was increased by both heterospecific neighbors. Together, these results show that consumptive and non-consumptive effects can explain the positive effect of *P. pratensis*. By contrast, the negative effect of *C. stoebe* is likely driven exclusively by intoxication. Our study suggests that different combinations of consumptive and non-consumptive effects are likely to contribute to the diversity of neighborhood effects in nature. Furthermore, the results show that neighborhood effects are important factors in below ground plant-insect interactions.

Keywords: Associational effect, diet mixing, *Melolontha melolontha*, neighboring plant, physiological response, plant, herbivore interactions, plant-plant interactions, root insects, species, specificity, *T. officinale*

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Poster 16

Interactions plantes-insectes dans un écosystème forestier : le cas de la chenille processionnaire du pin *Thaumetopoea pityocampa* (Denis & Schiffermüller, 1775) en région de l'Est Algérien

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La chenille processionnaire du pin, *Thaumetopoea pityocampa* est le principal lépidoptère ravageur rencontré chez *Pinus halepensis* croissants dans le sud de l'Europe et en Afrique du Nord. Les interactions pin d'Alep-chenille processionnaire ont une importance écologique, économique, sociétale et scientifique. La combinaison des défenses directes et indirectes des plantes attaquées offre à ces dernières une résistance durable dans l'écosystème. La composition et la dynamique des communautés d'insectes herbivores sont donc largement influencées par les traits des végétaux. Bien que tous les insectes phytophages infligent des dégâts sur les tissus végétaux, la quantité et la qualité des dégâts varient grandement selon les guildes trophiques. Les insectes utilisent des stratégies alimentaires différentes pour obtenir les nutriments nécessaires à leur développement. Les insectes spécialistes sont restreints à une ou quelques plantes de la même famille et utilisent les composés chimiques émis par la plante pour leur propre défense afin de faciliter l'exploitation de leur hôte. Nous avons développé une approche pluridisciplinaire couplant la caractérisation de traits écophysiologiques et dendrométriques impliqués dans la sensibilité/résistance des populations d'arbres aux attaques de scolytes avec la caractérisation de facteurs écologiques clés pour la démographie des scolytes (traits d'histoire de vie des scolytes et stratégies d'exploitation de l'hôte). Les analyses effectuées sur la qualité phytochimique du pin d'Alep des feuilles attaquées et non attaquées. Nous a permis de quantifier les sucres totaux, les polyphénols, les tanins, et les flavonoïdes. Leurs variations temporelles ne présentent pas de différence significative entre les constituants biochimiques chez les deux catégories foliaires. Par besoin d'expliciter nos résultats, nous avons eu recours à la comparaison des pentes des feuilles attaquées par rapport aux feuilles non attaquées. Les résultats obtenus nous ont permis de clarifier les changements des constituants phytochimiques au niveau des arbres attaqués et sains. L'analyse en composantes principales (ACP) nous a permis de résumer la variabilité entre les constituants phytochimiques de l'hôte et l'intensité de l'attaque.

Keywords: arbres attaque, arbres sains, dynamique des populations, écophysiologie, Interaction, *Pinus halepensis,* phytochimie, *Thaumetopoea pityocampa*.

Poster 17

Life history of two leaf bud gallers associated with the deciduous tree *Schoepfia jasminodora* (Schoepfiaceae) in Japan

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The association between a host plant and two different gallers attacking the same plant organ and inducing similar shapes of gall is not a well-studied phenomenon. We report such a case on a deciduous tree *Schoepfia jasminodora* (Schoepfiaceae) on which slightly swollen galls are induced on leaf buds by a gall midge, Asphondylia sp. (Diptera:Cecidomyiidae), and a galling wasp, Ceratoneura (Hymenptera: Eulophidae). In the present study, monthly surveys were conducted in 2015-2016 on Mountains Hinokuma and Koura, Kyushu, Japan, to investigate the life history of both gallers and their relationships.

Both gallers were clarified to have at least three generations per year and similar external gall shape, but they differ in overwintering place and stage as well as in internal structure of galls. Asphondylia sp. overwintered as first instars inside the galls while Ceratoneura sp. was not found in overwintering buds, suggesting that they overwintered as adults outside the galls. Bud galls induced by Asphondylia sp. consisted of a single chamber with white fungal hyphae covering the inner walls, while those induced by Ceratoneura sp. was comprised of 1-7, usually 3, black and hardened chambers.

A previous study divided life history of Asphondylia into several patterns and Asphondylia sp. associated with *S. jasminodora* was revealed to have the life history pattern III, i.e., multivoltine and completing their life cycle on one organ of a single host plant species. This pattern was known only in some species associated with evergreen trees. So this is the first example of Asphondylia adopting pattern III on a deciduous tree species. Life history of Ceratoneura species were unclear and previous studies suspected that Ceratoneura sp. might be gall inducers, inquilines or parasitoids on gall midges. The present study first showed the life history and the species is a true gall inducer.

Keywords: Cecidomyiidae, Eulophidae, gall midges, Schoepfiaceae

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Poster 18

Herbivore-mediated fitness effects of increasing chemical variation among neighbouring plants

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Intraspecific plant diversity can modify the properties of associated arthropod communities and plant fitness. We explored the effect of intraspecific chemical variation among neighbouring plants on the associated invertebrate community and whether this, in turn, has consequences for plant fitness. In a garden experiment, intraspecific variation among neigboring plants was manipulated using three plant populations of wild cabbage (*Brassica oleracea*) that differ in foliar glucosinolates. The herbivore community was monitored throughout the growing season in the first year. Seeds of individual plants were collected in the second year (*Brassica oleracea* is a perennial plant that does not flower in the first year of growth). Correlation indices were used to reveal relationships among plant chemistry, insect community attributes and plant fitness.

Keywords: *Brassica oleracea*, chemical ecology, community ecology, plant fitness, cabbage

Speaker*

Poster 19

Why are terrestrial ecosystems generally green with small herbivores biomass? Why are anti-nutritive and inducible defenses effective?: The realities that a novel fully-parameterized food web model tells

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Despite perfect adaptations of specialist herbivores to plant defenses, terrestrial ecosystems are generally green with vegetation and annual herbivory is small (< 10%), which means herbivore density is consistently low and stable. This plant-rich pattern called "The Green World" is common around the world where precipitation and temperature are adequate. Nonetheless, the mechanism underlying this pattern has been unclear without suitable food-web models for predicting the absolute density of the herbivore biomass in physical units. I established a fully-parameterized mathematical food-web model based on flux of nutrients among three trophic levels that can predict biomass densities of herbivores h and carnivores c from factors such as nutritive values of plants np, herbivores nh, and carnivores nc, searching efficiency of carnivores S, eating efficiency of herbivores eh and carnivores ec, respiratory decreases in biomasses, dh and dc, absorption efficiencies ah and ac, and probabilities of carnivores preying on herbivores or carnivores, Phc and Pcc. The model predicts a stable convergent equilibrium with biomass densities of herbivore h=ncf{(1-ac)Pcc(ahehnp{nhdh)+2dcPhcg}/2acPhc2nhS (kg/m3) and carnivore c=nc(ahehnp-nhdh)/PhcnhS (kg/m3) with low herbivore biomass h sufficient to keep the world green provided plants are less nutritive than animals (np> eh). These conditions are well-realized in above-ground terrestrial ecosystems where plant-rich "green worlds" are common, versus animal-rich belowground and aquatic ecosystems where both conditions are not realized. The h, c, and annual herbivory calculated from our model fit in the same order of magnitude with those from empirical observations in both forest and savannah ecosystems. The model reasonably explained why anti-nutritive or quantitative defenses (e.g., tannins, protease inhibitors) of plants function as plant defences in the out-door conditions, and why inducible defences are effective.

Reference: Konno K. (2016) Ecological Monographs 86(2), 190-214.

Keywords: mathematical food web model, prediction of the absolute herbivore and carnivore biomass, forest, savannah, parameterization, green world hypothesis, HSS hypothesis, nutritive value, searching efficiency, eating speed, relative growth rate, plant defense

Poster 20

Canola/cabbage aphid food web – underestimated top-down pressure in invaded range

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The lack of understanding of complex food web interactions has been a major gap in the history of biological control. Technical limitations associated with the deciphering of complex food-webs can now be largely overcome by the use of next generation sequencing technologies. The cabbage aphid, (*Brevicoryne brassicae* (L.) is a prevalent pest on canola (*Brassica napus* L. (Brassicaceae)) in New Zealand. The cabbage aphid has been a problem for almost a century in this invaded region, and biological control success tends to remains below 10%. In contrast, in its native range, which includes the UK, *B. brassicae* is considered only as locally and occasionally damaging. In this study, we used environmental DNA in aphid mummies and Illumina Miseq, to compare the variations in structure and composition of *B. brassicae* food web in its native range (UK) and in an invaded range (New Zealand). We found an increased top down pressure in the New Zealand (NZ) food web, which coupled to a large ratio of consumer species / prey species and a lack of potential inter-specific competition between primary parasitoids, could cause the NZ food web to be more vulnerable than the UK one. This study also reports for the first time the occurrence of a new hyperparasitoid species in NZ. We conclude that the complexity of aphid food webs in agricultural systems could often been underestimated, particularly at higher trophic levels; and that the use of next generation sequencing tools, could largely help to overcome this impediment and support the implementation of better biological control strategies.

Speaker*

Poster 21

Evolutionary and functional ecology of ant-plant-fungus symbioses

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The frequent occurrence of dense fungal mats of blackish hyphae (fungal patches) within ant-occupied domatia (plant provided nesting space) in myrmecophytes (plants living in symbiosis with ants) was noticed over 100 yr ago but the symbiotic nature of these fungi remained overlooked and was demonstrated only recently. Recent phylogenetic analyses show that most fungi within the ant nests belong to the Chaetothyriales (Ascomycota) and the fungal patches within domatia are mainly constituted of a few strains more or less specific to the ant species. The frequency and extent of associations of these fungi with ants were underestimated for a long time. Fungal patches in ant-occupied domatia are astonishingly abundant in tropical ant-plant symbioses. They occur in Africa, America and Asia, in a wide range of unrelated plant genera associated with a wide range of unrelated ants, including myrmecophytic plants from at least 19 different plant genera and six ant genera from five subfamilies. Female alates of neotropic Azteca ants colonizing Cecropia spp. carry hyphal parts in their infrabuccal pockets. The comparison of fungal patches from foundress queens with patches of established colonies revealed that the hyphal parts stem from the maternal nest. Young foundress queens start a new fungiculture immediately after entering the nesting space provided by the plant and before egg laying. This and the fact that the cultivated fungi are fed to the larvae indicates that the fungal patches may be crucial for establishment and survival of arboreal ant colonies living in symbiosis with ant-plants.

Keywords: Ant plant interactions, fungi, Chaetothyriales

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Poster 22

Plastic plant defence strategies as an optimal response to unpredictable multi-herbivore communities

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Plant defence strategies to single attackers are highly diverse and often tailor made to tol-erate or resist specific herbivore attackers. Upon initial herbivore attack, plants respond by altering their morphology and chemical composition, thus presenting a new phenotype to the insect community. However, induced responses infer a physiological cost and alter the plant's interactions with the insect community, potentially imposing an ecological cost by increasing its susceptibility to attack by other herbivores. The induced plant phenotype feeds back to the insect community, altering strength and sign of indirect plant-mediated interactions within the attacking community. Reciprocal and dynamic interactions between the plant and its associated insect community shape the plants development, ultimately affecting fitness.

Our aim is to improve our understanding of plant defence plasticity in context of the full dy-namic insect community. We argue that an optimal plant response to the current attacker should not outweigh the costs incurred through the sequential herbivore community. It is thus to be expected that plant species have evolved defence strategies in function of their full associated in-sect community, incorporating the physiological and ecological costs of induced responses. This infers that plants integrate a measure of predictability in terms of identity, order, and timing, of the insect community to optimise defence strategies. However, it is unknown which elements of the insect communities are predictable and to what extend plant physiology is adapted to the dynamic insect herbivore community.

By using a comparative approach across 12 Brassicaceae plant species we aim to I) identify a measure and form of predictability in the dynamic herbivore community II) explore the effects of indirect plant-mediated interactions in this complex insect community on plant fitness III) identify plant physiological mechanisms involved in coping with (un)predictable multi-herbivore attack IV) identify different physiological solutions to multi-herbivore attack across related plant species.

Keywords: plant defence plasticity, Brassicaceae, multi herbivore, induced responses, plant physiology, community ecology

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Poster 23

Pieris butterflies regulate two genes differently for adapting to wide range of Brassicaceae host plants

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Pieris butterflies use Brassicaceae plants as host plants. Whereas Brassicaceae plants possess strong glucosinolate defense system against general herbivores, Piers butterflies can overcome this defense system by a gut-expressed protein called nitrile specifier protein (NSP). In NSP gene family, two related genes (MA and SDMA) are included. The functions of MA and SDMA are still unclear. However, NSP and MA gene basically have similar structure and they are known to be found only in Brassicaceae-feeding Pieridae butterflies. This highly suggests that MA also has some functions, which relate to glucosinolate detoxification in Pieris larvae. In this research, we compared the expression levels of NSP gene family in Pieris butterfly larvae (*Pieris napi*). We compared the expression levels of NSP, MA and SDMA in larvae that feed on two different Brassicaceae plant species that have different glucosinolate profiles. We found that the expression level of SDMA showed no difference, however, NSP and MA showed different expression patterns depending on the plant species the larvae feed on. We also let larvae feed on Arabidopsis mutants, that have different glucosinolate profiles and compared expressions of NSP gene family. We observed different expressional patterns of NSP and MA in this experiments, whereas SDMA showed no difference. We found that the expression levels of NSP and MA are differently regulated depending on the profiles of glucosinolates the larvae exposed, whereas SDMA did not show such trend. This indicates NSP and MA are likely to have glucosinolate detoxification functions while SDMA might have a role in general digestion. Moreover, it is likely that the functions of NSP and MA are different each other potentially relating to the glucosinolate type that they can detoxify.

Keywords: Pieris butterflies, glucosinolates, NSP, MA

Speaker*

Poster 24

Teaching Insect-Plant Relationships - Template for a Successful Graduate Course

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I have taught a 3-credit graduate course in Insect-Plant Relationships (IPR) biannually since 1991. It is capped at 18 students, draws them from as many as six academic departments and receives consistently high ratings. We meet for 75 min, two days per week, alternating between lectures and Socratic-style paper discussions, starting at the historical roots of the field and proceeding through evolution of herbivory, chemical and physical plant defenses, sensory physiology, host-finding behavior and learning, adaptions to plant defense, variability and induced resistance, multi-trophic interactions, polyculture/monoculture theory, community ecology, plant defense and island biogeography theory, climate change, pollination ecology, and ecological aspects of transgenic crops. The reading list includes historical papers (e.g., Verschaffelt 1911, Brues, Dethier, Fraenkel), seminal reviews (e.g., Price/Tritrophic interactions; Root/Resource Concentration; Feeny/Coley/Plant Apparency/Resource Availability, Bernays/Neural Limitations, etc.), as well as interesting and controversial experimental papers. Writing assignments include 1) a critique of Ehrlich and Raven (1965) and three counterpoint papers concerning coevolution, and 2) an original grant proposal, with budget, describing hypothesis-driven research of the students' choice that must be grounded in IPR theory. The course ends with a mini-symposium in which students give short talks on their proposed projects. Class discussion grades are based 50% on peer evaluation. This poster provides examples of class materials and links to all course materials so that persons wishing to develop a similar course can use them as a template or to supplement their own vision for how to teach the topic.

Keywords: Teaching, Graduate Course, Instruction

Poster 25

Diverse phytochemical profiles and ecological interactions

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Diverse phytochemical mixtures play an important role in plant-herbivore-parasitoid interactions. In the pursuit of understanding these chemically-mediated interactions, we are often faced with the challenge of deciphering the ecologically and biologically important compounds from diverse phytochemical mixtures. Using a network based approach, we analyzed binned 1H-NMR data from 200 artificial mixtures of commonly studied secondary metabolites including, alkaloids, amides, terpenes, iridoid glycosides, saponins, phenylpropene, flanvanoids and phytosterols. Within these mixtures we manipulated multiple dimensions of chemical diversity, including molecular complexity, mixture complexity and differences in the relative concentrations of each compound. This approach was then applied to crude extracts of 20 species in the phytochemically diverse tropical plant genus Piper. Combining a multiple organism bioassays and 1H-NMR data we identified a prenylated benzoic acid from these mixtures that exhibits antifungal properties and identified small structural differences that potentially had a large effect in the bioactivity. In an intraspecific analysis of *Piper kelleyi*, we found ontogenetic differences in chemistry that may relate to changes in natural enemies. In sum, this approach allowed us to combine chemical and ecological datasets and identify potential biologically important compounds from crude extracts.

Keywords: Plant defenses, NMR

Speaker*

Poster 26

Portiera as a phylogenetic tool on white flies

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Whiteflies (Hemiptera: Sternorrhyncha: Aleyrodidae) are small phloem feeding insects that include several agricultural pests. In contrast to other insects, whiteflies taxonomy is based on nymphal stages morphology. However, these stages show phenotypic plasticity, which produces several inconsistencies at the genus level.

All whiteflies have specialized cells (bacteriocytes) that host a bacterial endosymbiont named Candidatus Portiera aleyrodidarum. Portiera is an obligatory mutualistic endosymbiont that complements its host's unbalanced diet, being essential for the whitefly. Portiera has been vertically transmitted since the divergence of whiteflies from their Psyllinea ancestor (circa 160 Mya), and therefore can reflect its host's phylogeny. Also, Portiera from *Bemisia tabaci* lineage has lost the polymerase proofreading subunit (dnaQ) and presents an uncommon genome instability.

