



Wild Plant Pathosystems

29-31 August 2016, Helsinki

Contents

Schedule	3
Information	6
Map of downtown.....	8
Map of University main building	8
Talk Abstracts	9
Monday 29.8. 9:00- 10:15	9
Monday 29.8. 10:45- 12:15	11
Monday 29.8. 13:30- 14:30	15
Monday 29.8. 16:15- 17:15	18
Tuesday 30.8. 9:30- 10:30	20
Tuesday 30.8. 11:00- 12:00	23
Tuesday 30.8. 13:00- 14:15	25
Wednesday 31.8. 9:00- 10:00.....	31
Wednesday 31.8. 10:30- 12:15.....	34
Wednesday 31.8. 13:15- 14:30.....	39
Wednesday 31.8. 16:15- 17:15.....	42
Poster Abstracts	44
Pitching on Monday 29.8. 14:30- 16:45	44
Pitching on Wednesday 31.8. 14:30- 14.45.....	55
Participants	69



Schedule

Sunday 28.8. Pre-conference cocktail party & registration at Natural History Museum

Address Pohjoinen Rautatiekatu 13

18.30 – 21.00

Monday 29.8. Talks and poster session in the University Main Building

Address Unioninkatu 34, 3rd floor, auditorium XIV

Session I chair: Ales Lebeda

9.00 – 9.15 Welcoming words

9.15. – 9.45 Eric Holub: Arabidopsis species provide insights for anticipatory breeding of durable white rust resistance in Brassica crops

9.45. – 10.15 Bruce McDonald: The origin and spread of wheat blast

10.15 – 10.45 *Coffee*

10.45 – 11.15 Laura Rose: The interplay of pathogens, microRNAs, and regulation of resistance gene transcript abundance in tomatoes

11.15 – 11.45 Eva Stukenbrock: Comparative population genomics of closely related plant pathogens from natural grasslands and agro-ecosystems

11.45 – 12.00 Agathe Jouet: The adaptive evolution of the plant pathogen *Albugo candida*

12.00 – 12.15 Detlef Weigel: Autoimmunity and evolution of the plant immune system

12.15 – 13.30 *Lunch*

Session II chair: Laura Rose

13.30 – 14.00 Michael Shaw: The endophytic-pathogenesis continuum in *Botrytis* species in wild hosts

14.00 – 14.15 Hanna Märkle: Bayesian inference of host-parasite coevolution: Revealing loci running with the Red Queen

14.15 – 14.30 Remco Stam: Using pooled enrichment sequencing to understand R-gene durability and diversity in wild tomato

14.30 – 14.45 Poster pitching

14.45 – 16.15 *Coffee* and poster session in a hall of other side of the building

16.15 – 16.45 Michael Hood: Resistance transitivity across endemic and host-shift pathogens.



16.45 – 17.15 Jeremy J Burdon: Long-term epidemic dynamics and its evolutionary implications.

17.45 *Boat to Suomenlinna departs from Market Square*

18.30 *Free walk in Suomenlinna*

19.30 *Conference dinner*

22.30 *Boat back*

Tuesday 30.8. Talks in Haltia, the Finnish Nature Centre and walk in Nuuksio national park

8.30 *Bus leaves from Mikonkatu-street, on the side of Railway Station Square*

9.15 *Bus arrives to Haltia*

Session III chair: Erin Mordecai

9.30 – 10.00 John Walsh: The genetic diversity and host range of Turnip yellows virus (TuYV), a common virus infecting cultivated brassicas and wild plants in Europe

10.00 – 10.30 Janis Antonovics: Vector-based disease transmission in a spatially explicit context; field studies and theory

10.30 – 11.00 *Coffee*

11.00 – 11.30 Pascal Frey: When a plant pathogen runs down a river: population genetics of the poplar rust epidemics in the Durance River valley

11.30 – 12.00 Samuel Soubeyrand: Exploring data from wild plant pathosystems with recent modeling and inference techniques

12.00 – 13.00 *Lunch*

Session IV chair: Eric Holub

13.00 – 13.15 Fletcher Halliday: Seasonal variation, within-host priority effects, and fungal interactions jointly influence parasite epidemics in a grass host

13.15 – 13.30 Mark McMullan: Plant pathogen evolution across the wild-agricultural boundary

13.30 – 13.45 Laura Masini: Unravelling the defence arsenal of the wild *Solanum dulcamara* to *Pythophthora infestans*

13.45 – 14.00 Philippe Roumagnac: Deciphering plant-associated viruses at the agroecosystem scale using metagenomics

14.00 – 14.15 Nilsa Bosque-Perez: The prevalence of Barley yellow dwarf viruses in grassland habitats is influenced by diverse agroecological and environmental factors

14.30 *Walk in Nuuksio*

17.00 *Bus back to Helsinki*



Wednesday 31.8. Talks and poster session in the University Main Building

Address Unioninkatu 34, 4th floor, auditorium XV

Session V Jeremy J Burdon

9.00 – 9.15 Oliver Furzer: Exploring Brassicaceae NLR diversity with Resistance gene enrichment sequencing

9.15. – 9.30 Antoine Persoons: Field pathogenomics: Developing new tools for interrogating cereal invaders

9.30 – 10.00 Ales Lebeda: Interactions between wild Lactuca species and *Golovinomyces cichoracearum* – complex view

10.00 – 10.30 *Coffee*

10.30 – 11.00 Marie-Laure Desprez-Loustau: Oak powdery mildew in Europe one century after the invasion: some hypotheses about ecological, evolutionary and anthropogenic changes in the pathosystem

11.15 – 11.45 Gregory Gilbert: Phylogenetic prediction of the disease landscape in wild plant pathogen networks

11.45 – 12.00 Levente Kiss: A hidden friend of allergic people? Deciphering the biology of *Phyllachora ambrosiae*, an enigmatic, obligate biotrophic fungal pathogen of common ragweed (*Ambrosia artemisiifolia*)

12.00 – 12.15 Jenalle Eck: Soil microbial community impacts on tropical tree seedling growth promote seedling diversity within a tropical tree population

12.15 – 13.30 *Lunch*

Session VI chair: Eva Stukenbrock

13.30 – 13.45 Emme Bruns: Disease at species range margins: Co-distribution of alpine plant species and their vector-transmitted pathogens.

13.45 – 14.00 Kari Saikkonen: Endophytic fungi latent pathogens or defensive plant mutualists?

14.00 – 14.30 Erin Mordecai: Generalist pathogens impact survival and reproduction in California grasslands

14.30 – 14.45 Poster pitching

14.45 – 16.15 *Coffee* and poster session in a hall of other side of the building

16.15 – 16.45 Alison Power: From Plant Communities to Coinfections: Plant Virus Ecology at Multiple Scales

16.45 – 17.15 Anna-Liisa Laine: Variation in within-host pathogen communities: causes and consequences

17.15 Next WPP



Information

General Information

Currency: Euro

Time zone: UTC/GMT +3 hours

Emergency number: including general emergencies, ambulance, fire and police is 112

Useful websites

Tourist site: <http://www.visithelsinki.fi/en>

Practical information: <http://www.visithelsinki.fi/en/come/welcome-to-helsinki/useful-information>

Pharmacies:

- Mon-Sun 7am-12midnight in the city centre, Yliopiston Apteekki, Mannerheimintie 5
- 24-hour service: Yliopiston Apteekki, Mannerheimintie 96, telephone +358 (0)300 20200 (nationwide customer service number)

Taksi-Helsinki, telephone +358 (0)100 0700 (1,17€/phone call +0,25€/10s + local call charge)

How to get from Airport to Helsinki city centre

- Platforms for buses and coaches serving the Helsinki city centre and metropolitan area are located in front of both terminals. Bus 615 goes to Central Railway Station in 40 minutes.
 - Bus tickets can be bought from driver, price is 5,50€
- The train station is located on the arrivals floor, between terminals 1 and 2. Both trains I and P go to city centre, but by different routes. It takes about 30 minutes to Central Railway Station.
 - At the Airport train station there are ticket machines that sell tickets for Helsinki region. Both VR (railway) and HSL (public transport) machines are valid.
 - You can also buy a ticket from conductor on the train in the ticket sales compartment.
 - Price is 5,50€
- Taxis are available in front of the doors of both terminals.

Public transport in Helsinki

- Note that the airport is located in Vantaa and thus you need a regional ticket to travel from there and back. Regional single ticket is 5,50€ and day ticket 12€
- Single ticket inside Helsinki is 3,20€ from driver and 2,70€ from machine.
- Day ticket inside Helsinki is valid for unlimited travel for 24 hours within Helsinki and costs 8€. Two day costs 12 €, three days 16€ and so on. One day tickets can be bought from machines, R-kioski (all around in Helsinki, also airport) and on bus/train/tram. Several day tickets can be bought from machines and R-kioski.
- You can also buy a travel card for 5€ from R-Kioski. You can load money onto the card and it gives cheaper transport costs for single tickets.
- Journey planner is very useful: <http://www.reittiopas.fi/en/>



For further information, e.g. you can't find a meeting place, you can call Krista Raveala: +358503185238

Helsinki

Helsinki, the capital of Finland, is a modern city with over half a million residents and is situated on the Baltic Sea. It was founded in 1550 and became capital in 1812. Helsinki, alongside its neighboring municipalities of Espoo, Vantaa and Kauniainen, form a metropolitan area of more than a million inhabitants.

University of Helsinki

The University of Helsinki (Finnish: Helsingin Yliopisto, Swedish: Helsingfors Universitet, Latin: Universitas Helsingiensis, abbreviated UH) is a university located in Helsinki, Finland since 1829, but was founded in the city of Turku (in Swedish Åbo) in 1640 as the Royal Academy of Turku, at that time part of the Swedish Empire. It is the oldest and largest university in Finland with the widest range of disciplines available. Around 36,500 students are currently enrolled in degree programs at the university, spread across 11 faculties and 11 research institutes.

Nuoksio National Park

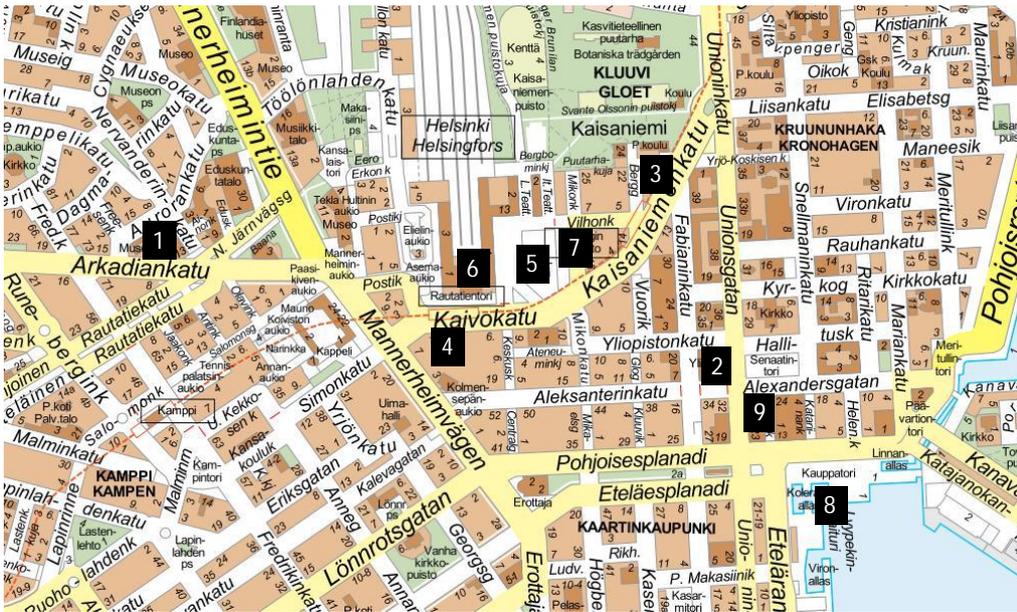
Nuoksio National Park (Finnish: Nuuksion kansallispuisto, Swedish: Noux nationalpark) is a national parks in Finland. Established in 1994, the park spreads over an area of forests and lakes in Espoo, Kirkkonummi and Vihti. The national park comprises the westernmost part of the so-called Nuoksio lake highlands. Dozens of endangered or near threatened species of animals, plants and fungi are known to live in the area; for instance the Siberian flying squirrel, the European nightjar and the woodlark.

Suomenlinna

Suomenlinna (Finnish) or Sveaborg (Swedish), until 1918 Viapori (Finnish), is an inhabited sea fortress built on six islands in front of Helsinki. Suomenlinna is a UNESCO World Heritage site and popular with tourists and locals, who enjoy it as a picturesque picnic site. In addition to the island fortress itself, sea facing fortifications on the mainland would ensure that an enemy would not acquire a beach-head from which to stage attacks. The plan was also to stock munitions for the whole Finnish contingent of the Swedish Army and Royal Swedish Navy there. In the Finnish War the fortress surrendered to Russia on May 3, 1808, paving the way for the occupation of Finland by Russian forces in 1809.



Map of downtown



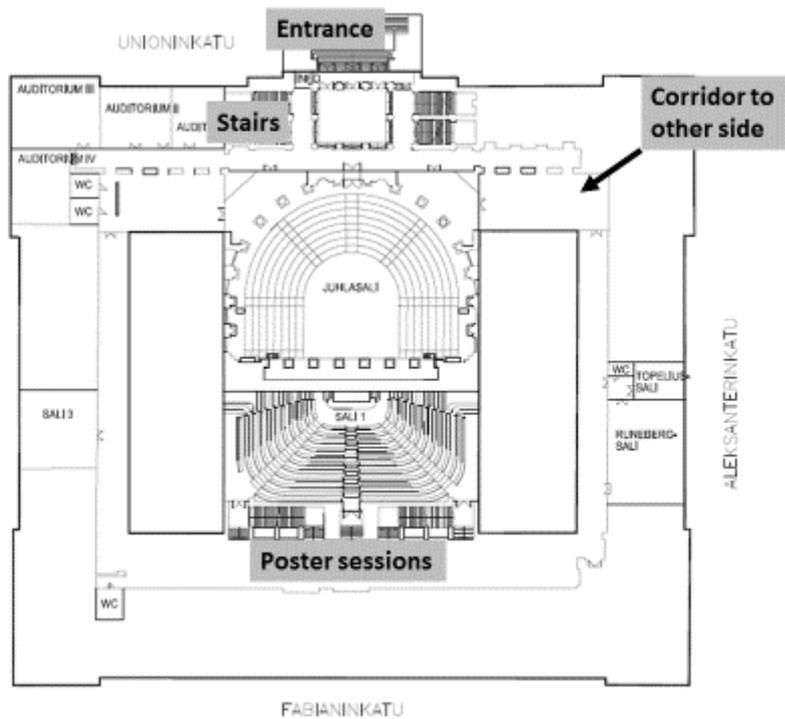
1. Natural History Museum (Pohjoinen Rautatiekatu 13)
2. University Main Building (Unioninkatu 34)
3. Hotel Arthur (Vuorikatu 19)
4. Hotel Seurahuone (Kaivokatu 12)
5. Railway Station Square
6. Central Railway Station
7. Bus to Nuukio
8. Boat to Suomenlinna
9. Restaurant Sunn (Aleksanterinkatu 26)

Map of University main building

Entrance floor from Unioninkatu side and 2nd floor from Fabianinkatu side

Auditorium XIV is on 3rd floor and XIV on 4th floor

Helsingin yliopisto
PÄÄRAKENNUS
Fabianinkatu 33
2.KERROS





Talk Abstracts

Monday 29.8. 9:00- 10:15

Eric Holub

University of Warwick

Co-authors

Fairhead, Sebastian; University of Warwick

Vicente, Joana; University of Warwick

Cevik, Volkan; The Sainsbury Lab, Norwich

Title

Arabidopsis species provide insights for anticipatory breeding of durable white rust resistance in Brassica crops.