Our main goal was to establish a phylogenetic framework based on several Portiera's genes. This framework will be used to improve whiteflies classification and to trace the dnaQ loss and the rise of genomic instability. For these reasons, a PCR screening with specific primers targeting five Portiera genes (16S and 23S rRNA, groEL, dnaK, rpoD and dnaQ), plus some Portiera rearrangements, was performed on 22 whiteflies species (including exsiccata museum specimens). Phylogenetic methods were used for tree inference, divergence dating, species delimitation and ancestral node reconstruction of dnaQ/rearrangements (RaxML, BEAST2, bPTP and ape).

We noticed that teh use of Portiera sequences outperform the universal mitochondrial cytochrome oxidase subunit I (mtCOI) region used so far. In summary, they show low signal saturation, avoid common misclassification of similar insects and can be used on parasitized samples. Therefore, it solves some problems/inconsistencies in current whiteflies phylogeny. The loss of dnaQ and the associated rearrangements are unique to the Bemisia genus.

Keywords: Phylogenetics, Endosymbionts, Molecular dating, Genome instability

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Poster 27

Overcompensation of herbivore reproduction through hyper-suppression of plant defenses in response to competition

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Spider mites are destructive arthropod pests on a variety of crops. The generalist herbivorous mite *Tetranychus urticae* induces defenses in tomato (*Solanum lycopersicum*) when feeding on it and this constrains its fitness. In contrast, the Solanaceae-specialist *T. evansi* upholds a high reproductive performance by suppressing tomato defenses. When present on the same plant, *T. evansi* outcompetes *T. urticae* as was found in natural settings as well as in laboratory experiments, but it is not known to which extent this is facilitated by the defenses of the plant. Here we show that *T. evansi* switches to hyper-suppression of defenses after its tomato host is also invaded by its natural competitor *T. urticae*. Jasmonate (JA) and salicylate (SA) defenses were suppressed stronger, albeit only locally at *T. evansi*'s feeding site, once *T. urticae* was introduced to an adjacent area on the same leaflet. The hyper-suppression of JA and SA defenses coincided with increased expression of *T. evansi* genes coding for salivary defense-suppressing effector proteins and was paralleled by an increased reproductive performance of the mite. Together, these observations suggest that *T. evansi* overcompensates its reproduction through hyper-suppression of plant defenses in response to nearby competitors. We hypothesize that the competitor-induced overcompensation promotes *T. evansi*'s competitive population growth on tomato.

Keywords: competition, defense suppression, effectors, overcompensation, plant, mediated interactions, spider mites, tomato

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Poster 28

Morphological adaptations of coccinellid species determined by host-plant architecture

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Communities of lady-beetles (Coleoptera, Coccinellidae) differ greatly in the plants they colonize. The differences originate because species of coccinellids differ in their tolerance of differences in prey abundance and quality, preference for particular microclimates and for plants of a particular size. The role of host plant in habitat selection is important, however, the correlates of different affinity of coccinelid species in particular hostplants still remain to be demonstrated. We tested two hypotheses predicting association between morphological characters of coccinellid larvae and hostplant stature; (i) Tree architecture is more complicated than herb architecture. Therefore larvae of tree adapted coccinellid species are more mobile than larvae of herb adapted species; and (ii) Coccinellid larvae dropped from trees have greater problems of return to host plant than larvae dropped from herbs. Therefore larvae of tree inhabiting species stick to host plant more firmly than larvae of herb inhabiting species and have greater anal disc. The hypotheses were tested using data on distribution of native and recently arrived invasive species *Harmonia axyridis*.

Keywords: Lady beetles, microclimates, prey abdundance, hostplant, morphological adaptation

Speaker*

Poster 29

Plant resistance ecology: what happens to insect communities when host plants evolve more resistant?

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Plant resistance is the ability of plants to escape attacking enemies, thus minimizing the amount of damage experienced by the plant. Strong resistance makes it possible for plants to maintain fit in hostile environments. In addition, as plant resistance is pivotal to prevent yield loss in crops, it is important to breed for. However, little is known about how increased resistance affects other ecological players (e.g. parasitoids and pollinators) in natural populations and crop plantations. I will introduce ongoing work dealing plant resistance ecology in The Strawberry Lab at SLU. We use woodland strawberry (*Fragaria vesca*), which show high genetic variation in important traits, as model plant to understand ecological consequences of increased resistance. The lessons we learn can be used to breed for integrated management of pests, and pollinators for strawberry.

Keywords: Plant resistance, Herbivory, Florivory, Pollination, Parasitism, Parasitoid, Diffuse interaction, Integrated Pest Management, IPM

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Poster 30

Paralell evolutionary changes in resource allocation to anti-herbivore traits in an invasive plant species

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One of the key factors that affect invasive plant species is the lack of their specialist herbivores in the invasive range. In absence of specialist herbivores it is expected that resources for obsolete defences against specialist herbivores are quickly diverted to other fitness increasing traits. By studying four independent invasive areas and the native area using more than 30 populations we find that the lack of specialist herbivores in the new range is accompanied by a parallel evolutionary change in all traits related to anti-herbivore strategies in invasive common ragwort (*Jacobaea vulgaris*). We find that invasive common ragwort (*Jacobaea vulgaris*) adapted its qualitative defences, quantitative defences, regrowth and growth leading to changes in competitive ability and seed production in this monocarpic plant. Competitive ability of invasive ragworts increased in the absence of herbivores and presence of a generalist herbivore but competitive ability decreased in the presence of a specialist herbivore. The increase in competitive ability and seed production in invasive ragwort are most likely explained by a profound decrease in carbohydrate storage to roots. None of the traits were correlated to climatic differences between the native and invasive populations.

Keywords: paralell evolution, alkaloids, specialists, generalists, tolerance, invasive, competitive ability

Poster 31

Pollination network analyzis by environmental metagenomics

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The plant-pollinator interaction network is a bipartite, mutualistic network between two groups with different interests. For plants, pollinators are essential pollen vectors required for reproduction, for pollinators, plants provide food resources. The study of plant-pollinator interactions is usually based on either field records of pollinator visits to plants, or pollen identification by microscopy. However, both of these methods have inherent limits that preclude an accurate description of pollination networks. For example, they do not take into account individual pollinator behavior and pollen flow. To analyze the pollen loads on pollinators and on plant stigmas, in a quantitative manner, a fine-scale approach is necessary. Recently, new, innovative methods are emerging that combine studies of environmental DNA by metabarcoding, high throughput sequencing and bioinformatics tools to thoroughly identify the taxa in environmental samples. However, the validity and efficiency of these news tools in studying pollination networks remains to be evaluated. The purpose of this work is to explore and analyse the application of environmental genomics in these mutualistic interactions. Our primary results show that, compared to visit observation, metabarcoding allows detection of many more interactions, and causes considerable changes to the properties of the pollination networks. Moreover, by allowing us to build individual pollination networks, metabarcoding adds an essential dimension to our comprehension of plant-pollinator interactions networks at a higher resolution than has previously been investigated.

Keywords: Plant, pollinator networks, metabarcoding, next generation sequencing, eDNA

Poster 32

Impact of endophytic entomopathogenic fungus on plant attractiveness in aphid-virus-plant interaction

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Endophytic entomopathogenic fungi (EEPF) are biological control agents able to live in their host plants in a symbiotic interaction and secrete secondary metabolites in the host plant tissues interacting with pests and phytopathogenic agents like plants virus. This is the case of Barley yellow dwarf virus (BYDV) transmitted by the Bird cherry oat aphid (*Rhopalosiphum padi* Linnaeus) and the Grain aphid (*Sitobion avenae* Fabricius). This virus is one of the most economically important phytoviruses affecting major world cereal crops such as wheat, rice and corn, causing significant yield losses. In this study, we investigated the influence of EEPF presence in the plant tissues on the aphid's orientation behavior by taking into consideration the infectious status of the insect. We performed Olfactometry assays complemented by a choice test in Petri dishes and collection of volatile compounds emitted by plants. The impact of these interactions between plant-fungi-virus is finally discussed.

Keywords: Endophytic entomopathogenic fungi, Aphid, BYDV, Plant attractiveness, multitrophic interaction

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Poster 33

Are aphid vectors manipulated by plant virus?

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Phytoviruses using insects as vectors can manipulate their host-plant or their insect vector for their own benefit. The indirect manipulation induces changes in host-plant phenotypes influencing the nature and the frequency of the host-plant/ vector interactions, promoting virus propagation. Conversely, the direct manipulation, described more recently, may lead to modifications of the vector behaviour, increasing the probability of colonization of non-infected plants by viruses. The purpose of this study was to investigate potential combined indirect and direct effects of a phytovirus on the behaviour of its vector in the pathosystem *Arabidopsis thaliana* / Turnip yellows virus (TuYV) / *Myzus persicae*. Non-viruliferous aphids exhibited no discrimination between odours of healthy or virus-infected plants, but their feeding behaviour was altered on virus-infected plants, showing an indirect effect of infected plant thus precluding any manipulation by the virus. On the other hand, viruliferous aphids exhibited no discrimination between healthy or virus-infected plants, but their feeding behaviour was negatively altered on healthy plants (compared with non-viruliferous aphids), showing a direct effect also precluding any manipulation by the virus. The only element in favour of manipulation was the increased intrinsic velocity of viruliferous aphids. To summarize, our results highlighted both indirect and direct effects of the virus on their host-plant and its vector respectively, but in these two situations virus manipulation was not involved because its dispersion was not promoted.

Keywords: *Arabidopsis thaliana*, Turnip yellows virus (TuYV), *Myzus persicae*, host plant, vector manipulation

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Poster 34

Insect-pathogen interaction in oilseed rape (OSR): *Myzus persicae* increases susceptibility of *Brassica napus* to *Rhizoctonia solani* AG 2-1.

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Crop plants are constantly exposed to a range of different attackers including plant pathogens and herbivorous insects. Each of them induces specific alterations in the host-plant, which potentially affect other organisms sharing the same host. *Brassica napus*, (oilseed rape, OSR), is the host of the necrotrophic soil-borne pathogen *Rhizoctonia solani* AG 2-1. Currently no resistant cultivar is available for AG 2-1 and it is unclear how the pathogen manipulates plant defences. Furthermore, OSR is one of the secondary hosts of *Myzus persicae*; a notorious aphid species with an impressive ability to adapt to plant-host defence mechanisms. The aim of the present work was to examine if there is an interaction between AG 2-1 and *M. persicae* and determine the role of the main plant-hormones in the interaction. Firstly, we assessed the effect of AG 2-1 inoculation on aphid performance by measuring aphid growth rate and population increase for a period of 7 days. Then we evaluated the effect of aphid infestation on OSR susceptibility to AG 2-1 by assessing disease symptoms in plant stems and quantifying fungal DNA in stems and soil 13 days post inoculation. We studied the expression of WAK1, NPR1, PR2, PR4, MYC2, LOX3 and WRKY38 genes involved in plant defences against *M. persicae* and/or necrotrophic fungi. Our results show that although there is no effect of AG 2-1 on aphid performance, *M. persicae* clearly and significantly alters the response of Canard plants to AG 2-1, making plants more susceptible. Although the amount of fungal DNA was not different between treatments within each cultivar, Canard plants exposed to aphid infestation had an almost two-fold increase in disease symptoms compare to control plants. Our findings suggest that aphids can have an immunosuppressive effect on plants that renders them more susceptible to pathogen attack.

Keywords: plant insect pathogen interaction, *B. napus*, *R.solani*, *M. persicae*

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Poster 35

Using dsRNA of the BtGST2 Detoxification Gene to Develop *Bemisia tabaci* Resistant Plants

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Bemisia tabaci, the sweet-potato whitefly, is one of the most devastating pests worldwide, causing enormous economical lost in agriculture. As other phloem-feeding insects, *B. tabaci* is mainly controlled by synthetic insecticides. Insecticide resistance is one of the major problems agriculture faces nowadays and developing alternatives to insecticides is necessary. As a highly polyphagous pest, *B. tabaci* utilizes an induced general detoxification system capable of dealing with a broad range of plant toxins. Our main goal was to develop an RNA interference technology that will allow the production of pest-resistant crops capable of silencing insect detoxification genes.

Artificial feeding assay was performed by exposing *B. tabaci* adults to double-strand (ds) RNA of the BtGST2 (dsBtGST2) gene, a known general detoxifier in *B. tabaci*. In addition, transgenic *Arabidopsis thaliana* plants expressing dsBtGST2 under a phloem specific promoter were produced and feeding and development assays were conducted. Finally, gene expression, in all the experiments, was analyzed by Real Time PCR.

Artificial diet showed significant down-regulation in BtGST2 gene expression in the mid-gut of adults compared to the control group. Individuals developing on transgenic *A. thaliana* plants showed significant developmental delay when compared to those developing on wild type (WT) plants. In parallel, BtGST2 gene expression in the mid-gut showed significant down-regulation in individuals fed on transgenic plants compared to individuals fed on WT plants. Slowing the development of *B. tabaci* on host plants by RNAi can increase the efficiency of its control by natural enemies, which will lead to minimizing the use of synthetic insecticides. Future experiments will assess the influence of combined down-regulation of two detoxification genes (BtGST2 & BtCYP6like5) on the ability of *B. tabaci* to utilize plant hosts.

Keywords: *Bemisia tabaci*, RNAi, detoxification, BtGST2, transgenic plants
Speaker*

Poster 36

Antibiotic treatment of *Pieris brassicae* attenuates egg-mediated anti-herbivore defenses in two brassicaceous species

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Several plant species are known to improve their defense against herbivorous larvae when they have received insect egg depositions prior to larval attack, resulting in stronger detrimental effects on performance of insect larvae compared to egg-free plants (1, 2). Previous studies revealed some similarities of plant responses to insect eggs and phytopathogenic microbes. To test whether bacterial associates of the butterfly *Pieris brassicae* are involved in egg-mediated anti-herbivore defenses of *Arabidopsis thaliana* and *Brassica nigra*, butterflies were treated with antibiotics (AB) to reduce their microbial load. Transcript levels of defense genes and larval performance were determined in plants deposited with eggs of either AB-treated or untreated control females. Plants with eggs from AB-treated females showed lower expression levels of several phytopathogen-responsive genes than plants with control eggs. As expected, control larvae performed worse on plants with control eggs than larvae on egg-free plants. However, performance of control larvae on plants laden with eggs from AB-females was not reduced compared to performance of larvae on egg-free plants. Hence, the AB-treatment of butterfly parents attenuated the egg-mediated plant responses that lead to worse performance of larvae feeding on them. Our study indicates (i) that bacteria associated with *P. brassicae* can affect a plant's anti-herbivore defense and (ii) that the egg-mediated improvement of plant defense against larvae is linked with high transcript levels of plant genes known to respond to phytopathogens.

1. Hilker and Fatouros 2015. Annu. Rev. Entomol. 60: 493-515.
2. Hilker and Fatouros 2016. Curr. Op. Plant Biol. 32: 9-16.

Keywords: egg deposition, antibiotics, insect microbiome, *Pieris brassicae*, *Arabidopsis thaliana*, plant defense
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Poster 37

Dispersal capacity of *Monochmus saltuarius* (Gebler) (Coleoptera: Cerambycidae) on flight mills

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The symptoms of pine wilt disease caused by the pine wood nematode (*Bursaphelenchus xylophilus*), which is recognized as a major forest pest. It was introduced into Korea in 1988, and two insect species, *Monochamus saltuarius* and *M. alternatus*, are known for vector of pine wood nematode. The pine wood nematode is transmitted by *M. saltuarius* to healthy Korean white pine (*Pinus koraiensis*). To understand and predict the spread of pine wilt disease in Korean white pine forests, we examined flight capacity of *M. saltuarius* using computer-linked flight mills in laboratory. Flight capability was individually measured during 30 minutes in each experiment, and repeatedly measured twice a week. In addition, we investigated the effects of age, sex, and biological characteristics (wing and body size) on flight performances of this vector insect. The variation of flight capability of *M. saltuarius* within population was high. And a maximum flight distance was about 4 km over the lifetime of the beetle. Flight performance was more frequently occurred in males than in females, but total distance was higher in females. The mean flight distance in female was highest in 7 days after emergence and decreased with aging, but those in males were not changed until at least 23 days after emergence.

Keywords: Flight capability, Pine wilt disease, Pine wood nematode

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Speaker

Poster 38

Phylogenetic farming: Can evolutionary history inform crop and insect management?

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In agriculture, we rotate crops to avoid the buildup of host-specific pathogens that accumulate under single-species cultivation. Scientific guidelines for evaluating which crops are ideal for rotations are lacking, however, except for the common “rule” to avoid successive plantings in the same plant family. Thus, there is an implicit phylogenetic underpinning to rotations, but surprisingly this has never been explicitly tested in an agricultural context. We use a plant-soil feedback framework to test how relatedness affects the strength of soil legacies of one plant on another. Further, we evaluated how this soil-mediated microbial factor impacted insects feeding aboveground. To do so, we conditioned field-collected soil using 36 common crops and agricultural weeds that varied along a phylogenetic spectrum in relatedness to our focal plant, tomato. After a 10 week conditioning period, this soil was used as inoculum to germinate tomato seedlings, on which we assessed plant growth and the performance of hornworm caterpillars (*Manduca sexta*) feeding on leaves. We also used PLFA (phospholipid fatty acid) analysis on conditioned soil to simultaneously track responses in the soil microbial community as a potential explanatory factor. Overall, we found that tomato grows differently in varying soil types (P=0.0023), but this variation was not explained by phylogenetic relatedness among plant pairs (P=0.5762). Rather, plant-soil feedbacks on tomato were species- and family-specific; for example, plants in the Cucurbitaceae and Amaranthaceae had particularly negative impacts on tomato via the soil. Although a PCA of the soil microbial community predicted the strength of this feedback, the explanatory power was relatively weak (R2=0.0336). Caterpillar performance also varied depending on soil types, but as with plant responses was unrelated to phylogeny. As a result, we conclude that plant-soil feedbacks in agriculture should be tailored to specific interactions rather than using broad rules guided by evolutionary history.

Keywords: plant, soil feedback, phytobiome, phylodiversity, microbe, plant, insect interaction, crop rotation

Speaker*

Poster 39

Fungal grass endophytes can influence host plant preference and fitness of a satyrine butterfly

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Fungal endophytes belonging to genus Epichloe are commonly regarded as mutualists of cool-season grasses. The prevailing hypothesis states that such fungi are mutualists contributing to plants' anti-herbivory defenses. Defensive mutualism is attributable to fungal-origin alkaloids such as ergot alkaloids, indolediterpenoids, lolines and peramine. Ergot alkaloids and indolediterpenoids are most well known for their toxicity to vertebrates whereas lolines and peramine are strongly insecticidal. However, the literature testing the hypothesis of defensive mutualism is likely to be biased by the disproportional use of agricultural model systems. To test the hypothesis using a wild Epichloe endophyte-grass-herbivore model system we selected tall fescue (*Schedonorus phoenix* with *E. coenophiala*) and red fescue (*Festuca rubra* with *E. festucae*) as grass-endophyte models. As the model herbivore, we selected *Coenonympha hero* butterfly. All the species are native to Europe. Endophyte infection influenced both preference and performance of the herbivore. Ovipositing *C. hero* females were shown to respond to both chemical and physical cues in host selection. Both these cues appear to be modified by endophyte infection. Neonate larvae were found to be able to select fungus-free grasses, with some indication of better growth performance on such hosts. Nevertheless, the effect of endophyte infection on both preference and performance considerably varied between the host species. Our results thus support the defensive mutualism hypothesis only partly.

Keywords: fungal grass endophyte, host plant preference, symbiosis, fungal alkaloids, anti herbivory defense, insect herbivore

Speaker*

Poster 40

Induced resistance to thrips by bacterial infection

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The pathogenic bacterium *Pseudomonas syringae* activates the jasmonic acid (JA) pathway producing the JA mimic coronatine (COR). In doing so it fools the plant by activating plant defence against insects although being itself a pathogen. We investigated whether infection of tomato with *P. syringae* leads to induced plant defence against herbivores using thrips (*Frankliniella occidentalis*), a key pest in agri- and horticulture worldwide, as a model. Inoculation of tomatoes with low concentrations of *P. syringae* led to a 50% systemically induced reduction of thrips damage 7 days after inoculation. Infected plants did not show bacterial symptoms nor reduced biomass. Likewise tomato plants treated with suspended medium, in which *P. syringae* had been grown but subsequently eliminated, as well as treatments of plants with COR led to substantial reductions in thrips damage. Polyphenol oxidase (PPO), a marker enzyme of the JA pathway was significantly increased in all treated plants. Likewise, metabolomic analysis of inoculated plants with nuclear magnetic resonance spectroscopy (NMR) showed significantly different metabolomes in comparison with the control. The avanoid Rutin substantially contributed to this difference being significantly increased in treated plants. Our results show that infection with low concentrations of *P. syringae* induces plant defence to thrips and thus constitutes a promising tool to reduce herbivore damage in crops.

Keywords: Induced resistance, thrips (*Frankliniella occidentalis*), bacteria (*Pseudomonas syringae*)

Speaker*

Poster 41

Strength in cooperation: bacterial symbionts help the insect host overcome plant defences

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During their evolution, plants have developed a variety of morphological and biochemical traits to fend off herbivores, including insects. Production of secondary metabolites is one of the most important plant biochemical defense mechanisms. In our study system, *Aconitum napellus* (Ranunculales: Ranunculaceae) produces alkaloids, such as aconitine and nepaline, which are extremely toxic to animals. Despite their high toxicity, the leaf beetle *Galeruca laticollis* (Coleoptera: Chrysomelidae) is able to feed and complete its life cycle on this plant. Up to date, the mechanisms by which the insect is able to withstand such high toxicity are not understood. In this study, we investigate the possible involvement of bacterial symbionts in this resistance phenotype. Exploring the gut microbiota of *G. laticollis* using 16S rRNA gene sequencing we identified potential candidates among which bacteria belonging to the genus Pseudomonas. After strain isolation, the ability to degrade this alkaloid was tested *in vitro* with kinetic experiments. This confirmed one Pseudomonas strain as the most efficient degrader among the isolated strains. Furthermore, Pseudomonas sp. activity was tested *in vivo*, using *Drosophila melanogaster* as a model. We were able to confirm that Pseudomonas sp establishes a beneficial symbiosis with their hosts and validate their key role in aconitine-degradation in *D. melanogaster*. We also investigated the genetic determinants of this degradative ability of the bacteria. The obtained results provide further evidence regarding the mechanisms by which insects are able to resist toxic molecules (plant secondary metabolites or insecticides) through the evolution of beneficial symbioses with bacteria.

Keywords: Insect, plant interaction, herbivory, Coleoptera, symbiosis

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Poster 42

The role of the *Pieris brassicae* microbiome during a host-plant shift

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Insect dietary behavior is well known as one of the most important factors shaping bacterial gut communities. However, it is only until recently that the role of gut bacteria in facilitating diet shifts by insects is being explored. Here, we investigated the impact of the microbiome of *Pieris brassicae* on the performance of larvae feeding on a host plant species that differs from that of their parents. In nature, this multivoltine lepidopteran species often shows a host shift from one generation to the next because of the plant's short life time. In a first experiment, we directly treated larvae with antibiotics and evaluated their performance on either, the parental diet or an alternative one, in comparison to untreated larvae feeding such diets. In a second experiment, and in order to discard antibiotic-related side effects, we treated *P. brassicae* for one generation with antibiotics and then used their (untreated) offspring for the same assessments. For both experiments we found a negative effect of the antibiotic treatment on larval biomass only when larvae were exposed to another diet than their parents. No effect was detected when larvae fed on the parental diet. PCR of the 16S rRNA gene showed a clear inhibition of bacteria present in antibiotic treated individuals, and preliminary sequencing analysis showed a significant disturbance of the bacterial community composition due to the treatment. Our results suggest a beneficial role of the *Pieris brassicae* microbiome only evident when the insect feeds on a host plant not experienced by the parental generation.

Keywords: Plant, insect, microbe interactions, gut microbiome, Brassicaceae, antibiotics, bacteria

Speaker*

Poster 43

Learning in two butterfly species when using flowers of the tropical milkweed *Asclepias curassavica*: no benefits for pollination

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The ability of visitors to learn to manipulate complex flowers has important consequences for foraging efficiency and plant fitness. We investigated learning by two butterfly species, *Danaus erippus* and *Heliconius erato*, as they forage on the complex flowers of *Asclepias curassavica*, as well as consequences for pollination. To examine learning with respect to flower manipulation, butterflies were individually tested during four consecutive days under insectary conditions. At the end of each test we recorded the number of pollinaria attached to the body of each butterfly and scored visited flowers for numbers of removed and inserted pollinia. We also conducted a field study to survey *D. erippus* and *H. erato* visiting flowers of *A. curassavica*, as well as to record numbers of pollinaria attached to the butterflies' body, and surveyed *A. curassavica* plants in the field to inspect flowers for pollinia removal and insertion. Learning improves the efficiency of both butterfly species in locating and extracting nectar of *A. curassavica* flowers. There were no learning effects for either species on the number of removed and inserted pollinia. *Heliconius erato* removed and inserted more pollinia than *D. erippus*. For both butterfly species, pollinia removal was higher than pollinia insertion. This study is the first to show that Danaus and Heliconius butterflies can learn to manipulate complex flowers, but this learning ability does not confer benefits to pollination in *A. curassavica*.

Keywords: Asclepias, complex flowers, Danaus, flower visiting, Heliconius, learning, pollination
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Speaker

Poster 44

Sweet Pepper-Thrips Interaction: Uncovering dynamics of the plant defense-signaling network to identify novel leads for maximizing crop protection

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Insect pest attack can seriously hinder plant development, reducing crop productivity and triggering further agronomic problems. Thrips are minute cell-content-feeding insects that are a major pest in many ornamental and vegetable crops. Additionally, they are also important vectors of viral plant pathogens. The objective of this study is to investigate at high temporal resolution the dynamics of the defense-signaling network of Arabidopsis and sweet pepper plants during their interaction with western flower thrips (*Frankliniella occidentalis*). To answer this, we monitored the early dynamics of the transcriptome of pepper using RNA-sequencing followed by advanced bioinformatical analysis. Advanced bioinformatical analysis includes co-expression analysis, promoter/motif analysis and building detailed gene regulatory network using different tools. Using a greenhouse setup, we collected leaf samples from infested and non-infested plants, and subjected these to RNA sequencing. This approach generates profound knowledge into highly accurate gene regulatory networks with unprecedented details and allows us to make models of plant immune signaling sectors with which we can predict and validate novel key regulators of plant defense against thrips. To elucidate the role of jasmonates in defense of pepper upon thrips feeding, we targeted CaLOX2, known to be involved in biosynthesis of jasmonic acid (JA), for silencing by Viral-Induced Gene Silencing (VIGs). For CaLOX2 -silenced pepper plants we assessed JA accumulation upon thrips feeding, susceptibility to thrips, and thrips host selection behaviour. These experiments were complemented with studies of the effects of exogenous JA application. In conclusion, this work unravels plant-signaling networks underlying defences against western flower thrips and specific pathways involved in such defences. This will be instrumental in finding new ways to combat thrips in pepper crops.

Keywords: Thrips, Sweet pepper, Transcriptome, Signalling network, Plant Defense, Genes
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Poster 45

Developmental and reproductive performance of a specialist herbivore depend on seasonality of, and light conditions experienced by, the host plant

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Seasonal and light-modulated changes in the phenotypic and phytochemical properties of leaves have been hypothesised to equivocally influence insect herbivore performance. Here, we examined the effects of seasonality (autumn versus winter) and light environment (shade vs full-sun habitat) on the leaf characteristics of the invasive alien plant, *Chromolaena odorata* (L.) King and Robinson (Asteraceae). In addition, the performance of a specialist folivore, *Pareuchaetes insulata* (Walker) (Lepidoptera: Erebidae), feeding on leaves obtained from both shaded and full-sun habitats during autumn and winter, was evaluated over two generations. Foliar nitrogen and magnesium contents were higher on shaded plants during winter while leaf toughness was noticeably higher on full-sun plants during winter. Leaf water content was higher on plants in autumn compared to winter. Irrespective of season, shaded leaves had higher nitrogen, magnesium, carbon, potassium, water and lignin contents compared to full-sun ones. Non-structural carbohydrate and phosphorus contents were higher in full-sun leaves in both autumn and winter. *Pareuchaetes insulata* developed faster and had larger pupal mass, increased growth rate and higher fecundity when reared on shaded foliage (relative to full-sun) or when reared on autumn leaves compared to leaves of plants growing in winter. Although egg hatchability and mating success did not differ between seasons and between habitats, Maw's host suitability index (HSI) indicated that shaded leaves during autumn were more suitable for the growth and reproduction of *P. insulata*. This study demonstrates that seasonality and light environment can indirectly affect insect folivore performance in ways that are less straightforward.

Keywords: *Pareuchaetes insulata*, invasive alien weed, *Chromolaena odorata*, sunlight, autumn, winter, leaf characteristics, herbivore performance, insect, plant interactions

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Poster 46

Earthworms indirectly mediate plant-herbivore interaction via changes in soil nutrient composition and plant chemical traits

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How plants cope with herbivore attack is partially dictated by the biotic and abiotic environment where the plant lives. For instance, plants growing in richer soil may grow bigger and produce more nutritious leaves, but at the same time, might allocate more resources to defence production. Soil fauna earthworms, by their borrowing and casting activities, are known to favour soil nutrient availability. Earthworms could thus indirectly modify plant-herbivore interaction by modifying plant growth and chemical composition. We tested this hypothesis using tomato plants attacked by one of the major greenhouse pests, the western ower thrips (*Frankliniella occidentalis*), and which were inoculated with single earthworm species and a mix of two earthworm species that differ in their ecological functions. We found that earthworm presence significantly affected soil biochemical properties, and overall, they enhanced plant growth and the concentration of leaf soluble amino acids and sugars. Nonetheless, we found variation in the results, which was driven by species-specific variation in the earthworm ecological types and functional diversity. Meanwhile, earthworm presence significantly increased the concentration of leaf defence-related hormone jasmonic acid, as well as the concentration of phenolics. Taken together, this resulted in earthworm presence near the roots to decrease thrips abundance. These results were corroborated using structural equation modelling, indicating that, independently of earthworm species, earthworm presence significantly increased plant growth and chemical defences, and in turn suppressed thrips abundance mainly through the increase of plant chemical defences. These results strongly build towards a better understanding of the earthworm functional roles in the ecosystems, and how they could be integrated into ecologically sound pest control programs.

Keywords: Earthworm ecological type, functional diversity, western ower thrips, bottom, up force, soil nutrient, plant defence

Speaker*

Poster 47

Herbivore-induced plant volatile blends are influenced by plant nutrition

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Due to climate change, dry regions like the Mediterranean face increasing water limitation; nitrogen leaching risks eutrophication. While resource input into agricultural systems has to be optimized, crop production has to stay feasible. In plants, nitrogen and water are involved in basic physiological processes and at the same time linked to defense compound production. Additionally, studies indicate that their availability influences the blend of volatile organic compounds (VOC) emitted by plants. When attacked, plants emit a specific blend of herbivore-induced plant volatiles (HIPV) which can be perceived by natural enemies of the respective herbivores. Constitutively emitted VOC blends can be affected by abiotic factors. If HIPV blends are likewise impacted, this indirect plant defense strategy could be impeded. Using solid-phase micro extraction (SPME) fibers we have collected volatile compounds from tomato plants (*Solanum lycopersicum*) receiving moderately reduced water and/or nitrogen, before and during infestation with one of two sap-feeding (*Macrosiphum euphorbiae* and *Bemisia tabaci*) or one of two leaf-chewing herbivore species (*Tuta absoluta* and *Spodoptera littoralis*). Compounds were analyzed via GC-MS, chromatograms evaluated via XCMS online, and results analyzed via MetaboAnalyst 3.0. We detected significant effects of the plant nutrient solution on HIPV, especially regarding blends emitted by plants infested by sap-feeders, and on constitutive volatile blends emitted before infestation. Additionally, principal component analysis indicates that leaf-chewer HIPV blends differ more from constitutive volatiles than sap-feeder associated HIPV. Our results suggest a bottom-up effect of plant nutrient solution on indirect plant defense, especially against sap-feeders. HIPV blends associated to leaf-chewers appear to be less susceptible to changes caused by abiotic factors. Indirect defense against leaf-chewers might be under higher selective pressure for resilience due to their higher potential to cause massive damage to the plant compared to sap-feeders.

Keywords: herbivore induced plant volatiles, HIPV, VOC, *Macrosiphum euphorbiae*, *Bemisia tabaci*, *Spodoptera littoralis*, abiotic factor, nitrogen, water. ***Speaker****

Poster 48

Disease in bloom - exploring the link between pollination and phytopathology

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Like all organisms, plants do not exist in isolation but interact with their environment in a multitude of ways. Plant signalling via secondary metabolites, e.g. volatile organic compounds (VOCs), is thus indispensable. Plant VOCs have been well-studied in the context of tri-trophic (plant-herbivore-natural enemy) interactions and as mediators of plant-pollinator interactions. However, the dynamic nature of floral VOC emissions and the potential for VOC bouquet shifts in response to environmental stimuli and stressors have been largely ignored to date. Among the many potential hazards are plant pathogens, often associated with severe consequences for plant survival and fitness. For instance, the two most severe diseases in pome and stone fruit growing areas, apple proliferation (AP) and European stone fruit yellows (ESFY), are caused by phytoplasma pathogens (Candidatus *Phytoplasma mali* and Ca. *P. prunorum*, respectively). Although fruit crop failure and the effects of phytoplasma infection on fruit development are well-documented, impacts on floral phenotype (e.g. flower colour, scent and nectar), and in turn pollinator behaviour, are unknown. Here, we propose the fruit tree - phytoplasma - bee pollinator model to explore tri-trophic interactions at the vital pollination stage. We compared the nectar and floral VOC bouquets of healthy apple flowers with those infected with phytoplasma strains Ca. *P. mali* 3/6 and 12/93. Moreover, we tested flowers of AP- and ESFY-infected trees for phytoplasma presence in floral tissue and nectar. PCR results confirmed phytoplasmas in petals and young shoots. The sucrose concentration in nectar did not differ between treatments. However, there is evidence for shifts in the floral VOC bouquets in response to infection. Thus, changes in floral phenotype may potentially influence pollinator behaviour and pollination success. Our model allows us to explore fundamental questions on ecological interactions under stress as well as pressing matters on plant and pollinator health and food security.