Abstract

Major effect genes that encode receptor-like proteins can potentially provide long-lasting resistance to a particular pathogen, if they can detect specific molecules that are vital to pathogen fitness. The white rust resistance gene WRR4 in *Arabidopsis thaliana* provides an example for investigation in the Brassicaceae. An allele of this TIR-NBS-LRR gene from accession Columbia confers resistance to four specialised races of *Albugo candida* from different Brassicaceae hosts. To explain this broad spectrum resistance, an avirulence protein was predicted which is encoded by a conserved allele in all four *Al. candida* races. However, since every pathogen is capable of evolving new virulence, our objective was to determine whether pathogen variants occur in wild hosts that can overcome WRR4-mediated resistance. Early identification of virulent pathogens that can overcome individual R-genes is essential to anticipate which alleles of multiple host genes could be assembled for the most effective R-gene combination. We began by collecting *Al. candida* from natural populations of *A. thaliana* that were growing in close proximity to *Capsella bursa-pastoris* (a prolific source of *Al. candida*). We also used perennial *Arabidopsis* as a pot-grown bait to 'trap' white rust throughout the year. Isolates were propagated in *Arabidopsis* accessions lacking WRR4-resistance, and then tested for virulence in Columbia. Floral tissue proved to be a useful source for *Al. candida*. Although rare, three Col-virulent isolates were identified including one from a natural population of *A. thaliana* and one each from bait plants of *A. lyrata* and *A. halleri*. Resistance to all three isolates has been mapped in a Norwegian accession (Oystese-0) to the WRR4 locus. Combining this allele with the WRR4-Col allele could provide a durable combination for white rust resistance in brassica crops. The Col-virulent isolates are avirulent in brassicas and are therefore not a direct threat to resistance that already occurs within crops. Genome-wide sequence analysis of the three Col-virulent isolates has been used to identify mutations that occur within two candidate avirulence genes (matching WRR4-Col) that encode highly conserved effector proteins amongst standard races of *Al. candida*.

Summary

Arabidopsis species provide insights for anticipatory breeding of durable white rust resistance in Brassica crops.



Bruce McDonald

ETH Zurich

Co-authors

Ceresini, Paulo; UNESP, Brazil

Maciel, Joao; EMBRAPA Wheat, Brazil

Castroadugin, Vanina; UNESP, Brazil

Carvalho, Giselle; UNESP, Brazil

de Assis Reges, Juliana; UNESP, Brazil

Croll, Daniel; ETH Zurich

Title

The origin and spread of wheat blast

Abstract

Wheat blast was first detected in 1985 in Paraná State, Brazil and spread across central and southern Brazil as well as Bolivia, Argentina and Paraguay. Hierarchical samples of the fungus were made from wheat fields and grass species growing in sympatry with wheat across its geographical range in Brazil to provide a collection of 553 isolates. These isolates were characterized for mating types, 11 SSR markers, sequences of 10 housekeeping genes, two genes associated with fungicide resistance, an avirulence gene. A subset of strains was phenotyped for virulence on a set of wheat differentials and resistance to Qol and azole fungicides. Genome sequences were obtained for 17 strains. Since its emergence ~30 years ago, the wheat blast pathogen evolved resistance to fungicides, adapted to cooler temperatures and became host specialized. Its population genetic structure indicates a mixed reproductive system with regular recombination and significant gene and genotype flow over spatial scales of 1000s of km. Sequence comparisons showed that the wheat blast and rice blast pathogens are closely related, but phylogenetically distinct. We named the wheat blast pathogen *Pyricularia graminis-tritici* to distinguish it from the rice blast pathogen *Pyricularia oryzae*. *Pyricularia* isolates from some poaceous hosts, including *Urochloa brizantha* (signal grass), were indistinguishable from *P. graminis-tritici* isolated from wheat. Because *Urochloa* is a pasture grass grown on more than 90 million ha in Brazil, we propose that *Urochloa* is a major source of wheat blast inoculum and may be the preferred host for pathogen recombination. We further postulate that *Urochloa* was the original host of *P. graminis-tritici* and that wheat blast emerged through a series of host jumps from *Urochloa* in Brazil. The recent outbreak of wheat blast in Bangladesh was caused by strains of *P. graminis-tritici* closely related to the Brazilian strains included in our analyses.

Summary

Wheat blast caused by *Pyricularia graminis-tritici* emerged in Brazil via a host jump from *Urochloa* and spread to Bangladesh on infected seed.



Monday 29.8. 10:45- 12:15

Laura Rose

Univ. of Duesseldorf

Co-authors

Kloesges, Thorsten; Univ. of Duesseldorf

de Vries, Sophie; Univ. of Duesseldorf

Title

The interplay of pathogens, microRNAs, and regulation of resistance gene transcript abundance in tomatoes

Abstract

Plant genomes typically contain hundreds of R-genes, most of which are under some form of negative regulation. The recent discovery of a group of miRNAs that specifically target R-genes has opened the door to discovering which set of R-genes are targeted by these miRNAs and how this form of regulation is modified during pathogen infection. We have investigated the evolutionary history of members of the miR482 gene family in the Solanaceae, with a special focus on the group of wild tomatoes and their close relatives within the genus *Solanum*. The genomes of the tomato species typically contain seven different, but evolutionarily related, miR482 genes. These genes are predicted to target approximately 20% of the tomato R-gene repertoire. To determine how the abundance of miRNA and their predicted R-gene targets is affected during pathogen infection, we used qPCR to quantify miRNA and R-gene transcript abundance on three different tomato species, *S. lycopersicum*, *S. pimpinellifolium* and *S. arcanum* at six different time points during infection by the oomycete pathogen, *Phytophthora infestans*. The use of multiple host and pathogen genotypes allowed us to evaluate the effect of genotype on miRNA and R-gene abundance. Pathogen isolates showed variation in their ability to spread and transition from biotrophy to necrotrophy on the different host species. As a consequence, the dynamic of miRNA transcript abundance also differed between hosts depending upon pathogen isolate. Experiments are currently underway to now investigate how differences in miRNA abundance correlate with the transcript abundance of the predicted R-gene targets and how modification of miRNA abundance during pathogen infection affects the outcome of this host-parasite interaction.

Summary

The genotype of the host and the pathogen together affect the negative transcriptional regulation of R-genes in tomato.



Eva Holtgrewe Stukenbrock

MPI for Evolutionary Biology

Co-authors

Grandaubert, Jonathan; MPI for Evolutionary Biology

Eschenbrenner, Christoph; MPI for Evolutionary Biology

Dutheil, Julien; MPI for Evolutionary Biology

Title

Comparative population genomics of closely related plant pathogens from natural grasslands and agro-ecosystems

Abstract

The emergence of new fungal pathogens in managed ecosystems is an urgent matter of consideration. A goal of our research is to infer diversification and speciation processes of plant pathogens in natural and managed ecosystems. We study a species complex of plant pathogenic fungi including the wheat pathogen *Zymoseptoria tritici* (synonym *Mycosphaerella graminicola*). Speciation of *Z. tritici* was associated with wheat domestication and dates back to 10-12000 ya. Several closely related species of *Z. tritici* exist in natural grasslands in Iran. We have taken a comparative population genomics approach to study the underlying evolutionary processes that drive adaptive evolution of *Zymoseptoria* in managed and natural ecosystems. We have performed population genomics analyses and document recent speciation times in the *Zymoseptoria* complex. Using within and between species rates of non-synonymous and synonymous variation we show a strong impact of natural selection in genome evolution of *Zymoseptoria* spp. This is at odds with small effective population sizes estimated and suggests that population sizes were historically large but unstable. Speciation of *Z. tritici* did not entail an apparent loss of variation in spite of the homogenous agro-ecosystem where it has evolved. In contrast *Zymoseptoria* species infecting wild grasses have smaller effective population sizes. Inferences of demography illustrate that effective population sizes of pathogens on wild grasses is strongly affected by recurrent population bottlenecks. The stable and uniform agricultural environment in which *Z. tritici* evolve on the other hand has supported the maintenance a large effective population size of this important crop pathogen.

Summary

Rapid evolution of the wheat pathogen *Zymoseptoria tritici* through maintenance of high effective population size.



Agathe Jouet

The Sainsbury Laboratory

Co-authors

Saunders, Diane; The Genome Analysis Centred

van Oosterhout, Cock; The University of East Anglia

Jones, Jonathan; The Sainsbury Laboratory

Title

The adaptive evolution of the plant pathogen *Albugo candida*

Abstract

Albugo candida is a plant pathogenic oomycete responsible for the white rust disease in the Brassicaceae, Cleomaceae, and Capparaceae families. Sometimes considered a generalist plant pathogen, it is nonetheless organized into multiple host-specific races which have long been identified through host-specificity assays. However, little is known about the genetic variation of these races in nature or about how the pathogen has adapted to its many hosts. Recently, the genomes of 5 isolates representing 3 races were sequenced which revealed that not only *A. candida* races are genetically diverged (~1%) but also that there is evidence for historical recombination between them, highlighting recombination as a potential driving force for broad host adaptation in *A. candida*. To investigate this further, sequence capture was used to sequence a 400 kb contig as well as 32 neutral genes from 85 *A. candida* isolates collected from 21 Brassicaceae host species. Phylogenetic analyses revealed at least 16 host-specific races that are ~0.7% diverged and, confirming previous results, many inter-race recombinant blocks were detected (some of which appearing to be very recent). In addition, nucleotide divergence within races was low (~0.00025%) suggesting high levels of clonal reproduction. Yet, almost all races appeared to also be able to reproduce sexually, either through outcrossing (races collected from the field) or selfing (races propagated in the lab). In contrast, some races appeared to be associated with a strict clonal reproductive system which may lead, in the long-term, to speciation. Interestingly, these races were found to be triploid and were collected from cultivated hosts. This study reveals that the *A. candida* complex which was left largely unexplored is quite heterogeneous. Moreover, in addition to hybridization, it has become apparent that polyploidization is an important driving force in *A. candida* evolution.

Summary

White rust *A. candida* of Brassicales adapted to its many hosts via a mixed mating system, hybridization and polyploidization



Detlef Weigel

Max Planck Institute for Developmental Biology, Tübingen, Germany

Title

Autoimmunity and evolution of the plant immune system

Abstract

My lab is broadly interested in questions of evolution. Starting from different angles, the diversity of NLR (NB-LRR) genes in natural populations has become a major focus of our work. For example, several years ago, we introduced *Arabidopsis thaliana* as a model for hybrid necrosis, a syndrome that is characterized by activation of the immune system due to inappropriate self-recognition in F1 hybrids. We have since shown that hybrid necrosis is often caused by mismatched NLR immune receptors. Additional cases involve RPW8, which confers broad-spectrum resistance against powdery mildew, and ACD6, known to underlie a growth/immunity trade off in *A. thaliana* accessions. Genetic and molecular studies of these factors are being pursued by Ana Cristina Barragan, Eunyoung Chae, Kavita Venkataramani and Wangsheng Zhu. In a separate strand of work, we converged on NLR genes through our population genomic studies in the genus *Capsella*, which has pointed to strong selection for retention of NLR diversity even during extreme genetic bottlenecks. These results have led us to ask what shapes immune system diversity in natural populations at both different spatial and temporal scales. Current efforts to answer this question include (i) describing species-wide NLR diversity in *A. thaliana* (Felix Bemm, Anna-Lena Van de Weyer), (ii) relating leaf microbiome diversity and bacterial infection dynamics to host genetic diversity in local *A. thaliana* populations around Tübingen (Dino Jolic, Derek Lundberg, Talia Karasov, Julian Regalado), (iii) understanding evolution of disease resistance in a near-clonal population of *A. thaliana* found across N. America (Moi Exposito-Alonso, Alba González Hernando, Gautam Shirsekar). I will very briefly introduce recent discoveries in these areas, some of which are pursued in collaboration with the groups of Joy Bergelson (Univ. of Chicago), Hernán Burbano (MPI), Jeff Dangl (UNC), Joe Ecker (Salk), and Jonathan Jones (TSL). External funding for our immunity work comes from the ERC (Advanced Grant IMMUNEMESIS) and the Gordon and Betty Moore Foundation.



Monday 29.8. 13:30- 14:30

Michael Shaw

University of Reading

Title

The endophytic-pathogenesis continuum in *Botrytis* species in wild hosts

Abstract

Botrytis cinerea is recorded as a pathogen on over 1400 hosts, most dicots. Most of the rest of the genus are specialised pathogens, with limited host ranges, but often with extended cryptic phases of growth. The obvious reproductive route for *B. cinerea* is via the abundantly produced airborne spores, landing on damaged or weakly defended plant tissue and developing a necrotrophic infection. However, in many phylogenetically distinct hosts, cryptic and distributed infection with *B. cinerea* and some distantly related *Botrytis* species may exist throughout much of the life of the plant, even in perennials. For example, in *Taraxacum* in both the Netherlands and England, internal infection of all plant organs can be found; *B. cinerea* is the commonest pathogen species involved, but other species can also be isolated. Since the vegetation in which these infections are found is diverse and many of the hosts have no agriculturally improved relatives, this appears to represent an ancient relationship. Several lines of evidence suggest a balanced relationship between host defence and growth of these cryptic infections, in which the number of isolates in a host plant is limited, but complete absence is unusual. Furthermore, plants in better environmental conditions support more isolates. The widespread nature of this form of infection raises the question of why it is not more common and what selective forces favour a more aggressive but specialised evolutionary path for some pathogens. Models with quantitatively varying levels of defence rather than on/off switches appear necessary to account for the diversity of infection type.