Keywords: pollination, phytopathology, phytoplasma, apple proliferation, European stone fruit yellows, *Malus domestica*, floral VOCs. ***Speaker****

Poster 49

A herbivore tag-and-trace system reveals contact and density-dependent repellence of a root toxin

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Foraging behaviour of root feeding organisms strongly affects plant-environment-interactions and ecosystem processes. However, the impact of plant chemistry on root herbivore movement in the soil is poorly understood. Here, we apply a simple technique to trace the movement of soil-dwelling insects in their habitat without disturbing or restricting their interaction with host plants: We tagged the root feeding larvae of *Melolontha melolontha* with a copper ring and repeatedly located their position in relation to their preferred host plant, *Taraxacum officinale*, using a commercial metal detector. This method was validated and used to study the influence of the sesquiterpene lactone taraxinic acid β-D-glucopyranosyl ester (TA-G) on the foraging of *M. melolontha*. TA-G is stored in the latex of *T. officinale* and protects the roots from herbivory. Using behavioural arenas with TA-G deficient and control plants, we tested the impact of physical root access and plant distance on the effect of TA-G on *M. melolontha*. *M. melolontha* larvae preferred TA-G deficient plants over control plants, but only when physical root contact was possible and the plants were grown at a distance of 5 cm. *M. melolontha* showed no preference for TA-G deficient plants when the plants were grown 15 cm apart, which may indicate a trade-off between the cost of movement and the benefit of consuming less toxic food. We demonstrate that *M. melolontha* integrates host plant quality and distance into its foraging patterns and suggest that plant chemistry affects root herbivore behaviour in a plant-density dependent manner.

Keywords: Root herbivore, foraging, imaging, *Melolontha melolontha*, *Taraxacum officinale*

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Poster 50

Can we use semiochemicals to control *Aphis craccivora* Koch?

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Amaranthus hybridus L. (Amaranthaceae) is among the most important vegetable crop in several sub-Saharan countries. *Aphis craccivora* Koch (Homoptera: Aphididae) is an aphid species that cause significant losses in absence of chemical control. In this laboratory research, we evaluate the efficiency of informative substances (E-β-farnesene, methyl salicylate, essential oil of *Ocimum gratissimum* L. and *Ocimum basilicum* L.) to repel aphids from their host plant. Our assays were carried out in plastic trays containing twenty-five amaranth plants. In each tray, twenty apterous *A. craccivora* adults were placed on the central plant (release plant) associated with a semiochemical releaser containing 100 µl of the substance to be tested diluted in paraffin oil. The number of aphids was then counted on each plant surrounding plants every three-days for twelve days.

We observed a significant repulsive effect of *O. gratissimum* and *O. basilicum* essential oils, that considerably reduced the aphid population on the treated plant, compared to control. However, no repulsive effect of E-β-farnesene and methyl salicylate on aphids was observed. Bioactivities of these substances and their using as alternative aphicidal in integrated pest management are discussed.

Keywords: Amaranth, Natural substances, Cowpea aphid, Pest control

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Poster 51

Soil wars: biological alternatives to pesticides to control wireworms

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Most of the studies on plant-insect interactions focus on the aboveground parts of the plant while belowground interactions are less explored. Yet, soil pests are equally dangerous for plant fitness and can interact with the aboveground pests and plant defenses. Amongst them, wire-worms (Coleoptera: Elateridae) are common polyphagous soil pests of various crops, including maize and potatoes, inflicting severe economic damage. Their management with pesticides is often not successful or sustainable, and more research on biological alternatives is required. One of them is to use traps baited with attractive volatile organic compounds (VOCs) and a microbial control agent. To achieve this general objective we defined four specific directions to follow: 1) developing a behavioral assay suitable for the study of wireworm orientation behavior; 2) profiling VOCs released in the rhizosphere of potato; 3) evaluating the role of the identified VOCs on wireworms foraging behavior; 4) developing a monitoring trap based on the previously identified VOCs, and associated with the entomopathogenic fungi *Metarhizium anisopliae* Sorokin (Hypocreales: Clavicipitaceae) to be tested in the laboratory and in the field. We will also evaluate the impact of larval development on the perception and orientation behavior toward host plant and specific VOCs released in the rhizosphere.

Keywords: Soil insect pests, indirect defense, biological control, semiochemicals, integrated pest management, microbial control.

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Speaker

Poster 52

Cellulases in phytophagous beetles: Characterization and molecular evolution of family 45 glycoside hydrolases in leaf beetles and weevils

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Cellulose is a polysaccharide made of glucose units. It could provide a potentially rich source of energy for plant feeding organisms except for the fact that it is recalcitrant to enzymatic breakdown. For a long time, it had been believed that only cellulolytic microorganisms were able to digest cellulose. Recent studies have revealed that genes encoding putative cellulases of several glycoside hydrolase (GH) families were present in genomes of various metazoans, such as nematodes and arthropods. Our previous work indicated that putative cellulases belonging to the GH45 family were present in beetles of the Chrysomeloidea (leaf beetles and longhorned beetles) and Curculionoidea (weevils and bark beetles).

My work aims to address whether GH45s are indeed true cellulases or whether they have evolved other functions. I also investigate their evolutionary history and their biological relevance. My current hypothesis is that these cellulases have been originally acquired by beetles through horizontal gene transfer (HGT).

Heterologous expression in cultured insect cells and several enzymatic assays allowed me to identify 13 cellulases and, interestingly 10 xyloglucanases (active on xyloglucan, the most abundant hemicellulose polysaccharide in primary plant cell wall) out of a total of 34 GH45s. The remaining 11 GH45s showed no activity on any substrate I tested. RNAi experiments suggested that in these beetles, the breakdown of cellulose is rather accessory and facilitates the access to the nitrogen-rich cell content.

According to our phylogenetic analyses, we hypothesize that this gene family has evolved from originally two genes present in the last common ancestor of the Chysomeloidea and the Curculionoidea followed by gene duplication events which lead to a differing number of GH45 genes in each species. Interestingly, a cluster of orthologs in the Chrysomelidae shows single activity towards xyloglucan. Still under investigation is whether GH45s in beetles were acquired by HGT.

Keywords: Chrysomelidae, Curculionoidea, Glycoside hydrolase, Cellulase, Endoglucanase, Xyloglucanase, Plant cell wall degrading enzymes

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Poster 53

Terpene chemotypes and interactions with insect herbivores

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Chemical polymorphisms or chemotypes are found across several plant families, in particular related to terpene composition. The Australian tea tree (*Melaleuca alternifolia*) presents terpene chemotypes based on its foliar composition, however there is little knowledge on the relevance of this intraspecific variation for ecological interactions that can be useful for pest management or genetic conservation efforts. I investigated how these chemotypes affect interactions with specialized herbivore beetles in laboratory and field conditions, and the intraspecific variation in volatile emissions. I found that the most common beetle (*Paropsisterna tigrina*) shows a preference for local chemoytpes at the adult stage, but larvae are not affected by chemotypic variation. A rarer species (Faex sp.) shows different oviposition preference to chemotypes that depends on the larval diet. Terpene emissions also show intraspecific variation based on the foliar composition, while herbivory increases the emissions. Overall, I found that chemotypes influence specialized herbivores to some degree and that chemical variation in leaves extend to other plant traits.

Keywords: chemical ecology, terpenes, chrysomelidae, chemical variation, plant volatiles

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Poster 54

Ecological study of pistachio bark beetle, *Chaetoptelius vestitus* Muls & Rey (Coleoptera: Curculionidae)

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The pistachio bark beetle, *Chaetoptelius vestitus* (Muls & Rey) (Coleoptera, Curculionidae, Scolytinae) is a serious pest of pistachio trees in Tunisia. Despite its phytosanitary importance, some aspects of its population dynamic are still unclear. In this study, we investigated the population fluctuations of *C. vestitus* between 2013 and 2016. The distribution of *C. vestitus* was also investigated both in the center and south of Tunisia. We recorded the direct damage caused by beetle on pistachio branches and buds. The highest pistachio bark beetle population density (for all developmental stages) was detected in Elguettar (*Gafsa goveronarate*). This bark beetle overwinters in larval stage on pistachio trees. The adults emerge to attack new suitable trees at mid-February. We found that the sex ratio of beetles recovered from pistachio buds and branches was approximately 1:1 at all experimental sites, and this trend did not vary seasonally. Reproduction starts in autumn, and the copulation takes place at the entrance hole. It was found that females initiated egg tunnel construction copulation takes place either on the bark in the initial phase of egg tunnel construction or inside the tunnel system. Mean achieved fecundity was 50.95 (+/- 9.68 SD) eggs/ female. The colonization process occurs in two phases; during the first phase, the construction of feeding galleries drilled through the buds, in the second phase reproduction galleries are constructed in the thickened branches of the tree. The results obtained in this work are considered essential for developing optimal control of the pest.

Keywords: *Pistacia vera* L., population dynamic, fecundity, colonisation, Tunisia.

Speaker*

Poster 55

The relationship between ant abundance and leaf biomass in ant-inhabited *Macaranga pearsonii* in human-modifed landscapes in SE Asia

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One of the most diverse mutualistic interactions occurring in SE Asia is between Macaranga trees and Crematogaster ants. These early succession trees, often comprising the majority of individuals in disturbed habitats, are ecologically important because they potentially provide shade for late-succession trees. However, little is known about how plant fitness is affected by the identity of their ant mutualists and how this varies across anthropogenically modified landscapes. *Macaranga pearsonii* is a frequently encountered species in both oil palm plantations and logged forest, which could potentially play an important role in the future restoration of these sites. This role might be altered by changes in the mutualistic relationship between ants and plants during habitat degradation. Here we analyse the relationship between ant occupation and herbivory damage of these plants, and compare a degraded habitat where severe logging has occurred but where *Macaranga pearsonii* density is very high with oil palm plantation, where densities are lower. Over 40 trees (0.5m to over 6.5m) were collected and dissected in each habitat. We quantified ant and coccid abundance in each branch as well as leaf biomass. We controlled for environmental factors including soil phosphate, nitrate, pH, soil density and canopy cover that may also influence plant fitness. Additionally we considered specific aspects of the mutualism relating to plant fitness such as ant patrolling and herbivory damage. We demonstrate that depending on the habitat the relation between ant abundance and herbivory is not always positively correlated. Other factors such as ant species identity, the number of colonising queens and how many different species simultaneously occupy the same tree influence the herbivory damage of plants, which may differ in relation to the habitat.

Keywords: herbivory damage, ants, oil palm, logged forest, mutualism, Macaranga, south east Asia

Speaker*

Poster 56

The consequence of plant domestication for resistance against insects: testing the role of the plant-breeding target

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Plant domestication has generally resulted in decreased chemical and physical defense in crop plants compared to their wild ancestors. A reduction in plant defensive traits is often expected to result in increased insect performance. However recent studies have shown that this pattern is not ubiquitous.

The reason for this may lie in the purpose or the organ targeted by domestication. Such that, a positive relationship between reduction in plant defense and increased insect performance will be only, or more evident for cultivars and plant organs that have been selected for consumption.

To test this hypothesis we used wild accessions and cultivated varieties of squash (genus Cucurbita) and larvae of three generalist herbivores: *Spodoptera frugiperda*, *Spodoptera eridania* (leaf-feeding herbivores) and *Diabrotica balteata* (root-feeding herbivore).We chose cultivated varieties that have been selected for different purposes (fruit and seed consumption, and ornamentals). Plants were analyzed and characterized for leaf trichome density and their concentration of cucurbitacins that are known to be toxic to generalist herbivores. In parallel, we conducted laboratory assays to determine insect performance. We found partial support for our hypothesis. Trichome densities were lower on leaves of cultivated varieties, but this did not correlate with insect performance. As predicted, only cultivars selected for fruit consumption had lower concentrations of cucurbitacins than seed varieties and ornamentals, and wild accessions had the highest concentrations. Insect performance was higher on fruit-selected varieties but only for *S. frugiperda*. The performance of *S. eridania* and *D. balteata* was not correlated with cucurbitacin concentration or domestication purpose, which suggests that these species are adapted to feed on plants containing high levels of these toxic compounds.

These results highlight the importance of incorporating plant traits and insect adaptations in studies on crop domestication and insect interactions.

Keywords: Domestication/Squash/Insect performance/Cucurbitacins/Plant resistance

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Poster 57

Insect herbivory may cause changes in the visual properties of leaves and affect the camouflage of herbivores to avian predators

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`Cry for help' hypothesis predicts that attraction of predators with chemical or visual cues can decrease insect damage of plants. Visual cues involve changes in photosynthetic activity and the reflectance of leaves, and there is some evidence that birds may use these changes as foraging cues. However, changes in the visual properties of leaves have not been quantified and it is not known how birds see these changes. We also presented and tested a new `reduction in camouflage' hypothesis (not mutually exclusive with `cry for help') stating that herbivore-mediated changes in leaf colour can increase the conspicuousness of herbivore against leaves. To define changes in the visual properties of leaves, their detectability to birds, and whether these changes affect the conspicuousness of herbivore, we manipulated the level of herbivory in silver birch trees (*Betula pendula*) with autumnal moth (*Epirrita autumnata*) larvae, and used blue tit (*Cyanistes caeruleus*) vision models to images of leaves and larvae. Hue, luminance (lightness), contrast, transparency, chlorophyll content, photosynthetic activity and water content of the leaves were compared between herbivore-damaged and control trees. The leaves of herbivore-damaged trees had a decreased chlorophyll *a* concentration, increased contrast and they reflected more longer wavelengths. However, these changes are likely not obvious to birds. In contrast to our expectation, there were only minor differences in conspicuousness of larvae against the leaves of damaged trees, which may be very subtle to predator vision. Nevertheless, according to visual models, larvae should be easily detectable to birds from both herbivore-damaged and control trees.

Keywords: trophic interactions, avian vision model, background matching, herbivory, camouflage
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Poster 58

Interspecific competition between dominant and infrequent parasitoid wasps of a leaf miner

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Parasitoid wasps are one major enemy of phytophagous insects and play important roles in ecosystem stability. Although each phytophagous insect species is generally attacked by several parasitoid wasps, the majority of individuals are often killed by respective specific dominant parasitoid species. This implies that asymmetric interspecific competition between dominant and infrequent parasitoid species. However, we know little about whether dominant parasitoid species in the wild win in the competition with other infrequent parasitoid species in the laboratory condition. Leaf-mining insects are generally small in their body size, so that majorities of their parasitoid wasps are solitary. In this study, we conduct the laboratory competition experiments between dominant and infrequent braconid parasitoid species of a leaf-minng moth, *Acrocercops transecta* (Lepidoptera: Gracillariidae). Previous study shows that *Aneurobracon philippinensis* (Hymenoptera: Braconidae: Agathidinae) is a single predominant enemy for *Ac. transecta*, and Choeras sp. (Hymenoptera: Braconidae: Microgastinae) is a second predominant enemy among braconid parasitoids. As a result, *An. philippinensis* were always dominant irrespective of the order of oviposition and the length of time intervals between ovipositions. These results suggest that the dominant parasitoid species in the field are also dominant in the experimental competition in the laboratory, suggesting that superiority in the competition is an important factor determining the parasitoid communities of leaf miners and host ranges of parasitoids.

Keywords: Braconidae, Gracillariidae, host range, leaf miner, parasitoid community, solitary
Speaker*

Poster 59

The role of butterfly eggs on plant-plant communication

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Plants are able to recognize eggs of specific herbivores and enhance their defences upon subsequent caterpillar feeding. In a field experiment, we found that egg deposition by a Pieridae butter y on black mustard, induced plant responses that negatively affect the performance of feeding caterpillars. Effects were cascaded up to higher trophic levels and increased attraction of natural enemies. Overall plants use egg-deposition as an "herbivore warning cue" and enhance their direct and indirect responses against subsequent herbivores. This resulted in increased plant fitness (i.e. seed production) compared with plants that did not receive eggs. Black mustard plants grow in patches therefore volatiles from egg-infested plants may be used as another predictable cue of herbivory from neighbouring non-infested plants. It remains unclear whether neighbouring plants can use cues from plants infested with eggs to enhance their defence responses against upcoming herbivory. The first objective was to test whether plants can use volatiles cues from neighbouring plants infested with butterfly eggs to mount enhanced responses upon subsequent herbivory. The second objective is to test whether there are any differences on plant volatiles and phytohormones that suggest an underlying mechanism for the plant response to egg deposition and plant-plant interaction. To investigate our objectives, we used a domestic plant, the white cabbage, which is resistant to herbivory (*Brassica oleracea*) and the wild plant black mustard, (*Brassica nigra*). Our first results suggest that plants, which growing next to egg-infested plants are able to use volatiles from the egg-infested plants and mount their defences against subsequent feeding herbivores. This results emphasize the importance of egg deposition as a warning cue within and between plants to anticipate future herbivory, and adds another dimension to understand phenotypic plasticity of induced plant defences. This may impact the structure of plant mediated communities up to higher trophic levels.

Keywords: plant defences, egg deposition, natural enemies, fitness, plant communication

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Poster 60

Transfer of stabilized and reactivated plant toxin derivatives to the third and fourth tropic level protects the western corn rootworm from its natural enemies

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Herbivore fitness is constrained by plant quality and predation by higher trophic levels. Numerous insect herbivores can redirect plant defenses against their own natural enemies. Yet, plant toxin stabilization and reactivation mechanisms by herbivores, as well as the extent to which they avert predation, remain poorly understood. Here we report that the soil dwelling maize pest herbivore, *Diabrotica virgifera*, tolerates plant benzoxazinoids and accumulates high amounts of the benzoxazinoids glucosides HDMBOA-Glc and MBOA-Glc in its hemolymph and skin. Larvae fed on benzoxazinoid mutant plants were more susceptible to infection by the nematode *Heterorhabditis bacteriophora* which injects and feeds on the entomopathogenic symbiontic bacterium *Photorhabdus luminescens*. We found that MBOA-Glc is a strong repellent to the nematode. Furthermore, upon tissue disruption, *D. virgifera* larvae hydrolyze the stored benzoxazinoid glucosides to produce MBOA. We demonstrate that MBOA reduces development and infectivity of both the nematode and its bacterial symbiont. Our results highlight that both stabilized and re-activated plant toxins can be used by herbivores to defend themselves against natural enemies. The presented findings also provide an explanation for the low success rate of certain biological control programs aiming at controlling *D. virgifera*.

Keywords: Tritrophic interactions, belowground herbivory, benzoxazinoids, *Diabrotica virgifera*, entomopathogenic nematodes

Speaker*

Poster 61

Plants as sources for insect odorscapes

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Insects recognize and localize their vital resources such as food or a mating partner by extracting specific odor signals from a complex and changing odor environment. Not only sources of cues to herbivores, terrestrial plants are the main sources for the huge diversity of volatile organic compounds forming odorscapes among which insects must obtain ecologically relevant information. Female moths for instance release a pheromone blend that attracts male from a distance. Plant volatiles may facilitate or decrease perception of the sex pheromone by males, depending on their chemical nature and concentration. However, emissions of VOCs are modified by plant metabolism and their mixing rates in the atmosphere are constantly changing due to aerial turbulence. We will describe some of the characteristics of the spatio-temporal structure of odorscapes and present results of our behavioral and physiological experiments aiming to understand how odor background affects perception of odor signal and behavior in moths.

Keywords: pheromone, olfaction, sensory ecology, neural coding, plant volatiles

Poster 62

Adaptation of Japanese Swallowtail butterfly to host plant

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Recent studies indicated that various plant secondary metabolisms have driven diversity of herbivores. In order to investigate the evolutionary process of adaptation on defense compounds, we focused on the interactions between Japanese swallowtail butterfly, genus Papilio, and its host plants, Rutaceae and Apiaceae.

First, we quantified "furanocoumarin" that is one of the defense compounds included in Rutaceae and Apiaceae. Second, we conducted feeding experiment utilizing *Papilio xuthus* and 8 Rutaceae plants to see how the furanocoumarin profiles affect larval performance. Finally, we analyzed sequences of CYP6B1 that is a detoxification related gene to investigate the evolution of the detoxification mechanism of Papilio species.

The result of furanocoumarin quantification revealed the species-specific profile of the compounds. In addition, it was revealed that some furanocoumarins were common among plant species, whereas isoimperatorin was found only from one species, *Skimmia japonica*. The comparison the result of feeding experiment and furanocoumarin quantification showed the difference in growth rates of larvae feed on different species. We found that the total amount of furanocoumarin negatively affected the host preference of Papilio larvae shown by existing literature. It is notable that the larvae feed on *Zanthoxylum ailanthoides*, which contained relatively large amount of xanthotoxin, also showed high growth. These results suggest that furanocoumarins might affect the host use of Papilio butterflies. However, it is also showed that not all the furanocoumarins are effective defenses against Papilio butterflies.

In addition, as the result of sequence analysis of CYP6B1, we found a large mutation in amino acid sequence at *P. machaon*. It is known that *P. machaon* is a phylogenetically derivative species that was originated from Rutaceae-feeding species. These suggested that the relatively large host jump from the Rutaceae to the Apiaceae of *P. machaon* might necessarily be accompanied by a large change in the detoxification related gene.

Keywords: chemical defense, detoxification, host adaptation

***Speaker**

Poster 63

Linking genotypic susceptibility to insects pests with plant chemistry: an example from the oilseed rape - pollen beetle interaction

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Pollen beetle (*Meligethes aeneus*) is one of the main insect pests affecting oilseed rape crops. Efficiency of insecticide use to control this pest is decreasing due to its adaptation to phytosanitary products such as pyrethroids. In this context, alternatives to this kind of control need to be found. Breeding oilseed rape for resistance to insect attacks could be an interesting way to deal with this issue. Actually, the primary benefit of this approach is the ease of its use by farmers. However, it remains complicated to breed plants for insect resistance, especially using field tests on large genotype collections. Our knowledge of the chemical ecology of interactions between oilseed rape and pollen beetles could allow to find biochemical markers of this resistance. In this way an indirect breeding approach based on makers of resistance could be adopted rather than direct confrontation of plants to insects. Laboratory tests have already shown that variation in resistance between oilseed genotypes could be explained by the biochemistry of bud tissues. These observations now need to be validated under field conditions. To test this, we conducted a multi-site experiment in France to observe resistance of different genotypes to pollen beetles. We phenotyped pollen beetle damage and sampled buds in the field to analyse their chemistry and, based on these results, discuss the potential use of identified compounds as markers of resistance to pollen beetle for breeding purposes.

Keywords: Plant resistance, *Meligethes aeneus*, *Brassica napus*, Chemical markers

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Poster 64

Is quantity or quality of food the issue in feeding site choice in oilseed rape by the pollen beetle?

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According to the optimal foraging theory, diet selection by herbivorous insects should result from a trade-off between food quality and food quantity. Indeed, these insects are expected to optimize their food choice by balancing nutrient intake on the one hand, while minimizing toxicity from specific secondary metabolites in their host plants on the other. While optimal foraging theory has been used to understand food foraging and selection by some generalist herbivore insects, it has seldom been applied to specialist herbivores to understand how they choose among different plant parts or tissues. Yet, within-plant variability of primary compounds such as carbohydrates and proteins can highly influence tissue nutritional quality. The same variability also exists for secondary toxic compounds. Profitability of plant tissues also depends on architecture, organ size and physical defenses. These three factors (nutritional quality, toxicity, morphology) are rarely studied together but all could condition within-plant feeding patterns. We tried to explain feeding patterns of the pollen beetle (*Meligethes aeneus*), a pollinivorous insect and a pest of oilseed rape (*Brassica napus*) in Europe. We observed a clear feeding pattern, with insects preferring young buds in the center of the inflorescence. However, this pattern seems rather counterintuitive because of the low quantity of pollen present in these non-mature buds. We used behavioral and performance experiments paired with chemical analyses of plant tissues and insects to understand how constraints such as nutritional quality, organ toxicity and accessibility of the pollen may explain such paradox.

Keywords: Feeding pattern, *Meligethes aeneus*, *Brassica napus*, optimal foraging, biochemistry

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Poster 65

The ecology and evolution of host preference in an aphid parasitoid

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The parasitoid *Aphidius ervi* is widely used in biological control programs of aphids. Its success as biocontrol agent relies upon its ability to efficiently find specific aphids. This behaviour is mediated by learning chemical signals from the aphid-plant in which females developed, preferring to oviposit on the natal aphid-plant host. This preference for the natal host (host fidelity), represents an important trait for this parasitoid searching for a suitable host in complex environments. However, host fidelity can be lost when in endogamy conditions, which may reduce its efficiency controlling aphids. We studied the host preference in parasitoids that come from crosses between inbred-females (i.e., taken from caged lines) and outbred-males (i.e., collected from natural populations), to test whether managing the genetic diversity of caged *A. ervi* populations could restore their host fidelity. Hence, experimental parasitoids were raised in a common natal aphid-plant system (pea aphid-broad bean; APA) and evaluated in terms of their ability to prefer for the natal or non-natal host (grain aphid-wheat; SA). The results indicate that inbred and outbred *A. ervi* females had preferences for the natal host; showing significantly faster oviposition behaviour on APA than on SA. Indeed, the outbred-females rejected more than 50% of the non-natal aphids. The admixed-females, however, did not show preference for any host. Our results suggest a strong genetic effect that could be result from deleterious genes in inbred females, which are negatively affecting host fidelity after a single generation (admixed population). Interestingly, the preference for the natal host displayed by inbred-females gives some insights that a mechanism other than host fidelity could be explaining the pattern of host preference observed on APA. Our findings should help to understand the complexity of host fidelity in aphid parasitoid waps.

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Keywords: Parasitoid, Host preference, Behavior

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Poster 66

Role of volatiles from cowpea varieties on the behavior of *Megalurothrips sjostedti*

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The bud flower thrips, *Megalurothrips sjostedti* is a major pest of cowpea in sub-Saharan Africa. Main damages are due to the abortion of flowers and their shedding. Chemical sprays generally used by farmers to control thrips have a negative impact on human health and environment. The contribution of semiochemicals in the interactions between cowpea and thrips were investigated to reduce *M. sjostedti* outbreaks in the fields. In order to evaluate the potential effect, a preference host selection, at vegetative and oral stages, was done by observing insect location 24 hours after introduction into a cage with four cowpea varieties. Then, the choice of thrips adults between air control and the vegetative or floral parts of cowpea varieties was observed into Y-tube olfactometer. The chemical analyse of cowpea volatiles was performed by coupled gas chromatography-mass spectrometry (GC/MS) to identify and quantify the compounds emitted by vegetative and floral parts of cowpeas. The preference test showed no significant difference between the four varieties of cowpea at both growth stages. The olfactometer test indicated repellent effect of vegetative and floral parts of the cowpea variety K80 to female thrips. The vegetative parts of varieties EL and M66 were repellent to females but their flowers were repellent to males. In addition, the odour from the vegetative part of cowpea variety KK1 was repellent to males but the flower part was attractive to females. There were no significant differences for most of the variety in pairwise comparisons. Only the variety K80 was significantly attractive to males than the variety KK1. The role of volatiles from different part of cowpea plants was discussed as part of the natural defence mechanism of cowpea against the thrips *M. sjostedti*.

Keywords: *Megalurothrips sjostedti*, cowpea, preference selection, Olfactometer, gas chromatography, mass spectrometry, volatiles, semiochemicals

Speaker*

Poster 67

Early-flowering induced by herbivory in wild Lima bean plants affects late-season seed predators but not their parasitoids

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Early-season herbivory can induce plant responses that affect herbivores later in the season. For wild lima bean, *Phaseolus lunatus*, plant development is well synchronized with that of the associated insects that attack the plant throughout the season. Therefore, any change in plant phenology can alter the interactions with the insect community.

Here, we examined how early-season herbivory affects plant phenology and reproductive traits, and how these changes influence the attack by late-season herbivores and their natural enemies. In a field experiment in Puerto Escondido (Oaxaca, Mexico), plants were either infested with herbivores or kept undamaged and followed throughout the season. We recorded flowering time, pod production and number of seeds per pod. Upon seed maturation, seeds were collected and we recorded the number of seed predators (Bruchinae) and the number of parasitoids that emerged from these seeds. We found that early-season herbivory significantly shortened plant flowering time, and reduced pod and seed production. On the other hand, bruchids were more abundant in herbivore-treated plants. No significant difference was found in the abundance of parasitoids across treatments.

These findings suggest a trade-off between growth and defense whereby, plants subjected to herbivory reproduce early but invest less resources in defensive compounds allocated to the seeds. Overall, these results show how small changes in one trophic level can result in complex cascading effects on higher trophic levels.

Keywords: Tritrophic interactions, Ecology, Plant fitness, Parasitoids, Seed predators, Plant phenology

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Poster 68

Whitefly fitness on tomato plants is reduced by spider mite colonization through jasmonic acid and salicylic acid signaling pathways

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Plants are attacked by herbivorous insects and evolved different defense strategies to prevent or reduce damage. Plants usually upregulate jasmonic acid (JA) based defenses against tissue-damaging arthropods, such as mites, and activate salicylic acid (SA) signaling defenses to prevent further damage by phloem-feeding insects, for example whiteflies. As plant consumers, herbivores have to face not only plant defenses but also interact with other herbivores because plants usually are under attack by multiple herbivores. The white fly *Bemisia tabaci* and the two spotted spider mite *Tetranychus urticae* are important generalist horticultural pests and infestation with both insects on the same plant is common. They represent two different feedings guilds since *B. tabaci* is a phloem feeder and *T. urticae* is a cell-content. Here, we investigated plant-mediated interactions between these two herbivores. We found that the oviposition of *B. tabaci* was negatively affected by the colonization of *T. urticae* above a threshold density. The assessment of expression of marker genes in the SA and JA pathways indicated that both pathways were activated by coinfestation with these two insects. Furthermore, white fly performance assays by using JA deficient mutant Spr-2 and SA deficient mutant NahG tomato plants and by mimicking spider mite infestation with exogenous application of JA and SA demonstrated that JA and SA were important in the plant-mediated interaction between *T. urticae* and *B. tabaci*. Although white flies are able to manipulate plant signaling, this strategy was not found to be used by *B. tabaci* to enhance their fitness on tomato plants infested with *T. urticae*. Instead, *B. tabaci* expressed a higher level of transcripts of detoxification enzymes, such as P-450 monooxygenases, carboxylesterases and glutathione S-transferases, to tolerate the plants defenses triggered by the other herbivore, which may cause a reduction in their fecundity.

Keywords: plant resistance, signal transduction, detoxification

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Poster 69

Parasitoid foraging behaviour in complex situations: Influence of weather, surrounding vegetation and learning

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Parasitoid foraging has been intensively studied in simple laboratory set-ups, but less is known about parasitoid host location in more complex natural environments. Herbivore-induced plant volatiles (HIPVs), which are emitted after an herbivore attack are important foraging cues for parasitoids. The ability of parasitoids to follow an odour plume upwind towards its source is likely influenced by weather conditions and surrounding vegetation. Experience with host or non-host related HIPVs may help parasitoids to orient in complex natural environments.

To study parasitoid foraging efficiency in complex situations, we use the parasitoid *Cotesia glomerata*, which attacks caterpillars of the Cabbage white (*Pieris rapae* and *P. brassicae*). Preliminary experiments, in which we released parasitoids in a circle of caterpillar infested plants in the field, suggest that the number of parasitoids that successfully located a caterpillar infested plant strongly depends on humidity, with more parasitoids reaching caterpillar infested plants at higher humidity. This indicates that parasitoid foraging activity or their ability to locate an odor source is reduced at low humidity. Preliminary data further hints that upwind dispersal may only be possible at low wind speed. In a wind tunnel study we showed that non-host infested cabbage plants distract naive parasitoids from the host infested plant, leading to longer foraging until location of the host infested plant. The ability of parasitoids to discriminate between host and non-host infested plants increased after non-host experience, but did not increase foraging efficiency in complex situations. Surprisingly, oviposition experience even decreased parasitoid foraging efficiency in complex situations.

Our experiments suggest that parasitoid foraging in complex (field) environments is less straight forward than in simple laboratory set-ups and that both adverse weather conditions and presence of neighboring plants can decrease foraging efficiency. Our results further show that learning may not always increase foraging efficiency in complex situations.

Keywords: parasitoids, foraging, HIPVs, weather conditions, *Cotesia glomerata*, *Pieris brassicae*

Speaker

Poster 70

The wolf in sheep's clothing: Entomopathogenic nematodes attract their insect herbivore hosts by manipulating plant and cadaver odors

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Plants under herbivore attack are well known to attract natural enemies. Whether natural enemies can attract herbivores by manipulating plants in turn is unknown. We investigated this question using the entomopathogenic nematode (EPN) *Heterorhabditis bacteriophora* and the western corn rootworm (WCR, *Diabrotica virgifera virgifera*), a specialist root herbivore of maize. Belowground olfactometer and Petri dish experiments revealed that WCR larvae are repelled by EPNs alone, but attracted to maize plants that are exposed to EPNs. Surprisingly, WCR larvae are also attracted to EPN-infested WCR cadavers. We are currently in the process of identifying the responsible plant and cadaver volatiles. Our study indicates that EPNs can manipulate the volatile bouquets of plants and herbivores to lure in their prey.

Keywords: Tritrophic interactions, entomopathogenic nematodes, werstern corn rootworm, below-ground herbivore, natural enemies

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Poster 71

Combined use of herbivore-induced plant volatiles and sex pheromones for mate location in braconid parasitoids

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Herbivore-induced plant volatiles (HIPVs) are important cues for female parasitic wasps to find hosts. Here we investigated the possibility that HIPVs may also serve parasitoids as cues to locate mates. To test this, the odour preferences of four braconid wasps, the gregarious parasitoid *Cotesia glomerata* (L.) and the solitary parasitoids *Cotesia marginiventris* (Cresson), *Microplitis rufiventris* Kokujev, and *Microplitis mediator* (Haliday), were studied in olfactometers. Each species showed attraction to pheromones, but in somewhat different ways. Males of the two Cotesia species were attracted to virgin females, whereas females of *M. rufiventris* were attracted to virgin males. Males and females of *M. mediator* exhibited attraction to both sexes. Importantly, females and males of all four species were strongly attracted by HIPVs, independent of mating status. In most cases, males were also attracted to intact plants. The wasps preferred the combination of HIPVs and pheromones over plant odours alone, except *M. mediator*, which appears to mainly use HIPVs for mate location. We discuss the ecological contexts in which the combined use of pheromones and HIPVs by parasitoids can be expected. To our knowledge, this is the first study to show that braconid parasitoids use HIPVs and pheromones in combination to locate mates.

Keywords: Plant, insect interactions, caterpillar, induced plant volatiles, leaf volatiles, mate finding strategy, tritrophic interactions, biocontrol

Poster 72

Multiple adaptations allow the cabbage stem flea beetle to tolerate plant defense compounds

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Herbivores feeding on crucifer plants are confronted with a potent activated defense -the glucosinolate-myrosinase system. Feeding damage triggers enzymatic degradation of glucosino--lates to reactive isothiocyanates which deter non-adapted herbivores. The host plant range of the cabbage stem flea beetle *Psylliodes chrysocephala*, however, is restricted to glucosinolate containing plants. We thus investigated how these specialists overcome this plant defense and avoid isothiocyanate toxicity by analyzing the metabolic fate of ingested glucosinolates. We found isothiocyanates to be only present in traces in samples from beetle bodies and feces; instead, we detected two novel metabolites derived from the isothiocyanate-glutathione-conjugate. The metabolism of isothiocyanates via conjugation with glutathione represents a common detoxification mechanism, and our results suggest that this strategy efficiently enables *P. chrysocephala* to overcome this chemical defense of crucifers. Additionally, we found that *P. chrysocephala* adults also selectively sequester intact glucosinolates into their bodies, and we also detected desulfo-glucosinolates in beetle bodies and feces. The conversion of intact glucosinolates to desulfo-glucosinolates is catalyzed by specific sulfatase enzymes and prevents the activation of glucosinolates to the toxic isothiocyanates. Together, glucosinolate sequestration and detoxification by desulfation accounted for the fate of up to 35% of the total ingested glucosinolate in *P. chrysocephala*. The presence of both general (detoxification of isothiocyanates with glutathione) and highly specific detoxification strategies (sequestration and enzymatic deactivation of intact glucosinolates) in this specialized flea beetle suggests a stepwise adaptation to glucosinolates within the genus Psylliodes.