Summary

Some plant species host largely cryptic *Botrytis* infections but in others necrotrophy is the dominant form of attack. Why?



Hanna Märkle

Technical University of Munich

Co-authors

Heinrich, Lukas; Technical University of Munich

Tellier, Aurélien; Technical University of Munich

Title

Bayesian inference of host-parasite coevolution: Revealing loci running with the Red Queen

Abstract

The detection of genes which are involved into host-parasite coevolution is of interest to many fields and to many applications. While many studies only focus on either the host or the parasite, the wide application of next generation sequencing techniques will enable access to genetic data of both interacting species simultaneously. As the polymorphism data of both species contain information about their joint coevolutionary history, using them together may help not only to detect genes under coevolution but also to infer parameters of the past coevolutionary dynamics such as costs of resistance. Our aim is to develop an Approximate Bayesian Computation (ABC) to infer loci under coevolution based on a joint analysis of host and parasite genetic data at candidate loci. We extend the framework by Tellier et al. (2014) to simulate polymorphism data for 40 host and 40 parasite sequences by constraining the coalescent simulator msms on the coevolutionary trajectory of a gene-for-gene model under different parameter values. So far, our ABC uses simple summary statistics such as Tajima's D, the number of segregating sites and π from host and parasite data. As a first proof of principle, we were able to infer the host and parasite effective population size and cost of infection with a very good accuracy. However, the inference of cost of resistance turned out to be more challenging. We will present current extensions of the method including an extended set of summary statistics such as comparisons to an outgroup and results concerning the statistical power of our ABC method. The work done so far shows the potential to infer loci under coevolution by using host and parasite data in a Bayesian inference framework. We will discuss the future of applying such an inference method in combination with molecular biology methods to improve the detection of loci under coevolution and to understand host-parasite coevolutionary dynamics in given natural or agricultural systems.

Summary

Approximate Bayesian Computation to infer loci under coevolution by jointly using host and parasite polymorphism data.



Remco Stam

Technische Universität München

Co-authors

Scheikl, Daniela; Technische Universität München

Tellier, Aurelien; Technische Universität München

Title

Using pooled enrichment sequencing to understand R-gene durability and diversity in wild tomato

Abstract

Many of the known pathogen Resistance (R)-genes in plants belong to the NLRs. NLRs or Nod-like Receptors are Nucleotide-binding domain and Leucine rich Repeats (NB-LRR)-containing proteins that are important in plant resistance signalling and introgression of NLR genes in cultivated plant species successful to generate resistance. However, many cases exist where the R-genes have been overcome by pathogens within a couple of years. In nature, most wild plant species seem to maintain a certain resistance over time. Which factors play a role in this is yet poorly understood. Comparative genomics has shown long-term evolutionary relationships of NLRs and has shown that different mechanisms might have been in place to accomplish such great NLR diversity as can be observed today. Also in short time scales, functional genes that play such an important role in the plant-pathogen interaction should be under selective pressure, thus studying within and between population differences can help decipher NLR evolution in different habitats and identify possible coevolution with local pathogens. Here we assess NLR diversity in wild tomato species, using R-gene Enrichment Sequencing (RENSeq) of pooled populations. We first show a proof of principle of our methods within one wild tomato population of *Solanum pennellii* and identify NLR under varying selective pressure. We expand our analysis to fifteen *S. chilense* populations from different habitats and known geographical locations and assess short term evolutionary changes, using population genetics methods to detect patterns of selection. We link these data to infection assays to understand plant and pathogen population dynamics and understand the evolutionary pressures driving the birth and death of NLR genes in wild populations. Our study can pave the way for further evolutionary and functional studies in NLR biology and can lead to important insights in R-gene mediated resistance that can be applied to many species.

Summary

R genes show different selection pressures within and between several wild tomato populations.



Monday 29.8. 16:15- 17:15

Michael Hood

Amherst College

Title

Resistance transitivity across endemic and host-shift pathogens.

Abstract

Pathogen host range is often seen as constrained primarily by pathogen specialization and by fixed, baseline resistances that must be overcome through pathogen adaptation. However, there is often within-species variation in the ability to defend against host-shift pathogens. The current study articulates the idea of resistance transitivity: that natural variation in resistance to endemic pathogens may correlate with variation in resistance to host-shift pathogens, thus serving as an additional force in shaping new disease emergence and pathogen host range. The *Silene*-*Microbotryum* system provides support to this theory through cross-inoculation experiments; among field-collected families of *Silene vulgaris*, resistance to its endemic fungal anther-smut pathogen (*Microbotryum silenes-inflatae*) correlates with variation in resistance to a host-shift pathogen (*Microbotryum lychnidis-dioicae* from *Silene latifolia*). Although the relationship is broadly positive, there are marked outlier families that suggest a second, negative axis. Implications of these results are explored by modelling approaches, and help identify conditions where resistance transitivity can protect versus predispose populations to the risk of host-shift disease emergence.

Summary

Polymorphism in resistance to endemic pathogens may predict the risk of the disease emergence by host-shift pathogens.



Jeremy J Burdon

CSIRO, Australia

Co-authors

Ericson, Lars; Umea University, Sweden

Title

Long-term epidemic dynamics and its evolutionary implications.

Abstract

The epidemiology of the rust pathogen *Triphragmium ulmariae* has been studied in a metapopulation of 130- 170 discrete populations of its host plant *Filipendula ulmariae* for the past 26 years. In this metapopulation, host populations are dispersed across a highly structured archipelago of islands in which position effects play a major role in the occurrence of disease, and extinction and re-colonization processes. Analysis of epidemiological patterns across multiple years shows that hot spots of disease occurrence vary from year-to-year and place-to-place. Evidence from studies of the impact of disease on young plants, and on the occurrence of disease resistance within host populations suggests that the pathogen places significant pressure on host populations. Long-term epidemiological studies of this type are important in demonstrating the highly stochastic nature of disease occurrence in both time and space a factor of considerable importance in influencing the intensity and longevity of potential selective forces experienced by individual host populations.

Summary

Long-term epidemiological studies are important in demonstrating the highly stochastic nature of disease occurrence in time and space.



Tuesday 30.8. 9:30- 10:30

John Walsh

University of Warwick

Co-authors

Teakle, Graham; University of Warwick

Barker, Guy; University of Warwick

Katschnig, Diana; University of Warwick

Hambidge, Angela; University of Warwick

Williamson, Martin; Rothamsted Research

Greenslade, Alex; Rothamsted Research

Newbert, Max; University of Warwick

Title

The genetic diversity and host range of Turnip yellows virus (TuYV), a common virus infecting cultivated brassicas and wild plants in Europe

Abstract

Turnip yellows virus (TuYV) is widespread in Europe with high incidences recorded in cultivated crops, especially oilseed rape (OSR) and vegetable brassicas. It is transmitted by aphids, with the peach potato aphid *Myzus persicae* considered to be the major vector in Europe. It is economically important with estimates of losses in OSR in the UK alone estimated to be £67 - £180 million per annum (Nicholls, 2013). We have detected 100% incidence of TuYV in some insecticide-treated OSR crops indicating there must be a large reservoir of the virus in other plant species providing a green bridge between the OSR cropping seasons. Little was known about the genetic diversity of TuYV and the host range of different genotypes. This is surprising given the level of TuYV infection we have detected across Europe, with the UK, France, Germany and Poland all having >90% incidence in some OSR crops. Previously only a small portion of the TuYV genome had been studied, we have sequenced the whole genome of TuYV isolates mostly from across Europe. Our provisional phylogenetic studies indicated four distinct genetic groups in the UK. Whole genome analysis has provided valuable information on TuYV genetic diversity and recombination. We have also investigated the host range of selected TuYV isolates and determined the proportion of flying *M. persicae* carrying the virus. TuYV often goes unnoticed due to its muted symptoms, which can be similar to those resulting from a number of abiotic stresses. To better understand the epidemiology of TuYV, the status of different wild plant species as hosts has been investigated and new wild plant hosts have been identified. As TuYV is not seed-borne, host range is an important factor in its epidemiology.



Summary

Turnip yellows virus is very common in plants and spread by aphids. We investigated its genetic diversity, wild plant hosts and the proportion of aphids carrying it.



Janis Antonovics

University of Virginia

Title

Vector-based disease transmission in a spatially explicit context; field studies and theory

Abstract

In vector transmission, fixed dispersal distributions (or kernels) for modeling disease spread are inadequate because vectors are likely to adjust flight behavior depending on the density of hosts. I present a simple agent based model that uses a perception kernel to capture the essential features of vector behavior. Simulations show that observation of vector movement between extant hosts, in and of itself, provides an incomplete picture of how transmission relates to local host density, because such observations fail to detect non-visits. This model is applied to field data on anther-smut disease (*Microbotryum* sp.) on *Dianthus pavonius* to estimate relevant parameters, and to predict disease dynamics when there is local spatial variation in host density.

Summary

We need to do a lot more work to understand vector transmission, especially where host densities vary, as in natural populations.



Tuesday 30.8. 11:00- 12:00

Pascal Frey

INRA

Co-authors

Xhaard, Constance; INRA

Pernaci, Michael; INRA

Becheler, Ronan; INRA

De Mita, Stéphane; INRA

Halkett, Fabien; INRA

Title

When a plant pathogen runs down a river: population genetics of the poplar rust epidemics in the Durance River valley

Abstract

Tracking pathogen movement, identifying source populations and understanding environmental factors including human activities that influence pathogen spread are central tasks in disease ecology. Here we focus on the spread of a plant pathogen in a wild pathosystem. Every year we monitored a yearly epidemic of the European poplar rust fungus, *Melampsora larici-populina*, in the Durance River valley, in the French Alps. This valley is particularly well suited for the study of recurrent biological invasions: the need of an alternate host plant (larch) to perform its sexual reproduction restricts the resident pathogen population upstream the river, in a poplar-larch sympatry area. Then, a clonal epidemic phase spreads downstream the valley during five months along a ca. 200km natural riparian stand of black poplar, *Populus nigra*. This landscape also includes a few cultivated stands with poplars carrying qualitative resistances, thus exerting a peculiar selection pressure on pathogen populations. In this study we used epidemiology and population genetics tools to (i) sort *M. larici-populina* individuals according to their wild or cultivated origin, (ii) to describe the spread of the epidemic on the wild poplar stands, (iii) to assess the evolution of the genetic composition of the pathogen populations along the epidemic wave, and (iv) to assess the evolution of life history traits during the epidemic. These results are discussed in the light of recent studies interested in the relative effects of demographic and selection events on the evolutionary changes accompanying biological invasions.

Summary

When a plant pathogen runs down a river: 2 simultaneous poplar rust epidemics occur each year in the Durance River valley



Samuel Soubeyrand

INRA

Title

Exploring data from wild plant pathosystems with recent modeling and inference techniques

Abstract

Medium- and large-scale data collected from wild plant pathosystems and the associated environments are more and more diverse and rich, especially with the development of genetic-spatio-temporal surveys. Additionally, our capacity to exploit new sources of data for inferring processes underlying plant-pathogen dynamics increases with the development of open data. Thus, potentially, we should be able to significantly improve our understanding of wild plant pathosystems. However, the mass and heterogeneity of data (and sometimes their novelty) require adapted modeling and inference techniques. During my talk, I will present recent modeling and inference techniques allowing original analyses of wild plant pathosystems. In particular, I will discuss (i) the use of genetic and epidemiological data for revealing the relative contributions of different pathogen strains to natural epidemics; (ii) the use of high-throughput sequencing data for inferring transmissions of fast-evolving pathogens between host populations; (iii) the combination of a mechanistic approach of plant-pathogen dynamics and a probabilistic approach of surveillance for handling heterogeneity, scale-discrepancies and incompleteness in data; and (iv) the use of archived meteorological data for building dispersal graphs incorporated into metapopulation models. These techniques, and many others, offer new perspectives for multidisciplinary research in the study of wild plant pathosystems.

Summary

Recent modeling and inference techniques allow the use of heterogenous data informing processes underlying plant pathosystems.



Tuesday 30.8. 13:00- 14:15

Fletcher Halliday

UNC Chapel Hill

Co-authors

Umbanhowar, James; UNC Chapel Hill

Mitchell, Charles; UNC Chapel Hill

Title

Seasonal variation, within-host priority effects, and fungal interactions jointly influence parasite epidemics in a grass host

Abstract

Interactions among plant parasites and mutualists may depend on priority effects across host populations due to seasonal variation and within host individuals due to differences in the force-of-infection during epidemics. We compared the roles of seasonal variation in epidemic timing, within-host priority effects, and other direct interactions on parasite epidemics by measuring parasite infection on three cohorts of sentinel tall-fescue plants, timed to detect seasonal dynamics, and grown with and without the fungal mutualist, *Epichloë coenophiala*. We focused on three foliar fungal parasites (*Colletotrichum cereale*, *Puccinia coronata*, and *Rhizoctonia solani*) that exhibit overlapping seasonal epidemics. To evaluate within-host priority effects, we tested whether previous infection status by each symbiont influenced the risk of subsequent infection by each parasite (i.e. disease risk), using a Cox-Proportional Hazards model. To test the role of direct interactions among infected hosts, we analyzed infection severity, which measures within-host parasite replication (i.e. growth rate). We found strong support that within-host priority effects and direct interactions among infected hosts simultaneously influenced parasite epidemics. Additionally, seasonal variation in epidemic timing profoundly influenced parasite epidemics and fungal interactions. These results were robust across all three foliar parasites, and indicate that strong seasonal priority effects do not necessarily preempt within-host priority effects, which do not necessarily preempt direct interactions between symbionts. Instead priority effects and direct interactions likely act in concert during symbiont community assembly.

Summary

Fungal parasite communities inside plants are historically contingent. And deterministic. Across multiple scales. At the same time!