Keywords: adaptation, detoxification, glutathione, isothiocyanate, flea beetle, glucosinolate, plant defense

****Speaker***

Poster 73

Salivary proteins of spider mites that manipulate plant defenses and promote mite reproduction

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Spider mites (Tetranychidae sp.) are widely occurring arthropod pests on cultivated plants. Feeding by the two-spotted spider mite *T. urticae*, a generalist herbivore, induces a defense response in plants that mainly depends on the phytohormones jasmonic acid and salicylic acid (SA). On tomato (*Solanum lycopersicum*), however, certain genotypes of *T. urticae* and the specialist species *T. evansi* were found to suppress these defenses. This phenomenon occurs downstream of phytohormone accumulation via an unknown mechanism. We investigated if spider mites possess effector-like proteins in their saliva that can account for this defense suppression. First we performed an in silico prediction of the *T. urticae* and the *T. evansi* secretomes, and subsequently generated a short list of candidate effectors based on additional selection criteria such as life stage-specific expression and salivary gland expression via whole mount in situ hybridization. We picked candidates from the top 10 most promising protein families and expressed representatives in *Nicotiana benthamiana* using *Agrobacterium tumefaciens* transient expression assays to assess their effect on plant defenses and mite performance. Some of these proteins suppressed defenses downstream of the phytohormone SA. Furthermore, *T. urticae* performance on *N. benthamian* a improved in response to transient expression of three of these proteins. Our results suggest that both generalist and specialist plant-eating mite species secrete proteins via their saliva to reduce the negative effects of these defenses.

Keywords: spider mites, susceptibility, S gene, effector, resistance, plant breeding, protein, interaction, tetranychus

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Poster74

Correlation between phytohormone patterns and gall induction by Phylloxera on grape leaves

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Galls are highly specialized structures arising from atypical development of plant tissue induced by another organism. Many different kinds of organisms can induce galls on plants, including viruses, fungi, bacteria, nematodes, mites and insects. However, gall-inducing insects produce the most diverse galls in nature, ranging from simple stem swellings to complex structures that are ornamented with bright colors and spines. These structures are thought to provide adaptive advantages to gall-inducers by enhancing their nutrition, and protecting them against natural enemies and environmental stresses. Gall formation is a complex and close interaction between the gall-inducing insect and its host-plant resulting from molecular cross-talk between two independent genomes; however, the mechanism underlying the gall induction and mainte-nance by gall-inducing insects is still unknown. In this study, we characterized phytohormones present (i) in the gall-inducing insect's body (*Daktulosphaira vitifoliae*) and (ii) in the galls they induce on grape leaves (*Vitis riparia*). This will allow us to determine which phytohormones are used as salivary effectors by the insect and how these secretions alter phytohormone profiles within the plant to induce gall initiation and growth. Because galls grow via hypertrophy and hyperplasia, phytohormones that influence cell growth and division, such as auxins and cytokinins, will most likely be involved in host-plant manipulation. These plant growth factors have already been detected in insect saliva in other studies, and these insect-derived plant hormones may be responsible for stimulating gall growth.

Keywords: Gall, Aphid, Phylloxera, Grape, Phytohormones, Cytokinins, Auxins
Speaker

Poster 75

Early cell responses of poplars to salivary extracts of a gall-inducing aphid, *Phloeomyzus passerinii*

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Saliva is considered as the molecular interface between most phytophagous insects and their host plant, and plays a critical role during plant manipulation by gall-inducing insects. We used a multidisciplinary approach to (i) characterize the saliva of *Phloeomyzus passerinii*, an aphid inducing galls in the bark of poplars, and (ii) assess the effects of salivary extracts on host plant cells. We first used the transcriptome obtained from the salivary glands to compare the *P. passerinii* secretome with those of other aphids and gall-inducing insects. In addition, we assessed the early cell responses to salivary extracts transcriptionally using leaves protoplasts from two poplar genotypes, either susceptible (I214) or resistant (Koster) to *P. passerinii*. For this, the expression profile of 45 genes involved in plant response to biotic stress was assessed by qRT-PCR upon short time treatment with salivary extracts from *P. passerinii* and from *Myzus persicae* as control. The secretome comparisons allowed us to unravel the presence of known orthologous effectors in other aphid species, Mp10, ACE, ARMET and an orthologous effector of gall induction, SSGP71, from *Mayetiola destructor*. The transcriptomic approach indicated a classical response to *M. persicae* salivary extracts for both poplar genotypes, activating several plant hormones pathways. The cellular response of the resistant genotype (Koster) also showed an activation of these pathways in response to *P. passerinii* salivary extracts. In contrast, jasmonate and salicylate pathways were repressed in I214 with this salivary extracts as well as genes involved in auxin homeostasis. The potential roles of salivary compounds in plant manipulation are discussed.

Keywords: *Phloeomyzus passerinii*, poplar, gall, inducing aphids, saliva, secretome, gene expression, protoplast, cell response
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Poster 76

Responses of *Cnaphalocrocis medinalis* resistant varieties in rice

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Rice leaffolder (*Cnaphalocrocis medinalis* Guenee) is one of major rice pests in Taiwan. Previous studies showed the migratory *C. medinalis* in Taiwan come from Mainland China every year. Thus, we collected *C. medinalis* throughout Taiwan to understand the genetic variation of *C. medinalis* in Taiwan. In addition, we have been selected several rice varieties which showed *C. medinalis* resistant trait in the field test. Thus, we further measured the several defensive enzyme responses (such as polyphenol oxidase (PPO), peroxidase (POD), phenyl ammonia lyase (PAL) and trypsin protease inhibitor) of *C. medinalis* resistant varieties against *C. medinalis*. Furthermore, the defensive responsive gene expression and phytohormone profiles in rice is also been examination. In addition, we measured the defensive responses of *C. medinalis* resistant varieties against *C. medinalis* exposed to elevated CO2 and temperature conditions.

Keywords: *Cnaphalocrocis medinalis*, resistant varieties
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Poster 77

The salivary protein repertoire of the polyphagous spider mite *Tetranychus urticae*: a quest for effectors

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The two-spotted spider mite *Tetranychus urticae* is an extremely polyphagous crop pest. Alongside an unparalleled detoxification potential for plant secondary metabolites, it has recently been shown that some spider mite lines can attenuate or even suppress plant defenses. Salivary constituents, notably effectors, have been proposed to play an important role in manipulating plant defenses and might determine the outcome of plant-mite interactions In order to collect salivary secretions, mites were allowed to feed on an artificial diet contained within Parafilm hemispheres. As the host plant species is known to have a major impact on mite gene expression profiles, mite lines adapted to distinct plant species (bean, maize, soy, and tomato) were used for the feeding assays. Each host specific sample consisted of 0.3 ml of diet containing the salivary secretions of only 500 spider mites. Analysis with a Thermo Scientific LTQ Velos Orbitrap mass spectrometer revealed the identity of about 90 putative *T. urticae* salivary proteins. Many were of unknown function, and in numerous cases belonged to multi-membered gene families. To distinguish salivary proteins from contamination, the proteomics data were supplemented with RNAseq expression data of the mite body region that includes the salivary glands. Furthermore, host plant dependent production was evident for some putative salivary proteins, which was studied in detail by micro-array based genome-wide expression profiling. Additionally, a subset of genes encoding putative salivary proteins was selected for whole-mount *in situ* hybridization, and were found to be expressed in the anterior or dorsal podocephalic (salivary) glands. This meta-analysis revealed for the first time the salivary protein repertoire of a phytophagous chelicerate. The availability of this salivary proteome is expected to lead to a fundamental understanding of plant-mite coevolution, and may ultimately facilitate the development of mite-resistant crops.

Keywords: effector, LC, MS/MS, host plant, mite-plant interaction
***Speaker**

Poster 78

Interactions between the courgette *Cucurbita pepo* L. and the cotton aphid *Aphis gossypii* Glover

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The cotton or melon aphid, *Aphis gossypii* Glover, is a pest on different crops. *Cucurbita pepo* is one of its host plants, and it has been used for studying plant response to aphid attack. Here we show the results of a study of the interplay occurring between aphids, the plant response to the aphid challenge, and the aphid behavior in a subsequent infestation. We observed that previous aphid infestation does not impact biological parameters such as longevity and fertility. Conversely it affects the distribution on the plant of the newly produced nymphs, that actively disperse on the plant, rather than starting their feeding activity where they were originally laid, as happens in the control plants. Expression profile of genes involved both in the biosynthesis of Salicylic Acid (SA) and in the SA-mediated defense response evidenced that both gene categories were induced in the infested leaves. This result provides a possible explanation for this behavior as methyl salicylate, a volatile product of SA pathway, is known to promote aphid dispersal.

Interestingly, the dispersal observed upon previous aphid infestation is induced also by saliva application, showing that a salivary component is responsible for the altered gene expression and behaviour observed.

Keywords: plant response, aphid saliva, methyl salicylate, SA pathway
Speaker

Poster 79

Nicotiana attenuata distinguishes between different herbivorous insect species by their eggs.

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Plants can recognize insect oviposition and use it as a signal to prepare their defences against the upcoming herbivorous larvae. For example, oviposition-experienced *Nicotiana attenuata* plants increase their induced defences in response to larval herbivory. Feeding by two of its lepidopteran herbivores, *Manduca sexta* and *Spodoptera exigua*, elicits distinct responses in *N. attenuata*, but oviposition by both herbivores enhances these feeding-induced defences in a similar manner. We therefore investigated how oviposition affects the transcriptional and phytohormonal regulation of the plant's species-specific responses to larval feeding.

In a full factorial experimental design, we disentangled the species-specific effects of oviposition and larval feeding by both species. One day after larvae started to feed, as well as one day after oviposition, leaves of oviposited and non-oviposited plants were analysed for levels of JA, JA-Ile, SA and ABA by LC-MS/MS and their transcriptome was examined using microarrays.

Phytohormonal and transcriptomic analyses confirmed two distinct plant responses to feeding of the different herbivores. At the time of larval feeding, the transcriptomic imprint of oviposition was only minor, yet the species-specific plant response to the feeding larvae of each herbivore was shifted on plants that experienced the oviposition by the other species: When prior oviposited by *S. exigua*, the transcriptomic plant response to *M. sexta* feeding became more similar to that of plants that were fed upon by *S. exigua*, and vice versa. Moreover, we found a strong species-specific response directly after oviposition. Oviposition per se did not alter the phytohormone levels at any of the measured time points.

We conclude that *N. attenuata* differentiates between these two herbivore species already by their oviposition, which shapes the species-specific plant response to the subsequent caterpillar feeding.

Keywords: Plant defence, *Nicotiana attenuata*, *Manduca sexta*, *Spodoptera exigua*, insect oviposition, priming, herbivory, microarray, transcriptional responses, phytohormones
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Poster 80

Within-plant distribution and susceptibility of hazelnut cultivars to Hazelnut Gall Midge, *Mikomya coryli* (Diptera: Cecidomyiidae)

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The hazelnut gall midge, *Mikomya coryli* (Kieffer) (Diptera: Cecidomyiidae), is widespread in Europe and the most important cecidomyiid pest of hazelnut. Within-plant distribution, susceptibility of 18 Turkish hazelnut cultivars (Aci, Allahverdi, Cakildak, Cavcava, Fosa, Incekara, Kalinkara, Kan, Karafindik, Kargalak, Kus, Mincane, Palaz, Sivri, Tombul, Uzunmusa, Yassi Badem and Yuvarlak Badem), and the phenology of larvae of this pest in hazelnut leaves and involucres were assessed in 2014 and 2015 in Giresun (Turkey). *M. coryli* distribution differed significantly within different parts of the hazelnut plant. The highest gall numbers of *M. coryli* were found in the middle part (0.70-1.40 m) of the plant in both years. Total gall numbers varied between years: 1779 and 2588 galls were counted in 2014 and 2015, respectively. Susceptibility to *M. coryli* damage varied significantly among the cultivars. The highest leaf gall densities and total numbers of galls were found on leaves and involucres of Allahverdi, Yuvaklak Badem and Yassi Badem cultivars in both years. *M. coryli* larvae were detected between April and June in the leaf galls. The number of larvae in the involucres changed between April and mid-June. Results of the within-plant distribution, *M. coryli* larval phenology, and cultivar pest-susceptibility analyses are presented to enable effective control of the pest as a part of hazelnut integrated pest management.

Keywords: host, plant resistance, hazelnut cultivar, filbert, gall midges, within, plant distribution

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Poster 81

Does cabbage seeds treated with jasmonic acid and chitosan affect diamondback moth performance?

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Plants respond to insect herbivore attack through both constitutive and inducible defensive strategies. The latter allow plants to manage energy reserves more efficiently by synthesising defence compounds only when needed, not spending energy unnecessarily with protection mechanisms. Although, when plants are challenged by herbivores, they may suffer considerable damage before the defence is mounted. Priming can lead to a state of readiness for the induction of the defence response, leading to a reduction of the damage received. It can be triggered by insect damage, pathogens, and exogenous chemicals, such as jasmonic acid. By using *Brassica oleracea* L. var. capitata cv. Derby Day seeds treated with jasmonic acid (JA) and chitosan (CH), we conducted an experimental study to verify whether JA or CH would affect *B. oleracea* leaf area and/or *Plutella xylostella* L (Lepidoptera: Plutellidae) performance. For that, second instar *P. xylostella* larvae were placed on the surface of *B. oleracea* fully expanded leaves and the plants were enclosed in perforated ower sleeves and were evaluated daily. Neither JA nor CH affected *B. oleracea* leaf area, duration of *P. xylostella* larval stage or adult emergency percentage, when compared to the control groups. On the other hand, JA significantly reduced *P. xylostella* mean relative growth rate (MRGR), duration of pupal stage and increased preimaginal mortality of *P. xylostella* up to 84%. Regarding oviposition, CH did not affect egg viability, but reduced the total number of eggs (we were not able to evaluate JA, due to high preimaginal mortality). Therefore, long-term defence priming by seed treatment with jasmonic acid and chitosan did not lead to reductions in *B. oleracea* photosynthetic area and affected *P. xylostella* performance.

Keywords: *Brassica oleracea*, *Plutella xylostella*, priming, defence, chewing herbivores

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Poster 82

Interaction of beetle polygalacturonases with plant cell wall proteins

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The herbivorous mustard leaf beetle *Phaedon cochleariae* feeds on brassicaceous plants and possesses various carbohydrases for the digestion of plant cell wall polysaccharides. Amongst those, polygalacturonases (PGs) facilitate the breakdown of the cell wall polysaccharide pectin. Several plant-derived, cell wall-associated polygalacturonase-inhibiting proteins (PGIPs) are known to inhibit microbial PGs and thus contribute to the plant's defence against phytopathogenic fungi and bacteria. However, direct interactions between beetle PGs and plant inhibitory proteins have not yet been investigated. Both, PGs and PGIPs, belong to multi-gene families that are believed to be shaped by an evolutionary arms race. Besides intact PGIPs, several inactive PG family members were detected in the beetle gut and PG activity was observed in the gut content. Kirsch et al. (2014) stated that "catalytically inactive proteins may act as "decoy" targets for PGIPs, thus protecting the active PGs from inhibition". We performed interaction studies of *P. cochleariae* PG family members (active and inactive) with crude cell wall protein extracts from the beetle's food plant Chinese cabbage (*Brassica rapa* ssp. *pekinensis*). Plant PGIPs and other leucine-rich repeat (LRR) proteins were identified by MS/MS as candidates for beetle PG inhibition. Furthermore, we found differential interaction of plant proteins with the tested PG family members, indicating different specfcities of plant proteins towards active and inactive PG family members. Heterologous expression of candidate proteins is currently in the process to elucidate the protein inhibitory activity and specificity *in vitro* and will shed light on plant defence against insect PGs in general.

Keywords: beetle, polygalacturonase (PG), polygalacturonase inhibiting protein (PGIP), plant defence, plant cell wall protein

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Poster 83

What is driving aphid abundance? Effects of intraspecific and intraindividual variation of plants on aphid preference and performance in relation to phloem chemistry

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Plant traits affecting aphid abundance can differ within plant species but even within plant individuals. *Tanacetum vulgare* (common tansy, Asteracae) varies in its leaf terpenoid profiles, forming distinct chemotypes. This intraspecific variation influences the abundance of the specialised aphids *Macrosiphoniella tanacetaria* and *Uroleucon tanaceti*. Furthermore, these aphids are found on different plant tissues, indicating also intraindividual variation in phloem quality. Here, aphid preference was investigated for two distinct chemotypes (thujone and trans-carvyl-acetate). Moreover, aphids were fixed on either the upper stems close to the bud, young or old leaves of both chemotypes to test their performance on these tissues. Aphids of both species preferred leaves of the thujone chemotype over those of the trans-carvyl-acetate chemotype. Yet, neither chemotype nor plant part affected survival of *M. tanacetaria* aphids, whereas the number of *M. tanacetaria* offspring was highest on the bud stem. In contrast, *U. tanaceti* aphids survived best on old leaves of the thujone chemotype and showed highest reproduction on old leaves of both chemotypes. Therefore, *M. tanacetaria* aphids seem to occupy a broader niche, while *U. tanaceti* aphids appear to be restricted to older leaves. To test the variation in food quality that affected the aphids, we collected and analysed phloem exudates. We found clear differences in the composition of sugars, organic acids and amino acid composition between different tissues. High concentrations of amino acids and a low ratio of sucrose to amino acids were found in bud stem exudates, which, however, did not necessarily improve aphid performance. In summary, we show that intraspecific and intraindividual variation can affect aphid preference and perfor-mance to different extents, mediated by distinct food quality. Therefore, this study highlights the importance to consider multiple scales to understand what drives aphid abundance.