Mark McMullan

The Genome Analysis Centre

Co-authors

Percival-Alwyn, Lawrence; The Genome Analysis Centre

Kroboth, Jakob; The Genome Analysis Centre

Clark, Matt; The Genome Analysis Centre

Title

Plant pathogen evolution across the wild-agricultural boundary

Abstract

Agricultural pathogens can adapt quickly to the disease control strategies deployed against them. Many plant pathogens are clonal, which suits their lifestyle on a monoculture. The evolution of novel variation in these plant pathogens is a slow stepwise process facilitated by mutation. However, plant pathogenic fungi and oomycetes may occasionally enter a sexual reproductive life cycle and the implications of this could be far reaching. The role of recombination as a process to swap favourable or detrimental alleles may be fundamental to increasing the adaptive capacity of a plant pathogen. Perhaps more importantly, sex also allows genetic exchange between races of pathogens living in different environments. Wild progenitors of crops often suffer from the same pathogens as their agricultural counterparts, the difference being that, in the wild, both host and pathogen co-evolve. In order to identify more durable resistances, we must understand plant pathogen interactions in the wild and furthermore, the subsequent interaction between plant pathogens across the wild-agricultural boundary. Here I examine these processes in two different wild-agricultural systems 1) *Albugo candida*, an unusually broad host range pathogen found on both wild and agricultural brassicas. 2) Sugar beet (*Beta vulgaris*), a recently domesticated crop grown in close proximity to its wild progenitor (sea beet), both of which are affected by powdery mildews and rusts. In the *A. candida* system we have observed that recombination (or introgression) can occur between pathogen races that grow on different host species (wild and agricultural brassicas). In the sugar beet system, we use genome sequencing of the leaf surface of both wild and agricultural beets. We are using population genetics to address the question, does wild pathogen genetic variation invade the agricultural system?

Summary

@mcmullan0 considers how pathogen evolution that takes place in the wild influences their success in agriculture.



Laura Masini

SLU Alnarp

Co-authors

Abreha, Kibrom B.; SLU Alnarp

Alexandersson, Erik; SLU Alnarp

Råberg, Lars; Lund University

Vetukuri, Ramesh R.; SLU Alnarp

Grenville-Briggs Didymus, Laura; SLU Alnarp

Andreasson, Erik; SLU Alnarp

Lankinen, Åsa; SLU Alnarp

Title

Unravelling the defence arsenal of the wild *Solanum dulcamara* to *Pythophthora infestans*

Abstract

Potato late blight, caused by the oomycete *Phytophthora infestans*, is a devastating disease that can wipe out a potato field within days. *Solanum dulcamara* is a diploid, perennial, wild relative of potato, and an occasional natural host for *P. infestans* in Sweden. A study on 12 *S. dulcamara* populations originating from south-west Sweden detected remarkable disease variability in response to *P. infestans*. Our goal is to understand the cause of this variability. On one hand we are characterising the phenotypic response of *S. dulcamara* genotypes with different levels of resistance to *P. infestans*, including accumulation of reactive oxygen species (ROS), callose deposition, and pathogen biomass quantification. On the other hand we aim at investigating whether the variability in defence responses is due to tolerance, the ability of a plant to limit the negative impact of a pathogen on its fitness. Because tolerance, as opposed to resistance, does not affect the pathogen fitness, it could contribute to a slow-down in the evolution of the pathogen to overcome resistance. We are studying the relationship between plant fitness and degree of infection under controlled conditions. Our data shows that different *S. dulcamara* genotypes display either tolerance or overcompensation. Overcompensation refers to the increase in fitness in response to damage. These different genotypes will be used for gene expression studies to identify candidate genes for pathogen tolerance/overcompensation and to find gene products sharing a common pathway, enabling identification of broader tolerance/overcompensation mechanisms.

Summary

Solanum dulcamara: a wild relative of potato that tolerates *Pythophthora infestans*. A new tool in the fight against late blight



Philippe Roumagnac

CIRAD

Co-authors

Charles-Dominique, Tristan; UCT

Fernandez, Emmanuel; CIRAD

Filloux, Denis; CIRAD

Ortet, Philippe; CEA

Barakat, Mohamed; CNRS

Rebelo, Tony; SANBI

Varsani, Arvind; University of Canterbury

Malmstrom, Carolyn; MSU

Martin, Darren; UCT

Roumagnac, Philippe; CIRAD

Title

Deciphering plant-associated viruses at the agroecosystem scale using geometagenomics

Abstract

As a consequence of past plant-virus interaction studies having been almost exclusively focused on cultivated areas, our knowledge of plant virus diversity in natural environments is still very limited. Without an understanding of the spatial and temporal patterns of natural virus diversity we will never be able to achieve a mechanistic understanding of either plant virus ecological dynamics, or the factors driving long-term virus evolution and emergence. Consequently, it is still difficult to quantify the impacts of human activities (e.g. agricultural intensification, the dissemination of exotic plant and pathogen species) on host-pathogen interactions. We have developed a new geo-metagenomics approach for producing quantitative information on virus diversity, prevalence and spatial distributions and have applied it to the study of two pilot ecosystems located in South Africa and France. This approach yields geographically tagged cDNA from virus species, and further allows viral sequences to be linked to specific host plants at a specific location and time. The objectives of this study were to assess 1) whether natural, unmanaged areas act as reservoirs of plant virus biodiversity, 2) whether the spatial distributions of different plant viruses at the agro-ecosystem scale display distinctive patterns and 3) whether ecological parameters could account for observed patterns of virus distribution. This new approach allowed us to discover 94 new plant viral species and to reveal distinctive virus spatial distribution patterns. Whereas the prevalence of plant viruses associated with cultivated areas in both countries was significantly greater than that associated with non-cultivated areas, exotic plants within natural fynbos areas of South Africa also displayed a significantly higher prevalence of viruses than indigenous plants. These results emphasize both the direct and indirect impacts that human activity has on plant virus dynamics at the agro-ecosystem scale.



Summary

Geometagenomics emphasize both the direct and indirect impacts that human activity has on plant virus dynamics at the agro-ecosystem scale.



Nilsa Bosque-Perez

University of Idaho

Co-authors

Ingwell, Laura; Purdue University

Title

The prevalence of Barley yellow dwarf viruses in grassland habitats is influenced by diverse agroecological and environmental factors

Abstract

Barley/Cereal yellow dwarf virus (B/CYDV) are among the most important pathogens of cereal crops, such as wheat, and infect over 150 Poaceae species. Among these are many grass species present in native prairies and Conservation Reserve Program (CRP) lands in the USA. The wheat-producing Palouse region of northern Idaho and southeastern Washington is characterized by fragmented native prairie and CRP habitats embedded in an agricultural matrix. Disease prevalence has been understudied in these two habitats. Virus infection of grasses may play a role in disease ecology and epidemiology in agroecosystems and impact native prairie conservation and restoration efforts. Field surveys of Poaceae species in prairie and CRP in the Palouse region were conducted over two-years to examine for presence of B/CYDV among potential plant hosts and vectors. Viral species were identified via cloning and sequencing. Landscape, soil and weather data were obtained from USDA databases. Analysis was conducted to examine effects of diverse factors on virus prevalence. BYDV was detected at every prairie remnant and CRP sampled. Overall infection was 47%, but virus prevalence varied according to year, site and plant host. BYDV prevalence increased in sampled habitats as grain crop cover increased within a 1 km radius of a habitat patch. Aphids were encountered only once suggesting non-colonizing aphids are responsible for disease spread in these habitats. BYDV was more prevalent in perennial vs. annual grasses and was correlated with the presence of several introduced species. BYDV infection of *Ventenata dubia*, a nonnative invasive species was detected for the first time. Invasive grasses in these habitats could serve as virus inoculum sources with implications for disease and vector management, competitive dynamics between invasive and native grasses, and conservation of endangered grasslands.

Summary

Barley yellow dwarf virus occurs in Palouse prairie and CRP. Year, site, plant host and nearby grain crops influence virus prevalence.



Wednesday 31.8. 9:00- 10:00

Oliver Furzer

The Sainsbury Laboratory, Norwich, UK

Co-authors

Çevik, Volkan; The Sainsbury Laboratory, Norwich, UK

Witek, Kamil; The Sainsbury Laboratory, Norwich, UK

Jones, Jonathan; The Sainsbury Laboratory, Norwich, UK

Title

Exploring Brassicaceae NLR diversity with Resistance gene enrichment sequencing

Abstract

In plants, Resistance genes (R genes) confer strong immunity against pathogens and pests such as bacteria, viruses, fungi, oomycetes and invertebrates. R genes typically encode nucleotide binding, leucine rich repeat proteins (NLRs). R gene enrichment sequencing, RenSeq, is an RNA-oligo based DNA capture method to select the putative NLR encoding gene complement of a plant DNA sample prior to sequencing (Jupe et al, 2013, The Plant Journal). We use RenSeq to investigate natural variation in NLR repertoires. NLR encoding gene clusters harbour extensive genetic diversity and are complex and difficult to resolve using Illumina reads. We are using RenSeq in combination with long-read PacBio sequencing to define the diversity of NLRs. We will present the striking level of NLR polymorphism in terms of presence/absence, novel NLR loci, and novel structural features within NLRs, uncovered within 20 *Arabidopsis thaliana* accessions sequenced using PacBio RenSeq. These data contribute to a model of long term balancing selection acting to maintain diversity, and possible mechanisms of transposon activity and unequal crossing over events generating novel diversity, at NLR loci within plant populations. We have also used RenSeq and Illumina based genetic mapping to identify functional NLR encoding R genes against various pathogens, in particular the White Rust-causing obligate biotroph *Albugo* species that infect the Brassicaceae including *Arabidopsis thaliana*. This work has led to new understanding of the basis by which this pathogen is recognised by its host, and its corresponding evolutionary strategy to evade recognition.

Summary

PacBio RenSeq of *Arabidopsis* accessions uncovers striking diversity in NLR repertoires and novel Resistance genes against *Albugo* #WPP2016



Antoine Persoons

TGAC, Norwich Research Park, Norwich, UK

Co-authors

Bueno Sancho, Vanessa; TGAC, Norwich Research Park, Norwich, UK

Hubbard, Amelia; NIAB, Cambridge, UK

Lewis, Clare; JIC, Norwich Research Park, Norwich, UK

Cook, Nicola; TGAC, Norwich Research Park, Norwich, UK

Judge, Christopher; NIAB, Cambridge, UK

Thomas, Jane; NIAB, Cambridge, UK

Uauy, Christobal; JIC, Norwich Research Park, Norwich, UK

Holdgate, Sarah; NIAB, Cambridge, UK

Saunders, Diane; TGAC, JIC, Norwich research park, UK

Title

Field pathogenomics: Developing new tools for interrogating cereal invaders

Abstract

Wheat yellow rust disease poses a substantial threat to wheat production worldwide and recently re-emerged as a major constraint on UK agriculture. The causal agent *Puccinia striiformis* f. sp. *tritici* (PST) is an obligate biotrophic fungal pathogen that can cause significant reductions in both grain quality and yield in susceptible wheat cultivars. In order to document the global population structure of the pathogen and understand why it re-emerged as a major agricultural threat in the UK, we developed a robust and rapid genotyping strategy termed field pathogenomics. This method uses gene sequencing of PST-infected wheat leaves taken directly from the field, to gain insight into the population structure of PST over successive seasons. Our analysis uncovered a dramatic shift in the UK PST population in recent years, and supports the hypothesis that recent introduction of a diverse set of exotic PST lineages may have displaced the previous populations. Furthermore, we identified isolates belonging to this emergent lineage across a further three continents. This illustrates that the emergent PST population identified initially in Europe is now widespread on a global scale. In addition, we identified a direct association between pathogen genotypes and host pedigrees. This study illustrates the utility of the field pathogenomics technique to reveal new insight into population shifts and dynamics, which is important for our understanding of emerging plant diseases and has consequences for the management of such diseases.

Summary

Field pathogenomics approaches for understanding the dramatic shift in the wheat yellow rust population



Ales Lebeda

Palacký University in Olomouc, Depart of Botany

Co-authors

Mieslerova, Barbora; Palacký University in Olomouc, Depart of Botany

Petrzelova, Irena; Palacký University in Olomouc, Depart of Botany

Kristkova, Eva; Palacký University in Olomouc, Depart of Botany

Title

Interactions between wild *Lactuca* species and *Golovinomyces cichoracearum* – complex view

Abstract

The genus *Lactuca* L. (family Asteraceae) is composed of one cultivated species - lettuce (*Lactuca sativa* L.), and about 100 wild *Lactuca* spp. The primary gene pool of cultivated lettuce comprises its cultivars and landraces and some wild relatives, e.g. wild *L. serriola* and *L. aculeata*. *Golovinomyces cichoracearum* s.s. (GC), an important powdery mildew pathogen mainly of representatives of Asteraceae subfamily Cichorioideae, is distributed worldwide and occurs on *Lactuca sativa* as well as wild *Lactuca* spp. and related taxa (e.g. *Cichorium* spp.). Detailed study of variation of GC isolates revealed high specialization to their hosts. Most of GC isolates collected on *Lactuca serriola* infected other wild *Lactuca* species only weakly, and did not infect other representatives of the family Asteraceae. More than decade lasting study of mixed occurrence of powdery mildew (*G. cichoracearum*) and downy mildew (*Bremia lactucae*) in the wild populations of *L. serriola* has brought important results. GC is rather common in populations of *L. serriola*, however prevalence of infection is mostly low. Data about intensity of infection of both pathogens compared with average monthly temperature and rainfall rate proved that climatic conditions have influence on the occurrence of both pathogens. Long lasting research was focused on sampling of GC isolates in wild populations of *L. serriola* in the Czech Republic and study of their intraspecific variability. Large variability in virulence was confirmed and existence of different races was supposed, including their differentiation. Resistance in wild *Lactuca* spp. as well as in *L. sativa* is characterized by race-specificity, but the genetic background of resistance is poorly understood. Detailed study of GC development on the set of *Lactuca* species and other Asteraceae revealed that the hypersensitive response is the main resistance reaction in this pathosystem. However, this reaction was not always successful to prevent development of GC.



Wednesday 31.8. 10:30- 12:15

Marie-Laure Desprez-Loustau

INRA - Univ Bordeaux

Co-authors

Dutech, Cyril; INRA - Univ Bordeaux

Marcais, Benoit; INRA - Univ Bordeaux

Vacher, Corinne; INRA - Univ Bordeaux

Title

Oak powdery mildew in Europe one century after the invasion: some hypotheses about ecological, evolutionary and anthropogenic changes in the pathosystem.