Keywords: intraspecific and intraindividual variation, specialised aphids, performance, preference, *Tanacetum vulgare*, phloem chemistry

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Poster 84
Modulation of legume defense signaling pathways by native and non-native pea aphid clones

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The pea aphid (*Acyrthosiphon pisum*), a phloem-sucking insect, is a complex of at least 15 genetically different biotypes that are native to specific legume plants, but can all develop on the universal host plant *Vicia faba*. It is still not clear why pea aphid biotypes are able to colonize their native hosts while other biotypes are not. When aphids test plant suitability they penetrate the plant and salivate into the plant. Thus plants might react differently to the various pea aphid biotypes and might vary in their defense responses to the different biotypes. In order to test this, we measured the amounts of salicylic acid (SA), the jasmonic acid-isoleucine conjugate (JA-Ile), other jasmonate precursors and derivatives, and abscisic acid (ABA) in four different species (*Medicago sativa*, *Trifolium pratense*, *Pisum sativum*, *V. faba*) after infestation by native and non-native pea aphid clones of various biotypes. We also assessed the performance of the clones on the four plant species. On *M. sativa* and *T. pratense* non-native clones were barely able to survive or reproduce, and triggered a strong SA and JA-Ile response. The infestation with native clones however, led to lower levels of both phytohormones. On *P. sativum*, non-native clones survived or reproduced to a certain extent, and induced uctuating SA and JA-Ile levels, whereas the native clone triggered only a weak SA and JA-Ile response. On the universal host *V. faba* all aphid clones triggered only low SA levels initially, but induced clone-specific patterns of SA and JA-Ile later on. Our results suggest that *A. pisum* clones manipulate plant-defense signaling to their own advantage, and perform better on their native hosts due to their ability to modulate the SA- and JA-defense signaling pathways.

Keywords: pea aphid, sympatric speciation, plant response, phytohormones

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Poster 85
Solanum dulcamara's response to insect eggs comprises ovicidal hydrogen peroxide production

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Plants show multifaceted responses to insect oviposition. However, little is known about which of these responses directly affect the eggs and how. We show that the bittersweet night-shade *Solanum dulcamara* kills the eggs of the generalist noctuid herbivore *Spodoptera exigua*. At sites of oviposition, the plant forms neoplasms and chlorotic tissue and accumulates reactive oxygen species as well as defensive proteins. Transcriptome analyses revealed that these responses were reflected in the transcriptional reprogramming of the egg-laden leaf. A plant genotype that does not show chlorotic leaf tissue at the oviposition sites and on which the eggs are exposed to less hydrogen peroxide did not kill the eggs. As we show that exposure to hydrogen peroxide increases egg mortality while supplementation of egg clutches on plants with the hydrogen peroxide decomposing enzyme catalase reduced egg mortality, we suggest that ROS formation directly acts as an ovicidal plant response of *S. dulcamara*.

Keywords: insect eggs, ROS, hypersensitive like response, plant defense, neoplasm

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Poster 86

Transcriptomic responses of *Solanum dulcamara* to natural and simulated herbivory

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Plants respond to insect herbivory with a variety of defense responses. To study the early transcriptional events after herbivore attack, herbivory is often simulated to standardize the temporal and spatial dynamics that vary tremendously for feeding by a live herbivore. However, to what extent such simulations of herbivory elicit the same plant response as real herbivory remains largely undetermined. We examined the transcriptional response of *Solanum dulcamara* to herbivory by *Spodoptera exigua* larvae and to application of the larvae's oral secretions to standardized wounds, a commonly used herbivory simulation. We designed a microarray for *S. dulcamara* and showed that the transcriptional response to real and to simulated herbivory overlapped moderately by about 40%. Interestingly, certain responses were mimicked better than others; 60% of the genes up-regulated but not even a quarter of the genes down-regulated by herbivory were similarly affected by application of oral secretions to wounds. The regulation of genes involved in signaling, defense and water stress were mimicked well by the simulated herbivory, but most of the genes related to photosynthesis, carbohydrate- and lipid metabolism were exclusively regulated by real larval feeding. Thus, wounding and application of oral secretions decently mimics herbivory-induced defense responses but likely not the reprogramming of primary metabolism induced by real herbivory.

Keywords: *Solanum dulcamara*, microarray, caterpillar herbivory, photosynthesis, plant defense, phytohormone signaling, transcriptomics

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Poster 87

EdenShield products: A new class of ecological substances for insect pests control

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Greenhouse environments provide a variety of benefits for plant production; however, many greenhouses favor pest development as well. The warm, humid conditions and abundant food are ideal for pest build up. Natural enemies that serve to keep some pests under control in the field are absent in the greenhouse. For these reasons, pest problems often develop more rapidly and are more severe in enclosed systems. Pesticides are important tools in managing greenhouse pests. However, applications in enclosed spaces increase the risk of worker exposure and plants Phytotoxicity. Several desert plants species are well known for their strong odor and their toxic natural products that are stored in the plants trichomes, or hairs. We use the characteristics of the desert plants to develop a family of natural, nontoxic products, to protect crops against insect's damage .Our products are based on extracts of indigenous plants in the Judean Desert. In our study we applied the plants extract in the greenhouse environment and found that it reduced insect's attraction to the plants by causing insects to choose feeding option in other locations. Field tests demonstrated a reduction in greenhouse penetration of thrips, white flies and *Tuta absoluta*. Based on these results we suggest that products as Edeneshield products could be considered as a new class of ecological substances for insect pests control.

Keywords: insect, pests control

Poster 88

Plant utilization by phloem feeder insects: Secondary metabolites interacts in primary metabolism

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The importance of plant secondary metabolites in determining patterns of host plant utilization is well established in herbivore arthropods, especially on chewing insects. As a matter of fact, the involvement of plant secondary metabolites in determining specific insect-plant interactions in phloem-feeding insects is questioned and controversial. At the same time, phloem feeding insects face a unique challenge when feeding on their host plants, as they are required to overcome the high osmotic potential of the phloem sap by converting sucrose into various oligosaccharides which are excreted as honeydew. Therefore, traits involved in sugar metabolism, have the potential to play an important role in host-plant adaptation in phloem-feeding insects, and might be under strong selection pressure. Taken together, we pose here the hypothesis that research on phloem-feeding-insects interactions with their plant hosts, should focus mainly on primary (sugar and amino-acid) metabolism and its interface with defensive secondary metabolic pathways. In this study, we zoomed-in on the interaction between glucosinolates producing plants and few hemipteran models belonging to the phloem-feeding guild: whiteflies, aphids and mealybugs. Honeydew analysis indicated that all analyzed members were capable of conducting a novel biochemical modification, which involve the sequential additions of multiple glucose moieties to glucosinolates. This modification was found to be unique and was not detected in the frass of other analyzed groups such as leaf-chewers. It is proposed, that the presence, simultaneously, in the gut lumen of phloem feeders, of both glucosinolates (or other defensive glucoside conjugates) and high-levels of non-assimilated glucose (derived from the hydrolysis of sucrose), allowed phloem-feeding insects to evolve an efficient, elegant and energetically cheap solution to handle two major feeding limitations that interfere with successful host utilization: the control of osmotic pressure and the need to detoxify plant defensive chemistry.

Keywords: phloem feeder insects, host plant adaptation, glucose, Secondary metabolites

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Poster 89

Transgenerational consequences of inbreeding and herbivory in *Solanum carolinense*

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Plants have evolved diverse physical and chemical defenses against herbivores and pathogens. While some of these defenses are expressed constitutively, others are induced only in response to specific challenges. Inducible defenses allow plants to conserve resources in challenge-free environments, and to tailor defense responses to particular antagonists. Recent evidence indicates that induction of anti-herbivore defenses in one generation may influence the expression of such defenses in subsequent generations, which might provide progeny with a competitive advantage by conferring adaptations to local environmental conditions. Our lab has explored the effects of population-level processes, including inbreeding, on plant-insect interactions involving the perennial weed, horsenettle (*Solanum carolinense*). Previous work has documented significant inbreeding depression for herbivore resistance in horsenettle and shows that inbreeding can compromise defense gene expression and the induction of physical and chemical defenses. In this study, *Manduca sexta* caterpillars were used to inflict weekly damage on inbred and outbred horsenettle plants from three maternal families. These plants were also cross pollinated to produce outbred seeds. The resulting progeny were used to test the hypothesis that both inbreeding and herbivory has transgenerational effects on fitness and defense-related traits in the next generation. Our results show that maternal breeding type and herbivory in the previous generation can have significant effects on fitness-related traits, including rhizome resprout, seedling emergence, and flower production. Additionally, we found evidence for transgenerational induction of leaf trichomes, which can subsequently affect herbivore performance, including leaf consumption rates in no choice tests and weight gain. Overall, our results suggest that herbivory in the previous generation can confer transgenerational responses that affect offspring quality and offspring resistance to herbivores, which could benefit progeny in environments with high levels of herbivore pressure.

Keywords: herbivory, inbreeding, induced defences, trangenerational inheritance, Solanaceae, *Manduca sexta*

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Poster 90

Evolutionary Changes in Floral Traits Mediated by Pollinators and Herbivores in Experimental Evolution

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Pollinators can impose strong selection on floral traits because they mediate reproductive success, however in nature plants interact with a broad biotic community, herbivory by insects being one of the most important interactions that plants are involved into. Therefore, plants are subject to selection exerted by both herbivores and pollinators simultaneously; however, our understanding of how plants, particularly floral traits evolve under herbivory pressure and how the reproductive system is affected is still scarce. The aim of the present study is to investigate the real-time evolutionary changes in flowers of *Brassica rapa* (fast cycling) after six generations of selection by only pollinators (BB, *Bombus terrestris*) and pollinators plus herbivores (BH, Bombus and *Pieris brassicae*). Hand pollinated control plants (CO) were used to test for the effects of genetic drift. Plants of an 8th generation were grown to measure the evolutionary changes. We found that 5 out of 13 flower volatiles showed a significant increase in the BB treatment compared to BH and/or CO. Floral morphometry did not change significantly among treatments, however the patterns showing that flowers from the BB treatment are bigger suggest that these traits can potentially split among treatments with more generations of selection. Changes in the reproductive system suggest that self-compatibility increased in frequency in plants under herbivory and pollinators (BH), as the percentage of plants producing seeds from selfing and outcrossing in this treatment are fairly similar (95 and 92% respectively), while in the BB treatment and CO only 57% and 59% (respectively) of the plants produced seeds from selfing. Seeds produced from spontaneous autogamy were also more frequent in BH (24%), than in BB (10%) and CO (0%). In conclusion, an experimental evolution approach applied to floral evolution questions can allow us to increase our understanding of how plants adapt to different evolutionary scenarios.

Keywords: Experimental evolution, flowers, pollination, herbivory, interactions

Speaker

Poster 91

Phyllotreta armoraciae flea beetles combine two strategies to sequester intact glucosinolates from crucifer plants: A rapid uptake and the inhibition of plant myrosinase activity

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Plants of the order Brassicales defend themselves against herbivores with the so-called “mustard-oil bomb”. In intact plant tissue, glucosinolates (GLS) are stored separately from the enzyme myrosinase, but upon tissue damage, both components come together which leads to the production of highly reactive isothiocyanates. Phyllotreta flea beetles (Coleoptera: Galerucinae) are specialists on crucifer plants and were previously shown to accumulate high amounts of GLS in their hemolymph. We want to understand how Phyllotreta flea beetles prevent GLS hydrolysis by the plant myrosinase to sequester intact GLS. One possible mechanism is that GLS sequestration is faster than hydrolysis by the plant myrosinase. To determine how fast *P. armoraciae* beetles sequester GLS, we allowed them to feed for one minute on wild-type *Arabidopsis thaliana* (Col-0) leaves, dissected them subsequently into gut and rest of body, and analyzed the plant derived GLS in these tissues via LC-MS/MS. We found similar amounts of GLS in the gut and the rest of body which shows a rapid but not complete uptake of dietary GLS within one minute. Together with the observation of GLS being excreted with the feces, these results indicate that *P. armoraciae* is able to control myrosinase activity during feeding and digestion. Thus, we tested whether *P. armoraciae* gut content influences plant myrosinase activity in enzyme assays by comparing myrosinase activity with and without *P. armoraciae* gut content extracts. Indeed, myrosinase activity was reduced by 53% in assays incubated with beetle extracts. Our next goal is to identify which compound(s) are responsible for this effect.

Keywords: Flea beetle, sequestration, Brassicales, glucosinolate, myrosinase, mustard oil bomb, acitvated plant defense, specialized herbivore, chewing insect

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Poster 92

Genetics of virulence in pea aphid on *Medicago truncatula* hosts differing in R gene complement

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Although pea aphid is a popular model for speciation and adaptation to different legume species, we know less about how genetic variation impacts on compatibility within a single host species carrying different complements of R genes. Here, we tested clones of pea aphid from different host race groups on *Medicago truncatula* genotypes carrying or lacking the previously mapped QTL, *RAP1*, that confers strong race-specific resistance to certain clones. These patterns of virulence/avirulence and resistance/susceptibility broadly conform to the classic gene-for-gene model. Using laboratory crosses of virulent and avirulent parents to generate several F1, F2 and backcross populations, we show segregation for virulence that is consistent with Mendelian inheritance of a relatively small number of genes with large apparent effects. A single heterozygous locus, dominant for virulence, appears to explain a substantial proportion of variation, with additional loci predicted to contribute to progeny phenotypes. Impact of host genetic background was also found in comparisons of the *M. truncatula* genotype Jemalong A17, in which *RAP1* was originally discovered, with near-isogenic lines (NILs) derived from a cross of Jemalong A17 with the susceptible (*rap1*) genotype DZA315.16. Although *RAP1* appears to contribute the majority of resistance, NILs carrying *RAP1* are significantly more susceptible compared with their Jemalong A17 progenitor. We highlight the potential of these aphid populations as resources to reveal the molecular basis of virulence and avirulence, thus providing better understanding of aphid-plant interactions.

Speaker

Poster 93

Identifying natural resistance factors conferring resistance to thrips in Capsicum

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The demand for more sustainable agriculture practices is becoming increasingly important, especially for control of insect pests. Capsicum is an important crop which strongly suffers from thrips infection. Thrips infestation causes damage of leaves and fruits and leads to the transmission of viruses. Only few insecticides are still effective against thrips, underlining the importance of finding natural resistance within Capsicum. By exploring defense mechanisms in Capsicum varieties we are striving to identify mechanisms conferring resistance to thrips.

First, we developed a high-throughput assay to screen leaf discs of 47 Capsicum accessions for resistance to Thrips tabaci and Frankliniella occidentalis. We screened each accession over the plant's ontogenetic development (vegetative, flowering and fruit ripening stages). Our results show that the level of resistance to thrips changes over the plants ontogenetic development. Selection of accessions for resistance breeding should thus not only rely on resistance measurements in vegetative plants. The combined resistance measures provided a subset of 11 accessions that were either consistently vulnerable or resistant to thrips.

Because thrips infection is a worldwide problem, the 11 accessions were subjected to field tests in Thailand and India, where *Thrips palmi* and *Scirtothrips dorsalis* are important pests. Preliminary results indicate that accessions resistant to *F. occidentalis* and *T. tabaci* are mostly also resistant to *T. palmi*. This provides evidence that Capsicum possesses general resistance factors to different thrips species.

In addition, we are applying LC-MS based metabolomics to investigate the chemical mechanisms of thrips resistance. The metabolomics profiles were found to be different between species and ontogenetic stages. More interestingly, profiles differed between vulnerable and resistant lines and we are currently identifying compounds of interest. Eventually, metabolites that consistently confer resistance or susceptibility may serve as leads to breed for thrips resistance, which will contribute to green defense against thrips in Capsicum.

Keywords: Capsicum, pepper, *Frankliniella occidentalis*, *Thrips tabaci*, *Thrips palmi*, *Scirtothrips dorsalis*, resistance breeding, insect resistance, vegetable crops, metabolomics

Speaker

Poster 94

Expansion, Diversity, and Function of Putative Effectors in Gall Midges (Mayetiola)

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Successful pathogens and parasitic arthropods require genes coding for effector proteins that compromise the hosts' ability to defend themselves, and also require the ability to change these proteins in response to a detrimental change in a host. Gall midges in Mayetiola are very successful in adaptation to changes in host plants. Genomic, transcriptomic, and proteomic analyses of genes expressed in the salivary glands of Hessian fly larvae revealed a large number of genes coding for effector proteins. Multiple members of effector gene families are clustered within short chromosomal regions. Diversifying selection on the clustered members has resulted in proteins with diverse functions. A synchronized mechanism appears to regulate the effector genes exclusively expressed in the salivary glands of the first instar larvae, a critical stage that determines whether or not the insects can make galls successfully. The unusual structure, unique expression profile, and highly polymorphic nature of these effector genes suggest that they are likely the tools for gall making. In addition, the super-diversity specific to the protein coding regions among family members and the unique arrangement of these members within the genome indicated a programmed mechanism to generate super-diversification in effector genes to overcome changes in host plants. Current effort focuses on using crispr cas9 system and RNAi to determine the essentiality and biological functions of specific effector genes.