Abstract

Oak powdery mildew is among the most common forest diseases in Europe. Disease prevalence is usually quite high and severity moderate, although highly variable within and among sites and years, so that it could be easily taken as an indigenous pathosystem. However, the first disease outbreaks only date back from the beginning of the 20th century. Contrary to the present situation, very severe damage, including high mortality and quasi local extinction of oak populations in some areas were reported at that time. What are the factors that can explain the trajectory of this pathosystem? Phylogenetic studies have clarified the identity of causal organisms which appeared to be a complex of cryptic species (*Erysiphe alphitoides* sensu lato), likely originating from a common ancestor in Asia. Contrary to most powdery mildews, *E. alphitoides* seems particularly well suited to perform host shifts, among oak species but even also to more distant plant groups. A higher resistance of extant oak populations than at time of invasion may be explained by two hypotheses. First, changes in silvicultural practices may have had an impact on disease susceptibility of oaks. Also, disease resistance may have evolved under natural selection pressure by powdery mildew. Oak cohorts originating before and after the invasion were compared phenotypically and genetically to test this hypothesis. The potential effects of biotic and abiotic environmental factors have also been investigated. Accumulation of hyperparasites or antagonists might have an impact on pathogen populations. Changes in climate affect the spring phenological synchrony between host and pathogen, conditioning the re-initiation of epidemics each year, which may drive further changes of the pathosystem in the future.

Summary

Forests can show resilience to some exotic invasive pathogens despite high initial impact: oak powdery mildew in Europe as an example.



Gregory Gilbert

University of California, Santa Cruz

Co-authors

Parker, Ingrid; University of California, Santa Cruz

Title

Phylogenetic prediction of the disease landscape in wild plant pathogen networks

Abstract

Because most plant pathogens are not host specialists, their spread and impact is best considered at the level of a plant community, rather than a single host species. The disease landscape includes the individual plants of all the local species that are susceptible to a particular pathogen. Pathogen spread and impact is responsive to the combined local densities of all the susceptible species, weighted by the competence of hosts to support pathogen reproduction. The species that contribute to the disease landscape are a non-random subset of the local plant community. Many important plant traits associated with susceptibility and resistance are phylogenetically conserved. This means that the structure of networks of hosts and pathogens can be predicted based on the phylogenetic structure of the plant community. Phylogenetic approaches to the evolutionary ecology of wild plant pathosystems provides new opportunities to understand and predict the structure and dynamics of the disease landscape.

Summary

The evolutionary distances among local plant species can indicate the likely spread and impact of a plant pathogen in wild ecosystems.



Levente Kiss

Centre for Agric. Res., Hung Acad Sci, Hungary

Co-authors

Kovacs, Gabor M.; Dept. Plant Anat., Eotvos Lorand Univ., Hungary

Boka, Karoly; Dept Plant Anat., Eotvos Lorand Univ., Hungary

Bohar, Gyula; Bioved 2005 Ltd., Hungary

Boharne Varga, Krisztina; Bioved 2005 Ltd., Hungary

Nemeth, Mark Z.; Centre for Agric. Res., Hung Acad Sci, Hungary

Shin, Hyeon-Dong; Korea University, Seoul, Republic of Korea

Hayova, Vera; Kholodny Institute of Botany, NAS Ukraine

Nischwitz, Claudia; Dept. Biology, Utah State Univ., USA

Seier, Marion K.; Invasive Species Management CABI Europe-UK

Evans, Harry C.; Invasive Species Management CABI Europe-UK

Gavin, James Ash; Univ. Southern Queensland, Australia

Muller-Scharer, Heinz; Univ. Fribourg, Switzerland

Title

A hidden friend of allergic people? Deciphering the biology of *Phyllachora ambrosiae*, an enigmatic, obligate biotrophic fungal pathogen of common ragweed (*Ambrosia artemisiifolia*)

Abstract

Phyllachora ambrosiae is a little known intracellular, obligate biotrophic fungal pathogen infecting the aerial parts of common ragweed (*Ambrosia artemisiifolia*), an invasive agricultural weed also known for its highly allergenic pollen. The pathogen is capable, infrequently, to naturally kill the pollen-producing inflorescences in large areas, while being almost undetectable most of the time in ragweed populations. In spite of its sometimes devastating effects on ragweed pollen production, lower priority was given to *P. ambrosiae* as a potential biocontrol agent (BCA) of common ragweed due to its little known biology. This triggered the present work based on light microscopy and TEM studies and molecular analyses using living *P. ambrosiae* materials collected from 1999 to 2014 in Hungary, Korea, Ukraine and the USA as well as North American herbarium specimens collected from 1893 to 1962. Common ragweed was introduced from North America to Europe in the 19th century, and much later to some parts of Asia. Thus, it is hard to explain how *P. ambrosiae* spread in the introduced Eurasian ragweed populations so efficiently. Common ragweed is an annual plant, reproducing exclusively by seeds, and *P. ambrosiae* is not known to be seed-transmitted. Also, *P. ambrosiae* is not known to be soil-borne and alternative host plants are unknown. Based on ITS, 18S and 28S nrDNA sequences it became clear that the Eurasian *P. ambrosiae* specimens are different from those collected in North America, representing two distinct, but closely related lineages,



which are only distantly related to any known lineages within the Ascomycota. This in itself makes these fungi very interesting from a fungal phylogenetic point of view. Based on these results, it is even more difficult to explain the spread of *P. ambrosiae* in the recently introduced Eurasian *A. artemisiifolia* populations. Our results may serve as a starting point for the development of *P. ambrosiae* strains into potential BCAs.

Summary

The highly allergenic ragweed plants are sometimes seriously diseased in the field. This is the first extensive study of this disease.



Jenalle Eck

The Ohio State University

Co-authors

Delavaux, Camille; Yale University

Mangan, Scott; Washington University in St. Louis

Comita, Liza; Yale University

Title

Soil microbial community impacts on tropical tree seedling growth promote seedling diversity within a tropical tree population.

Abstract

The Janzen-Connell hypothesis and plant-soil feedback theory both highlight the importance of species-specific pathogens in promoting tree species diversity in tropical forests. Agricultural and model plant studies suggest that microbial impacts also depend on plant genotype within a single species, but whether microbes that specialize within tree species exist in tropical forests is unknown. If present, genotype-specific microbes could promote tree genetic diversity within populations via the plant-soil feedback mechanism. We conducted a plant-soil feedback greenhouse experiment in Panama to test for evidence of genotype-specific microbes within a tropical tree population. We grew seeds from 11 maternal sources in one tree population for 8 months in experimental treatments containing the soil microbial community from beneath either the seedling's own maternal tree, a non-maternal tree in the population, or a heterospecific tree, then quantified seedling growth, survival, and colonization by arbuscular mycorrhizal fungi. We found that seedling biomass and colonization by arbuscular mycorrhizal fungi were both decreased when seedlings were grown in the soil microbial community from beneath their maternal tree vs. from beneath a less-related, non-maternal tree in the population. In addition, plant-soil feedback analysis of seedling growth yielded a negative system feedback value within the tree population. Our experimental results provide new evidence that soil microbial communities within tree populations provide a growth and mutualism advantage to non-offspring conspecific seedlings and generate a negative plant-soil feedback theoretically capable of maintaining genetic diversity in the tropical tree population. Additional studies are necessary to confirm genotype-specificity in tropical soil microbes, but our results suggest that genotype-specific soil microbes exist in tropical forests and promote seedling diversity in tropical tree populations.

Summary

Soil microbial communities promote seedling diversity within a tropical tree population in Panama



Wednesday 31.8. 13:15- 14:30

Emme Bruns

University of Virginia

Co-authors

Antonovics, Janis; University of Virginia

Hood, Michael; Amherst College

Title

Disease at species range margins: Co-distribution of alpine plant species and their vector-transmitted pathogens.

Abstract

While disease is widely recognized as an important factor affecting host abundance, the effect of disease on species distributions has received relatively little attention. This is because host population size tends to decline towards the range margins, and diseases with density-dependent transmission typically cannot be maintained in low-density populations. However, vector-borne and sexually transmitted diseases are transmitted relatively independent of density and can potentially be maintained in smaller populations at the range margin. We studied the landscape-level distribution of anther-smut disease, a sterilizing pollinator-transmitted disease, on six different alpine plant species to determine whether disease was present at the host range margins or if there was a disease-free halo. We found in all six species disease extended all the way to the range margin, and was present even in small populations. The presence of disease at host range margins indicates that disease could be affecting host geographic distribution.



Kari Saikkonen

Title

Endophytic fungi – latent pathogens or defensive plant mutualists?

Abstract

Endophytic fungi are generally considered to be defensive plant mutualists. However, defensive mutualism appears to be more commonly detected in systemic and vertically transmitted grass endophytes compared to horizontally transmitted tree endophytes. Here I summarize the results of our studies comparing phenotypic and genetic correlations of two endophytic fungi (*Fusicladium* and *Melanconium*) and birch rust (*Melampsorium betulinum*) with the performance of six invertebrate herbivores growing on the same half sib progenies of mountain birch *Betula pubescens ssp. czerepanovii*. We found little support for causal association between fungal frequencies and performance of herbivore species. Instead, genetic correlations, particularly between autumnal moth (*Epirrita autumnata*) and birch rust, suggest that herbivore performance may be affected by (1) genetic differences in birch quality for fungi and herbivores, or (2) genetic differences in responses to environmental conditions. Genetic analysis of *Venturia ditricha* revealed that (1) birch genotypes and environment influence the probability of infection by particular endophyte genotypes, (2) genetic variation correlated negatively with infection frequencies of the fungus, and (3) the susceptibility of the birch to a particular endophyte genotype may change when environmental conditions are changed (environment-host genotype interaction). I propose that: (1) the performance of horizontally transmitted endophytes, pathogens, and herbivores may be responses to genetically determined plant qualities rather than interconnected associations, (2) negative correlation between birch resistance to rust fungus and autumnal moth may constrain birch population from reaching optimal species-specific resistance, and (3) knowledge about multispecies coevolution is necessary to fully understand bilateral interactions between plants and the organisms living on them.

Summary

Knowledge of multispecies coevolution is necessary to fully understand species-species interactions.



Erin Mordecai

Stanford University

Co-authors

Spear, Erin;

Daws, Caroline; Stanford University

Title

Generalist pathogens impact survival and reproduction in California grasslands

Abstract

California grasslands are paradoxically one of the most diverse, abundant, heavily invaded, and threatened Mediterranean ecosystems. We know relatively little about which fungal pathogens infect the grasses that compose this important ecosystem. Because fungal pathogens can kill plants and reduce seed set, understanding the composition and function of the pathogen community is critical for understanding the outcome of competition between grass species, particularly between native and exotic grasses. Here, we characterize the species composition, host associations, leaf damage, and demographic impact of the fungal pathogen community in a Northern California grassland site. We present the results of a combination of field surveys and experimental manipulations of the host and pathogen community across two growing seasons. We show that a few fungal species and genera dominate the culturable fungal community, and that these species in large part have broad host associations. Despite this host breadth, pathogen community composition differed across host species and sites, indicating spatial and/or host species turnover in pathogen associations. Pathogen damage was associated with changes in host seedling survival and adult seed production. Across five focal host species, the most heavily damaged individuals produced the fewest seeds, while the highest seed production came from individuals with low pathogen damage. Despite the broad host ranges of most of the common fungal species, their differential host impacts may modify the outcome of competition between grass species, an avenue we plan to explore using empirically derived population growth models. Together, the results imply that fungal pathogens may play an important role in regulating California grassland plant composition.

Summary

Fungal pathogens of CA native & exotic grasses are generalist & impact fecundity and survival. Do they regulate the outcome of competition?



Wednesday 31.8. 16:15- 17:15

Alison Power

Cornell University

Title

From Plant Communities to Coinfections: Plant Virus Ecology at Multiple Scales.

Abstract

Despite the ubiquity and potential importance of pathogens in plant communities, our understanding of how biodiversity governs pathogen spread in wild plants is still rudimentary. Much disease research focuses on single pathogens infecting single hosts, but infection of a single host plant by multiple pathogens is common in nature, and pathogens with multiple host species are also widespread. Using an experimentally tractable system of generalist plant viruses infecting grasses, we have addressed the role of host diversity and within-host pathogen diversity in shaping patterns of pathogen transmission. Field experiments demonstrate strong feedbacks between host community structure and disease dynamics, along with impacts of pathogen diversity on disease spread and virulence.

Summary

Field studies of grass viruses show impacts of co-infection on disease and feedbacks between host community structure and disease dynamics



Anna-Liisa Laine

University of helsinki

Title

Variation in within-host pathogen communities: causes and consequences.

Abstract

Pathogens are prevalent across all ecosystems and they may have strong negative effects on their hosts. Hence, there is a pressing need to understand risks of infection and how these evolve. To date, host-pathogen interactions have been largely viewed within the one host-one parasite framework although in reality the same host may be attacked by a myriad of pathogenic microbes. As molecular tools have become increasingly available for the study of parasites, we now know that a single host individual can support a highly diverse pathogen community. However, remarkably little is known about the factors that determine which pathogens co-occur within the same host individual and how they interact. In my talk I will present a case study of within-host pathogen diversity, and identify some of the key determinants of this diversity, what consequences of variable within-host pathogen communities are both for the host and for the pathogens.

Summary

Within host interactions between pathogen strains are regulated by the host genotype.



Poster Abstracts

Pitching on Monday 29.8. 14:30- 16:45

Alexey Mikaberidze

Institute of Integrative Biology, ETH Zurich

Co-authors

Uecker, Hildegard; Institute of Integrative Biology, ETH Zurich

Title

The role of sex in adaptation of fungal plant pathogens: insights from population modeling

Abstract

Scenarios of pathogen adaptation often involve two or more beneficial mutations. One example, is evolution of fungicide resistance in crop pathogens such as *Zymoseptoria tritici* (an important pathogen of wheat). Widespread use of fungicide mixtures in cereal crops exerts a strong selection pressure on pathogens to acquire resistance to both fungicides in the mixture (double resistance). What is the role of sexual reproduction in this process? In particular, does it accelerate or slow down emergence and fixation of double resistance? How to impede adaptation of pathogens that can reproduce sexually? We address these questions using a powerful population dynamical modeling framework.

Summary

Sex in fungal plant pathogens can accelerate or slow down evolution of resistance to fungicide mixtures. We will figure it out for *Septoria*.



Åsa Lankinen

Swedish University of Agricultural Sciences

Co-authors

Abreha, Kibrom B; Swedish University of Agricultural Sciences

Bakhshandeh, Maryam; Swedish University of Agricultural Sciences

Masini, Laura; Swedish University of Agricultural Sciences

Ali, Ashfaq; Skåne University Hospital

Andreasson, Erik; Swedish University of Agricultural Sciences

Title

Plant immunity is seldom activated in natural populations and agricultural fields

Abstract

Ecological and evolutionary processes can be interrelated despite their different time scales, as exemplified by fast adaptation of pathogen ability to overcome plant resistance to infection. While the zig-zag theory predicts coevolution of pathogen infectivity vs. plant recognition of microbes, one inconsistency of this theory in ecological time concerns the prediction that conserved molecular patterns from pathogens activates induced defence responses (PTI) and the immune response down regulator is disease. As molecular patterns from pathogens are expected to occur all the time in nature and agricultural fields without causing disease, in contrast to in the laboratory, PTI could be predicted to be constantly activated. Effectors secreted by pathogens may also trigger immune responses, even if some responses are repressed. We investigated the actual status of immune responses in both natural (wild *Solanum dulcamara* and *S. nigrum*) and under agricultural field conditions (cultivated *S. tuberosum*). We analysed over 500 apoplastic samples of non-diseased material from three consecutive years in the three summer months in Sweden for presence of PR (pathogenesis-related) proteins, which are the most classic markers for activation of plant immunity. Our results show that the defence system in both natural populations and agricultural fields is activated only in one-third of all samples. We suggest that repression of defence responses in addition to repression of effector-trigger responses need to be taken into consideration in models for pathogen-plant interactions under natural conditions.

Summary

We show that the plant defence system in both natural populations and agricultural fields is activated only in one-third of all samples.



Ayco Tack

Stockholm University

Co-authors

Nemomissa, Sileshi; Addis Ababa University

Samnegård, Ulrika; Stockholm University

Tesfaye, Kassahun; Addis Ababa University

Zewdie, Beyene; Stockholm University

Hylander, Kristoffer; Stockholm University

Title

Coffee at the agro-ecological interface

Abstract

Arabica coffee originated in the Ethiopian highlands, and provides a livelihood for millions of poor smallholder farmers in this region. While expansion and intensification of coffee production degrades the natural forests, and the release of disease-resistant varieties threatens the wild genetic diversity of coffee, shade coffee systems can also harbour high biodiversity. In this project, we explore this dual role of coffee, with the ultimate goal of improving farmer's livelihood, preserving biodiversity and utilizing ecosystem services. In particular, we are interested how biodiversity within and around the coffee plantation can aid in the natural and sustainable control of coffee pests and pathogens.

Summary

Coffee at the agro-ecological interface: the relationship between farmer's livelihood, biodiversity and pest and pathogen dynamics.



Cécile Robin

BIOGECO, INRA, Univ. Bordeaux, France

Co-authors

Dutech, Cyril; BIOGECO, INRA, Univ. Bordeaux, France

Title

Clonal expansion and thermal adaptation of *Cryphonectria parasitica* clonal lineages.

Abstract

Accidental introduction and spread of pathogens into new areas often cause devastating epidemics in wild plant populations. These range expansions also present the opportunity to study pathogen adaptation to new host or new environment. *Cryphonectria parasitica*, the causal agent of chestnut blight, originating from Asia, is now established into different continents. *C. parasitica* has been officially reported for the first time in 1958 in France, and has rapidly spread in all the southern part of the country. We took advantage of this *C. parasitica* recent emergence in northern France to study the changes in population structure and in phenotypic traits associated with this expansion in a colder climatic area. Our work hypothesis was that northern populations were derived from Southern ones and are locally adapted to their new environment. 427 *C. parasitica* isolates, sampled in Northern France, were analyzed with microsatellite markers. In parallel, in vitro growth rate at sub-optimal temperatures, was measured for a subsample of Northern and Southern isolates, these later having not experienced the recent range shift. Our results indicate that *C. parasitica* invasion mostly occurred through a clonal expansion since nearly 50% of the isolates belong to dominant clonal lineages established in Southern France (Dutech et al. 2010). Northern isolates had higher in vitro rate growth at 12 and 15°C and smaller rate growth at 28 and 32°C than southern isolates belonging to the same clonal lineages. These results suggest the evolutionary potential of *C. parasitica* lineages along a temperature gradient and that clonal evolution is not a limit for rapid adaptation for invasive fungal species.

Summary

Clonal evolution of *Cryphonectria parasitica* is not a limit for its rapid adaptation to new climatic constraints.



Claire Neema

Montpellier supagro, BGPI

Author

Oro, Franck; UPGC, ICRAF

Co-authors

Blondin, Laurence; CIRAD, Bioagresseurs

Mfegue, Virginie; IRAD

Ducamp, Michel; CIRAD, BGPI

Herail, Claude; CIRAD, BGPI

Neema, Claire; Montpellier supagro, BGPI

Title

Invasion patterns of *Phytophthora megakarya*, an emerging cocoa pathogen in West Africa

Abstract

Phytophthora megakarya has emerged as the most aggressive among *Phytophthora* species affecting cocoa (*Theobroma cacao* L.) in Central and West Africa. The pathogen is still in an invasive stage in Ivory Coast, threatening the world's largest cocoa producer. Genetic data supplemented by observational and historical records suggested that *P. megakarya* probably emerged on cocoa in Cameroon in the early 1900s, and progressively invaded all the cocoa production zones in Africa, replacing the more ubiquitous species *P. palmivora*. A survey was conducted in Cameroon and Ivory Coast to estimate the genetic variability and the invasion pattern of *Phytophthora* species. In Cameroon, *P. megakarya* was the most prevalent species with a high genetic variability. The situation was totally different in Ivory Coast, where *P. palmivora* is still the most prevalent species. In this country, the two species were differently distributed in cocoa growing regions and a high clonality was found in the two pathogen populations. The results will be discussed regarding the origin of *P. megakarya* species and its invasion pattern in Ivory Coast

Summary

Phytophthora megakarya has probably emerged on the newly introduced cocoa in Cameroon and is in an invasive stage in Ivory Coast.



Ezgi Özkurt

Max Planck Institute for Evolutionary Biology

Co-authors

Stukenbrock, Eva; Environmental Genomics, Christian-Albrechts Univer

Title

Genome evolution of the fungal grass pathogen *Zymoseptoria pseudotritici* following homoploid hybrid speciation

Abstract

Hybridization is proposed to be a major force in the speciation of fungal plant pathogens. The ascomycete grass pathogen *Zymoseptoria pseudotritici* emerged recently from an interspecific cross between yet unknown parental species. In a previous study, the genomes of five individuals of *Z. pseudotritici* were sequenced and revealed a peculiar nucleotide diversity pattern: The genome consists of segments of high nucleotide diversity but comprising only two diverged haplotypes. The other segments comprising more than 40% of the genome are completely depleted of variation. This particular genome structure results from a cross between only two parental individuals that gave rise to a hybrid swarm that has recombined but never back-crossed to the parental species. *Z. pseudotritici* provides a unique model system to study genomics of a young hybrid species. Hence we set out to investigate patterns of selection and distribution of derived mutations by sequencing additional 22 individuals. Re-analyzing the new sequence alignment, we could confirm the diversity patterns of the genome as found among only five individuals. The sites harbouring three or four alleles represent those sites in the genome where derived mutations accumulate in the hybrid population. We assessed the site frequency spectrum to further investigate the distribution of variation in our population sample. The distribution of the allele frequencies was found to be remarkably different from the pattern in close relative species *Z. tritici* reflecting the different evolutionary histories of the species. Moreover, we assessed genome-wide signatures of positive selection by computing dN/dS ratios. Gene ontology analyses showed that 14 of the 77 positively selected genes encode secreted proteins, and are putative effector candidates involved in host-pathogen interactions. We are currently applying additional analyses to estimate age the hybridization and the amount of variation in the whole population.

Summary

Z. pseudotritici genome shows peculiar genome diversity patterns. It is a unique model system to study genomics of young hybrid species.



Gautam Shirsekar

Max Planck Institute for Developmental Biology

Co-authors

Devos, Jane; Max Planck Institute for Developmental Biology

Gonzalez Hernando, Alba; Max Planck Institute for Developmental Biology

Friedemann, Claudia; Max Planck Institute for Developmental Biology

Kersten, Sonja; Max Planck Institute for Developmental Biology

Lundberg, Derek; Max Planck Institute for Developmental Biology

Queiroz Dias, Maique; Max Planck Institute for Developmental Biology

Fenster, Charles; University of Maryland, College Park

Neher, Richard; Max Planck Institute for Developmental Biology

Weigel, Detlef; Max Planck Institute for Developmental Biology

Title

Arabidopsis-Downy Mildew in USA: A Pathosystem for Assessing Impacts of Co-evolution on Host-Pathogen Genomes

Abstract

In nature, host interactions with pathogens form an integral part of the adaptive landscape, but how they shape host genetics is poorly understood. Recent advances in genome sequencing have made in-depth studies of host-pathogen co-evolutionary interactions at population level possible, especially in model plant-pathosystem comprising *Arabidopsis thaliana* (ATH) and its oomycete pathogen *Hyaloperonospora arabidopsidis* (HPA). Introduction of ATH to N.America since ~200 years offers a host which has undergone a severe population bottleneck. Despite reduced genetic diversity, these ATH populations have managed to survive significant HPA pressure in N. America. In the present study, 32 ATH and 25 HPA populations were collected in Spring seasons of 2014-16 from nine states covering East coast, North-East and Mid-West regions of USA. Earlier reports based on SNP genotyping of a different host population collection set have indicated >50% ATH individuals belong to a lineage termed Haplogroup-1 (Hpg1). Interestingly based on RAD-Seq data, current study have shown presence of Hpg-1 individuals to the extent of 0-15% in the 2014-16 ATH populations. Although Hpg-1 is pervasive, several other host haplogroups are dominant regionally. Importantly, several admixed ATH individuals were also identified in the populations. Based on the visual observation of downy mildew and HPA sequence reads obtained by RAD-Seq approach, around 10-25% of ATH individuals in different populations were infected by HPA. Genotyping-by-sequencing approach is being employed to assess HPA population structure. Preliminary lab based screening of ATH-HPA interactions show pathogen adaptation to host haplogroups and possible lack of local adaptation. Further utilization of admixed individuals in screening coupled with detailed analysis of genomic regions that are



preferentially admixed will unravel whether HPA pressure could be a selective force behind admixture events seen in the wild.

Summary

North American Arabidopsis-Downy Mildew: a pathosystem to understand how co-evolutionary forces shape host and pathogen genomes #WPP16



Janine Haueisen

Environmental Genomics, Christian-Albrechts

Co-authors

Martinelli, Elis; Environmental Genomics, Christian-Albrechts

Grandaubert, Jonathan; Environmental Genomics, Christian-Albrechts

Stukenbrock, Eva; Environmental Genomics, Christian-Albrechts

Title

Plant-associated lifestyles and host specialization of closely related grass-colonizing fungi

Abstract

Zymoseptoria tritici (syn. *Mycosphaerella graminicola*) is a pathogen highly specialized to infect domesticated wheat in agro-ecosystems worldwide. However, *Z. tritici* possesses an amazing degree of intra-species diversity that translates into distinct infection morphologies and development of individual isolates. *Z. tritici* originated in the Middle East where also its closest relatives *Z. pseudotritici* and *Z. ardabiliae* were found. These fungi are endemic to natural grasslands in the north of Iran and have been isolated from leaves of diverse wild grasses. In contrast to *Z. tritici*, very little is known about their lifestyles and how they colonize and reproduce inside grass leaves. Certainly, due to their adaptation to different host niches, the *Zymoseptoria* species complex provides an ideal model system to study speciation and host specialization of fungal plant pathogens. We analyze and compare host infections of *Zymoseptoria* species to investigate how adaptive evolution has shaped infection programs. Leaves of different grasses were inoculated with *Zymoseptoria* spp. isolates and plant-fungus interactions studied by combining confocal microscopy and RNA-seq. Unlike *Z. tritici*, *Z. pseudotritici* and *Z. ardabiliae* are not able to infect living wheat leaves. Hyphae are arrested in the substomatal cavities and no infection symptoms develop. We analyzed transcriptome data of the three *Zymoseptoria* species on wheat to compare expression of orthologs and species-specific genes. Initial results indicate that during early wheat colonization only 5 - 10 % of the orthologous genes are differentially expressed between the species. However, we observe that *Z. pseudotritici* and *Z. ardabiliae* can develop fructifications on wheat tissue and on several other grass species when leaves are compromised or senescing. This suggests that the closely related fungi not only have specialized to different ecological niches but also might have adopted different plant-associated lifestyles.

Summary

Zymoseptoria spp. have specialized to different niches and might also have adopted different plant-associated lifestyles #pathogen #endophyt



Layla Maria Höckerstedt

University of Helsinki

Co-authors

Laine, Anna-Liisa; University of Helsinki

Title

Spatial gene flow driving natural selection of host resistance

Abstract

How resistance to disease distributes across space and time can affect fundamental components of disease evolution and epidemiology. Here, we studied the mechanisms of spatial connectivity and the coevolutionary history with a pathogen driving local adaptation among natural plant populations. We surveyed resistance patterns in a large cross-inoculation experiment and combined epidemiological data collected over 14 years. In agreement with ecological and evolutionary theory, isolated and naive *Plantago lanceolata* populations provided the highest susceptibility to *Podosphaera plantaginis* infection. The resistance increased in connected populations; yet, in contrast to isolated populations, hosts indicated no local adaptation. The sympatric pathogen strains performed higher than allopatric strains regardless of the connectivity of the host population. Our results suggest that the interaction between directional selection and gene flow may change the resistance patterns in connected populations. This finding provides evidence of gene flow into a population counteracting gene frequency changes and limiting local adaptation. Jointly, our results highlight how both spatial structure and coevolutionary history with a pathogen influence host population resistance.

Summary

Swamping genes shaking local adaptation mechanisms.



Levente Kiss

Centre for Agric. Res., Hung Acad Sci, Hungary

Co-authors

Pintye, Alexandra; Centre for Agric. Res., Hung Acad Sci, Hungary

Nemeth, Mark Z.; Centre for Agric. Res., Hung Acad Sci, Hungary

Title

How specialized are mycoparasites in a wild tritrophic pathosystem?

Abstract

The question as to why parasites remain generalist or become specialist is still little understood in evolutionary biology. We investigated this question in a wild tritrophic pathosystem consisting of *Lycium halimifolium*, a widespread ruderal solanaceous weed in Central Europe, its powdery mildew pathogen *Arthrocladiella mougeotii*, and pycnidial mycoparasites belonging to the genus *Ampelomyces* which commonly occur in *A. mougeotii* colonies covering *L. halimifolium* leaves. We isolated >150 *Ampelomyces* strains from *A. mougeotii* infecting *L. halimifolium* in different sites in Hungary, from 1990 to 2015, and genotyped these strains using 8 microsatellite markers and nrDNA ITS, ACT1, RPB1 and EukNR sequences. All the data revealed that these strains were genetically diverse; moreover, a number of *Ampelomyces* genotypes detected on *L. halimifolium* were also found in other powdery mildew species infecting different host plants. To determine whether mycoparasites belonging to different genotypes can naturally be transmitted to other powdery mildews, potted powdery mildew-infected tobacco and cucumber plants, infected with *Golovinomyces orontii* and *Podosphaera xanthii*, respectively, were used as traps for *Ampelomyces* in the vicinity of *L. halimifolium* bushes naturally infected with powdery mildew, and parasitized by *Ampelomyces* mycoparasites. A part of the trap powdery mildew colonies became parasitized by *Ampelomyces* and these strains represented some of the microsatellite genotypes naturally occurring in *A. mougeotii* on *L. halimifolium*. Therefore, *Ampelomyces* appears to be one of the rare genuine generalist parasitic fungi, able to parasitize multiple mycohosts in natural populations, and could be used as an excellent model for studying the evolution of pathogens towards a generalist rather than a host-specific strategy. This work was partly supported by a grant (NN 100415) of the Hungarian National Research, Development and Innovation Fund.