Keywords: Gall midge, Hessian fly, Mayetiola, Effectors, Plant manipulation

Poster 95

Muting, distorting and deafening: How ozone pollution affects plant communication

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Plants provide information to other members of their community by releasing complex blends of volatile chemicals. The composition of the chemical blend reflects the physiological status of the plant and the information content can stimulate responses in a range of organisms. A classic example is the plant "cry for help", whereby herbivore-feeding induces the emission of a volatile blend that is attractive to predatory natural enemies of the herbivores. However, predators are not the only possible recipients of this informative volatile blend; neighbouring plants are also potential recipients and have been shown to respond to herbivore-induced plant volatiles by altering their defences.

Although volatile cues and signals have the potential to structure a myriad of interactions between and within trophic levels, they are vulnerable to disturbance. Noise is a critical obstacle to effective communication; in the case of volatile-mediated communication processes, noise can be created by atmospheric pollution. Not only do pollutants mix with volatiles altering the chemical blend, but they react with the chemicals destroying the original compounds and creating new products. The original blend of chemicals is distorted, potentially beyond recognition. Effective volatile-mediated interactions require an organism to release volatile chemicals, for those chemicals to move in the air to a receiving organism, and for that organism to decipher information from those chemicals. In the case of plant-plant interactions, pollutants such as ozone have the potential to undermine each of these junctures. Phytotoxic ozone may alter the emissions of emitter plants, degrade volatile chemicals in the air, and induce stomatal closure in receiver plants.

In this talk, our recent work on the effects of ozone pollution on plant-plant interactions in brassicaceous plants will be presented. Particular focus will be given to progress in understanding the functioning of plant-plant interactions, and the significance of ozone pollution on those interactions.

Keywords: Volatile mediated interactions, ozone, pollution, volatile adsorption, herbivores, Brassicaceae
***Speaker**

Poster 96

Climate change: impact on plant-aphid-ant interactions

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While the impact of climate change on plant or insect communities has been receiving increasing attention during the last decade, plant-insect interactions under a changing environment remain under studied. These interactions are of particular importance as regard to the economically dimension of some crop plants and to the pest status of some insect species. In this project, we raise the hypothesis that the predicted changes in climate for the end of the 21th century will impact multitrophic relationships between herbivorous pests, their host plants and mutualist partners. Some modifications in atmospheric temperature or greenhouse gases concentration could alter the semiochemical interactions and behaviours in such multitrophic systems. Studying relations between plants, aphids and ants is an emblematic case of multitrophic relations involving insect pest and mutualism. In this case, we will evaluate the impact of elevated atmospheric carbon dioxide concentration and elevated temperature, alone or in combination, on the secondary metabolites previously identified as important mediators of a multitrophic interaction model including a plant (*Vicia faba*), an aphid pest (*Aphis fabae*) and an aphid-tending ant (*Lasius niger*). Special attention will be given to the plant semiochemicals, aphid and ants biologies and pheromones. In a first experiment, winged aphids have been tested in a dual choice assay between two plants grown under ambient or elevated CO_2 concentrations. The results showed that aphids prefer plants which are grown under elevated CO_2 concentration.

Key words: climate change, aphids, ants, plants, multitrophic, crop pest

Poster 97

Elevated CO2 concentration reduces alarm signaling in aphids

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Insects often rely on olfaction to communicate with conspecifics. While the chemical language of insects has been deciphered in recent decades, few studies have assessed how changes in atmospheric greenhouse gas concentrations might impact pheromonal communication in insects. Here, we hypothesize that changes in the concentration of atmospheric carbon dioxide affect the whole dynamics of alarm signaling in aphids, through modification in host plant quality. We investigated: (1) the production of the active compound (E)-β-farnesene (Eβf), (2) emission behavior when under attack, (3) perception by the olfactory apparatus, and (4) the escape response. We reared two strains of the pea aphid, *Acyrthosiphon pisum*, under ambient and elevated CO2 concentrations over several generations. We found that an increase in CO2 concentration reduced the production (i.e., individual content) and emission (released under predation events) of Eβf. While no difference in Eβf neuronal perception was observed, we found that an increase in CO2 strongly reduced the escape behavior expressed by an aphid colony following exposure to natural doses of alarm pheromone.

Keywords: Carbon dioxide, Acyrthosiphon pisum, (E)-β-farnesene, Signal dynamic
****Speaker***

Poster 98

Plant-aphid-hover fly interaction under elevated CO2 concentration: oviposition behavior and larval development

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Performance of natural enemies of insect pests is mainly driven by their ability to find food sources or oviposition sites. These suitable resources are often detected through the perception of volatiles cues. Nevertheless, rising atmospheric carbon dioxide (CO2) concentration may affect the semiochemistry of plant-insect relationship and thus affect the associated behaviors of predators. Here we test the hypothesis that an increase in atmospheric CO2 concentration will modify the laying behavior of aphidophagous hover fly females *Episyrphus balteatus* De Geer, as well as their larval development. Plants infested with aphids were grown either under ambient or elevated CO2 conditions. Infested plants grown under aCO2 and eCO2 conditions were presented simultaneously to hover flies. The clutch size on each plant was then analyzed. Even if females have laid eggs on both plants for almost replicates, the results revealed a significant great number of eggs laid on aCO2 plants. In addition, *E. balteatus* larvae fed with aphids from either aCO2 or eCO2 conditions ad libitum were daily measured (length and weight) until pupation. Any significant difference was observed between these two groups of larvae, indicating that CO2 concentration do not affect the diet quality of aphid predators. We can conclude that odors emitted by plant/aphid complexes may be altered by atmospheric changes and influence the behavior of syrphid females, but the adaptation of the clutch size is not associated with the diet quality.

Keywords: Carbon dioxide, *Episyrphus balteatus*, Semiochemicals, *Acyrthosiphon pisum*
****Speaker***

Poster 99

Testing the Preference-Performance hypothesis on natural populations of *Arabidopsis halleri* distributed along an elevation gradient

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The Preference-Performance Hypothesis (PPH) states that gravid female insects will prefer to lay eggs on plants on which their offspring fitness will be greatest. Females can distinguish between different plant species, as well as among genotypes within a species, that vary in their quality as larval food resources. However, it is less clear how plant adaptation along environmental gradients, such as elevation gradients, might directly or indirectly impact on the preference of gravid females for different populations. Adaptive variation in defensive traits in response to changing herbivore pressure along elevation gradients has been observed, with associated changes in larval performance on these populations. In addition, adaptation to abiotic factors that change with elevation can indirectly affect larval performance. However, in most cases variation in herbivore performance on populations from different elevations has not been linked to adult preference. In this study, we assess whether a specialist, *Pieris brassicae*, differs in oviposition preferences for genotypes from different elevations and test whether *P. brassicae* prefers plants on which their offspring perform best. Our results suggest reduced preference of *P. brassicae* for laying eggs on genotypes from two of the highest elevation populations. A second experiment focusing on just these two high and two low populations confirmed this pattern, and also showed significantly reduced larval growth rates on one of the highest elevation populations, consistent with the PPH. We will compare these results to variation in chemical defence induction and leaf structural traits (e.g. specific leaf area) among populations to understand the factors driving variation in larval performance on these four populations from different elevations. Together, these results help understand how environmental gradients can shape variation in key plant traits and how this can affect higher order interactions with herbivorous insects.

Keywords: host preference, elevation gradients, adaptation, defense induction

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Poster 100

Light intensity-mediated induction of trichome-associated defenses increases resistance against thrips in tomato

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Photosynthetically active radiation (PAR) levels play an important role in plant-insect interactions by modulating plant defenses. In particular, tomato type-VI leaf glandular trichomes, which are important physical and chemical defensive structures against arthropod herbivores, are induced under increasing PAR conditions. The biological significance of PAR-mediated induction of trichomes for tomato defenses, however, has been poorly characterized. Here we used the tomato mutant odourless-2 (od-2), deficient in type-VI trichomes density and chemistry, to test the influence of different PAR conditions on trichome-mediated defenses and resistance against the Western ower thrips *Frankliniella occidentalis*. Our results showed that, compared to low PAR, high PAR increased resistance against thrips in wild-type plants, but not in od-2. Furthermore, preference assays demonstrated that thrips preferred high PAR-treated od-2 plants over high PAR -treated wild-type plants. PAR conditions had a great impact on plant physiology, independent of the plant genotype; plants grown under high PAR had a reduced stem length, increased leaf number, and increased leaf thickness. In addition, a non-targeted NMR metabolic analysis revealed that leaves from both genotypes experienced similar metabolic changes when exposed to high PAR conditions. However, whereas type-VI trichome density was higher under high PAR in both tomato genotypes, only wild-type plants produced more trichome-associated allelochemicals, i.e. terpenes and phenolics. Overall, our results suggest that high PAR -mediated induction of trichome-associated chemical defenses have a greater impact on tomato resistance against thrips than the reinforcement of leaf thickness or changes in non-trichome related primary and secondary plant metabolites. This highlights the importance of light conditions to increase crop protection against pests in agriculture systems.

Keywords: *Frankliniella occidentalis*, light intensity, photosynthetically active radiation, thrips, tomato, trichomes, volatiles, terpenes.

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Poster 101

Effect of temperature on development of *Chaetoptelius vestitus* (Muls & Rey) (Coleoptera: Curculionidae) on *Pistacia vera* L.

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The pistachio bark beetle, *Chaetoptelius vestitus* Muls & Rey (1860) is a major pest of pistachio trees. In the world, there is a little work relating to the biology and ecology of the species. Thus, in this study, the effect of temperature on developmental process, survival and reproduction of the insect was studied at three constant temperatures 25, 30 and 35.0 C and at 16:8 (L:D) hour photoperiod in the laboratory. The developmental periods for egg, larval, and pupal stages decreased in correlation with increased temperature. In this study, we determined rates of immature stages (larval and pupal) for *C. vestitus* in each temperature, developed linear regression models to describe the effect of temperature on developmental rate. There were signifcant differences in the rate of development among the temperature for larval developmental (from oviposition to peak emergence of larvae) and pupal developmental (from larval to peak emergence of adults). The larval instars, consisting of 5 instars, took significantly less time in each increasing temperature. *C. vestitus* development from egg to adult took significantly less time at each increasing temperature. Results concerning the development of immature stages showed that mean duration of total larval development and pupa were 55.37 +/- 7.010, and 14.79 +/- 4.857 days at 25 C, 36.69 +/- 3.203, and 9.32 +/- 1.106 days at 30 C, and 26.74 +/- 2.984, and 4.60 +/- 0.876 days at 35 C, respectively. These facts indicated that *C. vestitus* accomplished its total immature stage development in 128.93 +/- 18.797 days at 25 C, 84.651 +/- 9.097 days at 30 C, and 52.60 +/- 9.524 days at 35 C. The basis for these development data will be a useful key factor to assess control strategies.

Keywords: *Chaetoptelius vestitus*, Pistacia, development time variation, developmental rate, temperature, population, mortality, fecundity

Speaker

Poster 102

Impact of climate change on below ground tritrophic interactions in maize

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Climate change has tremendous effects on plant-herbivore interactions, but little is known about its impact on predation by the third trophic level. We investigated the effects of soil moisture on interaction between maize plants, the western corn rootworm (WCR, Diabrotica virgifera) and soil-borne natural enemies of WCR. A pot experiment in the field revealed that increasing soil moisture levels positively influenced plant growth (biomass, height, ASI) and cob mass. WCR infestation strongly reduced plant height. Cob weight was decreased by WCR under low moisture levels, but increased under high moisture. Inoculation with entomopathogenic nematodes (EPNs) did not influence the interaction, as the EPNs died rapidly in the warm and dry soil. Ants of the species *Solenopsis molesta* on the other hand invaded the experiment, were more abundant in WCR infested pots and predated WCR independently of soil moisture levels. Root biomass was increased in the presence of ants. Furthermore, the ants attenuated the moisture-dependent effects of WCR on cob weight. Our study identifies *S. molesta* as a new natural enemy of WCR and suggests that *S. molesta* reduces the climate-dependent impact of WCR on plant performance. Enhancing the abundance and efficacy of adapted natural enemies may therefore protect crops from the negative impact of herbivores under climate change.

Keywords: climate change, tritrophic interaction, *Diabrotica virgifera*, natural enemies

Speaker [z]Corresponding authors

Poster 103

Impacts of drought stress on caterpillars and defensive responses of tomato

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The ability for plants to respond accurately upon specific stressor or stresses combination is important to the survival of plants. Water stress and herbivory often co-occur as two of the most important stressors affecting survival and distribution of plants. The ability for plant to respond to single stressor, either herbivory or water stress, are well studied. However, how water stress affects the ability for plant to respond against insects are less addressed. Using Tomato, *Solanum lycopersicum* L. cv. Better Boy, and two pest species, tomato fruitworm, *Helicoverpa zea*, and tobacco hornworm, *Manduca sexta*, we study the impact of drought stress on (1) plant primary metabolites, (2) herbivore performance, and (3) plant defensive response against insects. Drought stress were divided into three levels: severe, moderate and well-watered. Insect damages were introduced after the establishment of drought stress. Primary metabolites, and activity of two defensive proteins, polyphenol oxidase and protease inhibitors, were analysed to determine the nutritional status and defensive responses of treated plants. Drought stress lead to slight changes in primary metabolite compositions in tomato leaf tissue. Moderate drought stress has a positive impact on generalist pest species *H. zea* on tomato leaf, whereas, specialist pest *M. sexta* are negatively affected by drought stress. Severe drought stress increases the constitutive defensive response of tomato leaf, but decreases the inducibility of defensive response. Well-watered tomato have a lower constitutive defensive response, and a higher inducibility of such defense. We observed altered defense allocation patterns in plant challenged by insect under different drought severity. In conclusion, herbivore of different host specificity were indirectly affected by drought stress differently. The results suggested that drought stress differentially alters the dynamics of plant-insect interaction among insect herbivores, potentially having a broader impact on community and ecosystem dynamics.

Keywords: drought, biotic stress, abiotic stress, tomato, water stress, generalist, specialist

Speaker

Poster 104

Root-derived attractants for larvae of the cabbage root fly *Delia radicum* to be used in novel control strategies

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Cabbage root fly *Delia radicum* L. (Diptera: Anthomyiidae) is an important pest of brassica crops. We are currently screening for possible root-derived attractants that can be used in a lure and kill formulations to fight the pest. In laboratory assays it was confirmed that cabbage root fly larvae are strongly attracted to dimethyl disulphide (DMDS), which is emitted by root fly-infested roots of Brassica plants. Current efforts are focused on identifying additional root-derived attractants and feeding stimulants. These compounds will then be incorporated in alginate-based beads bearing entomopathogenic nematodes, with the aim to attract the larvae and have them feed on beads with the lethal nematodes. Our progress on this novel pest control strategy will be discussed.

Keywords: *Delia radicum*, root herbivores, attractants, entomopathogenic nematodes, lure and kill strategy

***Speaker**

Poster 105

Unravelling the role of *Bemisia tabaci* - plant associations in the species diversification

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Bemisia tabaci is considered a generalist species complex containing at least 35 species. The understanding of the mechanisms driving this unusual diversification is limited, but largely focus on allopatric forces (separation by migration of the continents), and assume that most species share a similar broad host range. Recent meta-analysis of field sampling data suggests, however, that sympatric species within each continent, are more host-specific than commonly thought, with only few species showing true generalism. Therefore, it is quite likely that during evolution, various species acquired many genetic changes that relate to their ability to utilize plant hosts. These plant-related differences might have contributed to the speciation process that led to the establishment of multiple species at the same geographic range. In this study, we compared the expression pattern of a set of 298 P450s, GSTs, COEs, UGTs, sulfotransferases and ABC transporters detoxification genes, present in the *B. tabaci* transcriptome, using six symatric and allopatric species and four plant hosts: eggplant (common non-toxic host) and pepper, cassava and kale (known to produce toxic plant chemicals). We also monitored the performance of the six species on the four plant hosts. These performance assays indicated that the six species can be divided into two groups, one with extended (generalists) and one with restriced host range. In parallel, we found the same grouping pattern when the species were clustered according to the expression pattern of their detoxification genes, despite the fact that the three generalist species (which clustered together) represent three different genetic (continental) gropus. The observed putative correlation between the expression pattern of the detoxification system and the insect's feeding habit, supports the possibility that plant hosts played an important role in the evolution of the species complex. The possible links between our findings and the oscillation hypothesis of speciation will be discussed.

Keywords: Polyphagy, Species complex, Host, plant association, Microevolutionary changes, Genomic signatures, Positive selection, *Bemisia tabaci*

***Speaker**

Poster 106

Distinct shaping of gene expression profiles in an oligophagous beetle by long-term versus short-term experiences with different host plants

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Herbivorous insects need to adjust their enzymatic machinery to their specific host plant diet. Such short-term physiological adaptations are likely also influenced by long-term experiences with certain host plant species. Applying an experimental evolutionary approach, we investigated effects of long-term experience versus reciprocal short-term responses to different host plants in the oligophagous mustard leaf beetle *Phaedon cochleariae* (Coleoptera: Chrysomelidae). After 26 generations of exclusive experience with one of three host plant species, *Brassica rapa*, *Nasturtium officinale* or *Sinapis alba*, freshly hatched larvae were maintained on these plants or moved to one of the other host plants for ten days. Subsequently, global transcriptional signatures were investigated in these larvae. Microarray experiments revealed that, dependent on the original and recent host plant experience, between 1 and 16 % of all 25,227 putative genes were differentially expressed compared to the control line constantly kept on *B. rapa*. For lines that were maintained on their host species for long-term, differences in gene expression levels were moderate. In contrast, short-term switches from *B. rapa* to another host caused only minor changes in the transcriptome, whereas shifts to *B. rapa* led to substantial changes. Mainly genes related to metabolism, digestion and general cellular processes were differentially regulated. In conclusion, transcriptional plasticity in these genes plays a key role in long- and short-term responses of herbivores to adjust to changing host plant conditions.

Keywords: detoxification, host plant shift, molecular evolution

Speaker

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