Summary

Are generalist parasites genetically differentiated? This was studied in a solanaceous weed infected with powdery mildew and mycoparasites.



Pitching on Wednesday 31.8. 14:30- 14.45

Beate Proske

Stockholm University

Co-authors

Tack, Ayco; Stockholm University

Ehrlén, Johan; Stockholm University

Title

Spatial and temporal dynamics of the smut fungus *Urocystis primulicola* on the island of Öland, Sweden

Abstract

Ovary smut fungi are a broad group of fungi infecting a plants reproductive organs, resulting in the abortion of the fruit and development of smut spores that spread the disease. While infections by smut fungi can lead to major financial losses in agricultural crops, we know little about the spatial and temporal dynamics of smut fungi in natural systems. Here, we aimed to investigate (1) the abundance and spatial distribution and (2) the temporal consistency of infection in natural populations of the wild perennial *Primula farinosa*. For this, we focused on *Urocystis primulicola*, which is a smut fungus found on the bird s eye primrose *P. farinosa*. Infections can be easily identified in summer when the host has developed mature fruits, while infected fruits contain brown smut spores instead of seeds and appear swollen compared to healthy fruits. The conidial stage described in the older literature could not yet be identified in field. In July 2015 we visited 78 known *P. farinosa* populations on the Great Alvar on Öland and assessed infections of *U. primulicola* in the fruits. 24 of these *P. farinosa* populations have been monitored since 2007 on a yearly basis in the northern part of the Alvar. We present the current and past spatial distribution and temporal dynamics of *U. primulicola* infections on the Great Alvar.

Summary

Poster on the distribution of a rare pathogen on #Primula_farinosa on Öland Sweden #WPP2016 @DEEP_Sthlm_Uni @beate_proske @AycoTack



Elise Vaumourin

University of Helsinki

Co-authors

Elina, Numminen; University of Helsinki

Lucie, Poulin; University of Helsinki

Anna-Liisa, Laine; University of Helsinki

Title

Contrasting pathogen life-history strategies revealed by trade-offs

Abstract

Understanding the mechanisms by which diversity is maintained in pathogen populations is critical for predicting where pathogens will occur and how risk of infection evolves. Life-history trade-offs have been proposed as a hypothesis for explaining long-term maintenance of variation in pathogen populations, yet the empirical evidence supporting trade-offs has remained mixed. This is in part due to the challenges of documenting successive pathogen life-history stages in many pathosystems. Here, we focus on the fungal pathogen *Podosphaera plantaginis* infecting host plant *Plantago lanceolata* to study life-history traits and possible trade-offs in seven pathogen strains throughout their full life-cycle. We examine key traits in the pathogen's asexual and sexual stages. We find significant variation among the seven strains in the life-history stages that constitute the infection cycle. Moreover, we find positive correlations among the life-history traits – initially fast strains tend to be fast also in the subsequent life-history stages and they have higher fecundity. However, we find that rapid growth, early maturity, and many sexual resting structures is traded off with low quality offspring, while slower strains produce higher quality offspring. Interestingly, strains that represent two of the most common multi-locus genotypes in the natural pathogen metapopulation exhibit contrasting life-history strategies, suggesting that there are different, but equally successful, ways to persist across space and time. These different life-history strategies are likely to promote the maintenance of variation in wild pathogen populations that are subject to spatial and temporal variation in their environments.



Juliana Benevenuto

University of São Paulo (USP), Piracicaba, Brazil

Co-authors

Croll, Daniel; ETH Zurich, Zurich, Switzerland

McDonald, Bruce A.; ETH Zurich, Zurich, Switzerland

Monteiro-Vitorello, Claudia B.; University of São Paulo (USP), Piracicaba, Brazil

Title

The genetic basis of host specialization in smut fungi

Abstract

The evolution of host specialization is a key step in the emergence of new pathogens. However, the genetic basis of host specialization is poorly understood. Smut fungi are biotrophic pathogens that infect many Poaceae hosts, including agriculturally important crop plants, such as cereals, sugarcane, and forage grasses. Despite being phylogenetically close, species of smut fungi have distinct and narrow host ranges. Pathogen species also differ in their mode of plant colonization and symptoms development. Smut fungi are thought to become specialized following host jumps, as the host and pathogen phylogenies show incongruent topologies. The estimated divergence times of smut fungi are neither associated with host speciation nor with the domestication of individual crop species. Hence, we aim to identify the genetic basis of host specialization using comparative genomics analyses. We analyzed eight species of smut fungi isolated from maize, barley, sugarcane, wheat, oats, *Zizania latifolia* (a wild-rice relative), and *Persicaria* sp. (a dicot plant). We additionally assembled the genomes of *Ustilago hordei* isolated from oats and *U. tritici* isolated from wheat. We will establish an accurate phylogenomic tree using concatenation of single-copy orthologous genes in order to improve divergence time estimates among smut fungi. Then we will perform analyses of selection on orthologous genes as we predict that positively selected genes will have significantly contributed to host specialization. We are particularly interested in genes encoding predicted effectors as drivers of host adaptation and specialization.

Summary

Using comparative genomics approaches to further understand the genetic mechanisms that drive host specialization of smut fungi.



Katherine Hayden

Title

Differential expression associated with natural and phosphite-induced resistance to *P. ramorum* in tanoak

Abstract

Tanoak (*Notholithocarpus densiflorus*) is a culturally and ecologically important, and is the most susceptible US host to *Phytophthora ramorum* (sudden oak death), but has not been cultivated commercially. Host thinning and phosphite treatment are currently available as control strategies, and some family groups which carry a resistant phenotype have been identified. To better understand and predict phosphite responsiveness and “natural” resistance (untreated with phosphite), we first identified open-pollinated family groups that carried resistance in up to 25% of offspring. Multiple inoculations were performed on previously unchallenged members of these families, half of which had been treated with phosphites. We examined gene expression before inoculation and during the disease response in phosphite-treated, resistant hosts (in which the treatment worked as expected); in phosphite-treated but susceptible hosts (in which phosphite was not effective nor was there innate resistance); and in untreated susceptible and resistant trees. *P. ramorum* sequences were detected in most susceptible and some resistant phenotypes after inoculation, but no significant patterns of differential expression were detected in the pathogen. In the host, tanoak families differed in the presence of natural resistance and in the effectiveness of phosphite treatment. There were 9705 genes that were differentially expressed between untreated resistant trees and untreated susceptible trees. In contrast, there were 7 genes differentially expressed in the same comparison between susceptible and resistant phosphite-treated trees. Of 80 tanoak gene regions of interest which were validated using expression probes in unrelated trees, 12 differential expression patterns were supported. These arose from only two categories of pairwise comparisons: between phosphite-resistant and untreated-resistant trees at 7 dpi, and between untreated resistant and untreated susceptible trees prior to inoculation. Our results demonstrate pre-inoculation differences in expression in resistant phenotypes, post-inoculation differences of expression associated with phosphite treatment and response, and an intriguing lack of difference in gene



Lucie Poulin

Metapopulation Research Center, Helsinki, Finland

Co-authors

Safdari, Pehzman; Metapopulation Research Center, Helsinki, Finland

Salojärvi, Jarkko; Bioinformatics for molecular biology, Helsinki, Fi

Laine, Anna-Liisa; Metapopulation Research Center, Helsinki, Finland

Title

A genomic approach to unravel plant-pathogen coevolution in the wild

Abstract

Since the beginning of plant domestication plant diseases have caused concern because of their ability to considerably reduce harvest yields. Given the globally increasing food demand, there is more than ever a need to find durable ways of battling plant disease. The success of pathogens is best explained by their tremendous evolutionary potential that enables them to quickly respond to new host resistances. Theoretically antagonistic survival battle between hosts and their pathogens has been proposed to lead to coevolutionary arms race with balancing selection maintaining variation in both host resistance and pathogen infectivity. Despite considerable efforts, the genetic basis of infectivity traits in pathogens is typically poorly understood. To date, effectors (proteins expressed by plant pathogens to aid infection) have become the best described molecular underpinning of infectivity. The main goal of our study is to find a set of candidate effector proteins responsible for different infectivity levels and investigate their natural diversity in the fungal pathogen *Podosphaera plantaginis* on *Plantago lanceolata* hosts occurring in the Åland archipelago. For that purpose, the genome and transcriptome of two well characterized strains *P. plantaginis* have been sequenced and will be subsequently used for genome annotation. Comparative analyses will provide sufficient information with regard to potential effector repertoire that could be further screened on a panel of strains to unravel how these effectors vary across space and time, and how this variation links to realized epidemiological dynamics.

Summary

Candidate effector proteins responsible for different infectivity levels in a wild fungal pathogen in the Åland islands.



Michael Smith

Department of Entomology, Kansas State University

Author

Girvin, John; Department of Entomology, Kansas State University

Co-authors

Whitworth, Jeffrey; Department of Entomology, Kansas State University

Smith, Michael; Department of Entomology, Kansas State University

Title

Factors Affecting Barley Yellow Dwarf Virus and Vector Occurrence in Kansas

Abstract

Barley yellow dwarf virus (BYDV) causes consistent, significant yield loss to North American wheat. Nevertheless, factors governing the frequency of aphid vector occurrence, level of infestation, and BYDV concentration and movement are poorly understood. The bird cherry oat aphid, *Rhopalosiphum padi* (L.), is commonly associated with BYDV infection in the U. S. High Plains and a highly efficient vector of the most severe BYDV strain, BYDV-RPV (*R. padi* virus). Other common vectors include corn leaf aphid, *Rhopalosiphum maidis* L., English grain aphid, *Sitobion avenae* Fab., and greenbug, *Schizaphis graminum* Rondani. Spring sampling in ~16 mill ha of wheat in the state of Kansas in 2014 and 2015 determined *R. padi* to be predominant. *S. avenae* and *S. graminum* were rare in 2014 but their presence increased dramatically in 2015, with *S. avenae* present in 95% of samples and *S. graminum* present in 45% of samples. BYDV-RPV infection within vectors differed both within and between years. The reduced incidence of vector and BYDV-RPV in western Kansas appear to be related to the fact that sample sites occur at elevations > ~1,000 m; receive annual precipitation < ~55 cm; and have limited landscape vegetation. In contrast, eastern Kansas sampling sites occur at elevations < ~ 500 m; contain riparian and tree landscape; and receive > ~100 cm annual precipitation. Viruliferous vectors were found to be 4 times more likely to occur at eastern Kansas sites than western Kansas sites. Geospatial analyses presented will demonstrate how elevation, precipitation, soil fertility and sample site landscape contributed to BYDV-RPV and vector occurrence during the sample period.

Summary

BYDV-RPV infection and aphid vector occurrence in wheat are linked to sample site climate, landscape and geography.



Michael Smith

Department of Entomology, Kansas State University

Author

Girvin, John; Department of Entomology, Kansas State University

Co-authors

Smith, C. Michael; Department of Entomology, Kansas State University

Whitworth, Jeff; Department of Entomology, Kansas State University

Title

Effects of aphid vector, landscape, climate and geography on occurrence of Barley Yellow Dwarf Virus in Kansas wheat

Abstract

Barley yellow dwarf virus (BYDV) causes consistent, significant yield loss to North American wheat. Factors governing the frequency of aphid vector occurrence, level of infestation, and BYDV concentration and movement are poorly understood. The bird cherry oat aphid, *Rhopalosiphum padi* (L.), is commonly associated with BYDV infection in the U. S. High Plains and a highly efficient vector of the most severe strain of BYDV-RPV (*R. padi* virus). Other common vectors include corn leaf aphid, *Rhopalosiphum maidis* L., English grain aphid, *Sitobion avenae* Fab., and greenbug, *Schizaphis graminum* Rondani. Spring sampling in ~16 mill ha of wheat in the state of Kansas in 2014 and 2015 determined that *R. padi* occurred in 100% of samples in 2014 and 67% of samples in 2015. *S. avenae* and *S. graminum* were rare in 2014 samples (11% and 3%, respectively) but their presence increased dramatically in 2015, with *S. avenae* present in 95% of fields sampled and *S. graminum* present in 45% of fields sampled. The degree of BYDV-RPV infection in each vector also differed both within and between years. The reduced incidence of the three aphid vectors and BYDV-RPV in western Kansas appear to be related to increased elevation, reduced annual precipitation (~55 cm), low soil fertility and minimal sample site flora. In contrast, eastern Kansas sampling sites occur at lower elevation, contain greater vegetative landscape; are planted on richer soils; and receive substantially greater (~100 cm) annual precipitation. Viruliferous vectors were found to be 4 times more likely to occur at eastern Kansas sites than western Kansas sites. Geospatial analyses presented will demonstrate how elevation, precipitation, soil fertility and sample site landscape contributed to BYDV-RPV and vector occurrence during the sample period.

Summary

BYDV-RPV infection and aphid vector (*R. padi*, *S. avenae*, *S. graminum*) in wheat are linked to sample site climate, landscape and geography.



Miia Kauppinen

University of Oulu

Co-authors

Ruotsalainen, Anna-Liisa; University of Oulu

Schmid, Bernhard; University of Zurich

Leuchtmann, Adrian; ETH Zurich

Wäli, Piippa; University of Oulu

Title

The effects of *Epichloë festucae* endophyte on root- and leaf-associated pathogens of *Festuca rubra* in subalpine and subarctic habitats

Abstract

Systemic endophytes of cool-season grasses are a widely studied model system. However, little is known about the interactions of these endophytes with other grass-associated fungi, especially in natural habitats. Thus, we explored whether the endophyte *Epichloë festucae* affects root and leaf fungi of *Festuca rubra* in the native habitat and similar foreign habitat. We conducted a three-year field experiment with reciprocal transplantations of *F. rubra* with and without *E. festucae* endophyte among Swiss and Finnish tree-line meadows. We carried out Ion Torrent sequencing of ITS2 rDNA from the root and leaf samples in order to study the effects of the endophyte on overall fungal communities of *F. rubra*. Here we present the results with special attention to fungal pathogens. Our preliminary results show that the overall fungal communities of grass leaves and roots differed between the two countries. *Epichloë* infection had varying impacts on certain fungal pathogens (e.g. *Fusarium* and *Ilyonectria*) depending on pathogen genera and and the country of origin of grasses. These results suggest that endophyte infections can have very specific effects on grass fungal pathogens depending on plant origin, pathogen identity and environmental conditions. There are no easy generalizations to be made in this complex interaction between multiple partners.

Summary

Epichloë-endophytes have varying effects on grass fungal pathogens depending on plant origin, pathogen identity and environmental conditions.



Pezhman Safdari

University of Helsinki

Co-authors

Poulin, Lucie; University of Helsinki

Title

A genomic approach to unravel plant-pathogen coevolution in the wild

Abstract

Due to relatively well studied role of effector proteins and established bioinformatics methods to identify them in fungal genomes, effector proteins are a suitable means to investigate the genetic basis of infectivity traits in pathogens. The interaction between *P.lanceolata* and its fungal pathogen *P.plantaginis* offers unique opportunities for linking effector variation to infectivity traits and epidemiological dynamics. The key aim of this study is to identify candidate genomic loci in *P.plantaginis* associated with infectivity traits and analyze these for the presence of candidate effectors and to quantify variation at these loci from an existing extensive sample database.



Piippa R. Wäli

Department of Ecology, University of Oulu, Finland

Co-authors

Ruotsalainen, Anna-Liisa; Department of Ecology, University of Oulu, Finland

Ericson, Lars; Department of Ecology and Environmental Sciences,

Markkola, Annamari; Department of Ecology, University of Oulu, Finland

Title

Impact of moth outbreaks on *Empetrum nigrum ssp. hermaphroditum* and its fungal pathogens in mountain birch forest treeline

Abstract

Some moth species have outbreaks in Fennoscandian mountain birch forests and may cause birch deaths in large areas. Also cover of *Empetrum nigrum ssp. hermaphroditum*, the dominant species in understorey declines severely during moth outbreaks even though *Empetrum* is not actual food for moths. We followed the changes in the *Empetrum* cover during four adjacent summers after moth outbreak in Kaldoaivi wilderness area, in the northernmost Finland. In addition, we established a controlled field experiments with 1) manipulative moth outbreaks with either a) variable duration of moth outbreak or b) different moth species and different larval densities and 2) artificial defoliation and fertilization treatments. Purpose of this research was to shed light on the mechanisms causing dramatic decline in *Empetrum* with special attention to fungal pathogens of *Empetrum* during and after the moth treatments. Neither fertilization nor defoliation alone caused the severe browning of *Empetrum* detected in moth treatments. According to the experiments autumnal moth is capable of harming the *Empetrum* at lower larval densities than winter moth. Incidences of some pathogens increased in moth treatments indicating that fungal pathogens participate the browning of *Empetrum* during the moth outbreaks. Effects of different treatments on pathogen prevalence and fungal community of *Empetrum* leaves are discussed.

Summary

Moths outbreaks cause dramatic decrease of *Empetrum nigrum* in mountain birch forest. Role of fungal pathogens is *Empetrum* evaluated.



Rachel Penczykowski

University of Wisconsin-Madison

Co-authors

Laine, Anna-Liisa; University of Helsinki

Title

Specificity, durability, and epidemiological consequences of immune priming in a plant-pathogen system

Abstract

Coinfection by multiple pathogen strains can alter disease dynamics at the within-host and population level. Yet, in wild plant populations, little is known about how sequential challenge by multiple pathogen strains affects epidemiology. We tested the genetic specificity and durability of immune priming of *Plantago lanceolata* by its fungal pathogen *Podosphaera plantaginis*. In Experiment 1, four host genotypes were divided into control and primed treatments. Priming involved inoculating a single leaf with one of four pathogen strains, then sealing the inoculated (or uninfected control) leaf in a spore-proof pouch. At 4 and 8 days later, plants were challenged with all four pathogen strains. In Experiment 2, the same host genotypes were exposed to epidemics in 3 natural populations for 10 days. These plants were either healthy controls, or were infected with a pathogen strain from that population 4 or 8 days prior. After both experiments, leaves were screened for infection, and lesions were genotyped to determine which pathogen strains succeeded in infecting. Previous infection did not protect plants from subsequent pathogen attack in either experiment. Instead, prior infection of a single leaf which was sealed off to prevent transmission to other leaves on that same plant increased the probability that other leaves on the plant became infected following later inoculation or exposure to ambient pathogen strains. These results are consistent with previous work showing that coinfection by multiple pathogen strains promotes disease levels at the within-host and population levels. Forthcoming results from a SNP genotyping panel will reveal the degree of genotype specificity in priming. Because our experiment employed multiple host genotypes, we will also be able to test whether specificity in priming varies with host genetic background. Our results contribute valuable information about the epidemiological consequences of sequential infections.

Summary

Specificity, durability, and epidemiological consequences of immune priming in a wild plant-pathogen system.



Suvi Sallinen

University of Helsinki

Co-authors

Penczykowski, Rachel; University of Wisconsin-Madison

Laine, Anna-Liisa; University of Helsinki

Title

Limited role of host genetic resistance in explaining epidemiological patterns in wild plant populations

Abstract

Disease does not occur evenly across space, and not all individuals are as likely to get infected during epidemics. Instead, hot spots and cold spots of disease can be detected. Understanding these dynamics in population level is important in understanding local epidemics. Disease aggregation can be explained with environmental variation or the genetic difference of the hosts or the pathogen, or with both. To understand the role of the genetic heritage of the host in these dynamics, I performed a laboratory inoculation experiment using the interaction between *Plantago lanceolata* and *Podosphaera plantaginis*. In this study, seeds of five infected and five uninfected wild plants were collected from five Ålandic *P. lanceolata* populations. The offspring of these plants were tested against mildew isolates from the same populations. In addition, I tested these mildew isolates against five trap plant lines used in a field experiment to reveal whether the infection rate of these traps was caused by susceptibility/resistance to the isolates, or some other factors. I find no difference in susceptibility between trap plants and wild plants apart from on population. The five trap plant lines differed in their susceptibility to mildew from different populations, which suggests that the genetic heritage may partly explain the infection rates of the traps in the field experiment. Mildew isolates did not differ in their average success of causing infection on their natural hosts, but mildew isolates and plant lines varied in their ability to infect/block specific isolates/plant lines. Together with the field experiment, these results shed light on processes determining small scale disease distribution.

Summary

Genetic heritage may partly explain uneven disease distribution within a plant population.



Tomáš Koubek

Charles University in Prague

Co-authors

Chalupníková, Jana; Charles University in Prague

Koupilová, Klára; Charles University in Prague

Title

Using Ellenberg's indicator values as a proxy for effect of environment in three different pathosystems

Abstract

The traditional view of a pathosystem being influenced by three main components (host, pathogen and environment) is frequently addressed in agro-ecosystems but has been often simplified in wild plant pathosystems. Most studies show effects of host resistance and pathogen virulence and their spatial distribution but the role of environment is either taken as unimportant or hard to measure. However the variation in prevalence and incidence of disease in populations is often too large to be attributed only to the first two factors. Easy to obtain environmental data might give us some clues about the factors in play and prepare the way for targeted experiments. We gathered population data on 3 fairly different pathosystems (Falcaria-rust, Impatiens-powdery mildew and Dianthus-Microbotryum) along with vegetation data. The individual plant presence-absence data can be used to compute Ellenberg's indicator values (EIVs) that are frequently used as proxies for environmental factors namely temperature, light, soil pH, nutrients and moisture. Our results suggest that of all the EIVs, those for light and moisture tend to correlate with prevalence and incidence most often; EIV for soil reaction is also sometimes significant. The direction of the effect can be different for different pathosystems though. The prevalence of the rust on Falcaria is increased in populations with higher soil pH and moisture this might be connected to better survival and relict character of the calcareous grassland populations that are more infected. In the flower smut-Dianthus system the EIVs are not significant, only populations with less light tend to be little more infected. The mildew-Impatiens system is the most interesting with incidence influenced by light, moisture and soil pH. However, in all of the studies, EIVs are weaker predictors than population characteristics and configuration. The causes of the correlations are speculative but might still give us some insight into the systems.

Summary

The effect of environment in wild plant pathosystems can be detected using Ellenberg indicator numbers.



Evsey Kosman

ICCI, Tel Aviv University, Israel

Co-authors

Gregorius, Hans-Rolf; University of Gottingen, Germany

Scheiner, Samuel M.; Division of Environmental Biology, NSF, USA

Title

Dispersion, Diversity and Decomposing Functional Variability in Communities and Populations

Abstract

Biological variation is generally measured by counting distinct types observed (e.g. species in a community, geno-, pheno-, chemo-, pathotypes in a population, behavioral modes, cells, processes etc.) or/and by assessment dissimilarities among the types. These two perceptions express different aspects of variability – diversity and dispersion, respectively, though they are usually not distinguished. We suggest new approaches to measuring functional variability, which reflect the functional role of species within a community, geno- or phenotypes within a population etc., based on individual trait profiles and incorporating both the diversity and dispersion (distinctiveness) characteristics. The diversity component is expressed as effective number of types (n_e) generated from the corresponding dissimilarity matrix (Hill numbers) or dispersion measure, while the distinctiveness (d_e) is a kind of average dissimilarity between types. New metrics of functional variability can also be expressed in terms of richness (n), distinctiveness and functional evenness ($e = n_e/n$) as $1+(n-1) \times e \times d_e$, and may and may not include frequency (relative abundance) of types data. These metrics measure the effective number of functionally-distinct types and range between 1 and n . When a hierarchical structure is considered (e.g., spatial - communities within landscapes, or temporal – annual populations within a time interval), our metrics can be decomposed into parts within and among ranked subunits. Standard methods of diversity partition aimed at calculating variability among subunits (β -diversity) as a derivative (additive or multiplicative) of average variability within subunits (α -diversity) and total variability within the entire set of individuals (γ -diversity). However, those methods are incorrect for hierarchical decomposition of functional variability. Our method starts with independent measuring α - and β -components and derives a measure of total functional variability as $\gamma = \alpha \times \beta$.

Summary

New metrics of functional variability are expressed in terms of richness, distinctiveness and evenness, and allow hierarchical decomposition



Participants

Janis	Antonovics	ja8n@virginia.edu
Juliana	Benevenuto	julianaxbenevenuto@gmail.com
Nilsa	Bosque-Perez	nbosque@uidaho.edu
Emme	Bruns	elb5m@virginia.edu
Jeremy	Burdon	Jeremy.Burdon@csiro.au
Marie-Laure	Desprez-Loustau	loustau@bordeaux.inra.fr
Jenalle	Eck	eck.34@osu.edu
Pascal	Frey	pascal.frey@nancy.inra.fr
Oliver	Furzer	oliver.furzer@sainsbury-laboratory.ac.uk
Gregory	Gilbert	ggilbert@ucsc.edu
Fletcher	Halliday	fh@live.unc.edu
Janine	Haueisen	jhaueisen@bot.uni-kiel.de
Katherine	Hayden	k.hayden@rbge.ac.uk
Marjo	Helander	helander@utu.fi
Katy	Holub	ksholub@googlemail.com
Eric	Holub	Eric.Holub@warwick.ac.uk
Michael	Hood	mhood@amherst.edu
Pauliina	Hyttinen	pauliina.hyttinen@helsinki.fi
Layla	Höckerstedt	layla.hockerstedt@helsinki.fi
Tove H.	Jorgensen	tove.jorgensen@bios.au.dk
Agathe	Jouet	agathe.jouet@sainsbury-laboratory.ac.uk
Miia	Kauppinen	mii.kauppinen@oulu.fi
Levente	Kiss	kiss.levente@agrar.mta.hu
Evsey	Kosman	kosman@post.tau.ac.il
Tomáa	Koubek	tomas.koubek@gmail.com
Anna-Liisa	Laine	anna-liisa.laine@helsinki.fi
Åsa	Lankinen	asa.lankinen@slu.se
Ales	Lebeda	ales.lebeda@upol.cz
Laura	Masini	laura.masini@slu.se
Bruce	McDonald	bruce.mcdonald@usys.ethz.ch
Mark	McMullan	mark.mcmullan@tgac.ac.uk
Alexey	Mikaberidze	alexey.mikaberidze@env.ethz.ch
Erin	Mordecai	emordeca@stanford.edu
Hanna	Märkle	hanna.maerke@tum.de
CLAIRE	NEEMA	claire.neema@supagro.fr
Etsuko	Nonaka	etsuko.nonaka@helsinki.fi
Elina	Numminen	elina.numminen@helsinki.fi
Ezgi	Ozkurt	ozkurt@evolbio.mpg.de
Steven	Parratt	steven.parratt@helsinki.fi
Rachel	Penczykowski	mpencykows@wisc.edu
antoine	persoons	antoine.persoons@tgac.ac.uk
Lucie	Poulin	lucie.poulin@helsinki.fi
Alison	Power	agp4@cornell.edu
Beate	Proske	beate.proske@su.se
Krista	Raveala	krista.raveala@helsinki.fi
Cécile	Robin	robin@bordeaux.inra.fr
Laura	Rose	laura.rose@uni-duesseldorf.de
Philippe	Roumagnac	philippe.roumagnac@cirad.fr
Pezhman	Safdari	pezhman.safdari@helsinki.fi
Kari	Saikkonen	kari.saikkonen@luke.fi



Suvi	Sallinen	suvi.sallinen@helsinki.fi
Torsti	Schulz	torsti.schulz@helsinki.fi
Michael	Shaw	m.w.shaw@reading.ac.uk
Gautam	Shirsekar	gshirsekar@tuebingen.mpg.de
C. Michael	Smith	cmsmith@ksu.edu
Samuel	Soubeyrand	Samuel.Soubeyrand@avignon.inra.fr
Remco	Stam	stam@wzw.tum.de
Eva	Stukenbrock	estukenbrock@bot.uni-kiel.de
Ayco	Tack	ayco.tack@su.se
John	Walsh	john.walsh@warwick.ac.uk
Ben	Watkinson-Powell	bmw45@cam.ac.uk
Elise	Vaumourin	elise.vaumourin@helsinki.fi
Detlef	Weigel	weigel@tue.mpg.de
Isabella	Weilbacher	isabella.m.weilbacher@student.jyu.fi
Piippa	Wäli	piippa.wali@oulu.fi
Pauliina	Wäli	pauliina.wali@oulu.fi