



Sciences biologiques,
Écologie et Environnement
**CONFÉRENCES
JACQUES-MONOD**



Roscoff (France), 6-10 septembre 2014

**Les maladies infectieuses comme moteur de l'évolution :
les défis à venir**

Infectious diseases as drivers of evolution: the challenges ahead

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Rapport sur la Conférence

Conference Report

Report

In September 2011, a Jacques Monod Conference entitled “Coevolutionary arms race between parasite virulence and host immune defence: challenges from the state of the art research“ was held in Roscoff, organized by Gabriele Sorci (President) and Manfred Milinski (Vice-President). This conference was a big success and the participants voted in favour of a follow-up conference. Ana Rivero was elected as the new Vice-President. The follow-up conference took place in Roscoff from 6-10 September 2011. This document summarizes the key issues of the 2014 JMC.

Part 1: Programme overview

According to the original proposal we had four sessions:

- *Session I: The ever-changing diversity of infectious diseases as a complex challenge for host evolution /La diversification incessante des maladies infectieuses comme challenge à l'évolution de l'hôte*
- *Session II: Host diversity through standing genetic variation as an evolutionary response to infection / Variabilité génétique et diversité d'hôtes comme réponse évolutive aux infections*
- *Session III : Phenotypic plasticity both as a host response to infection and as a parasite strategy /La plasticité phénotypique : à la fois réponse de l'hôtes à l'infection et stratégie parasitaire*
- *Session IV : The Red Queen's moving equilibrium – is it inevitable? /L'équilibre instable de la Reine Rouge - est-il inévitable ?*

For the poster sessions, we used an open format, i.e. we did not allocate posters to sessions. There were 2 sequential poster sessions (on Sunday and on Monday), each lasting ca. 2 hours, with a total of 68 posters.

Part 2: Participants

The conference encountered a big success. All invited speakers (without exception) enthusiastically accepted our invitation. We were even approached by several senior level scientists who had heard about the conference through the grapevine, asking about the possibility of obtaining an invitation.

We had 90 external applications(for a maximum of 85 slots) coming from 12 different countries. Many of these applications came from senior level researchers.

Invited speakers by session.

We sent 30 invitations. Six of the invited speakers had to cancel for personal reasons: only two of them (Marlene Zuk, Curt Lively) could be replaced, the other four (Sarah Reece, Angus Buckling, Troy Day and Mike Siva-Jothy) cancelled a few days before the conference and the decision was made not to replace them but to allot more time for short (contributed talks), and for discussion.

In the end we had 26 invited speaker contributions. Each invited speaker gave a 30 minute presentation about her/his work.

Session	Speaker	Gender	Institution	Country
1	Joanne Webster	f	Imperial College London	UK
1	Andy Dobson	m	Princeton University	USA
1	Paul Schmid-Hempel	m	ETH Zurich	Switzerland
1	Samuel Alizon	m	CNRS Montpellier	France
1	Karen McCoy	f	CNRS Montpellier	France
2	Scott Edwards	m	Harvard University	USA
2	Camille Bonneaud	f	University of Exeter	UK
2	Nathalie Charbonnel	f	INRA Montpellier	France
2	Manfred Milinski	m	Max Planck Institute Ploen	Germany
2	Daniel Bolnick	m	University of Texas Austin	USA
2	Brian Lazzaro	m	Cornell University	USA
2	Yannick Moret	m	CNRS Dijon	France
3	Christoph Grunau	m	University of Perpignan	France
3	Danid Schneider	m	Stanford University	USA
3	Andrea Graham	f	Princeton University	USA
3	Gabriele Sorci	m	CNRS Dijon	France
3	Tatiana Giraud	f	CNRS Paris-Sud	France
3	Ana Rivero	f	CNRS Montpellier	France
3	Sylvain Gandon	m	CNRS Montpellier	France
3	Julien Viraldi	m	CNRS Villeurbanne	France
4	Dieter Ebert	m	University of Basel	Switzerland
4	Christophe Eizaguirre	m	Queen Mary University London	UK
4	Britt Koskella	f	University of Exeter	UK
4	Sunetra Gupta	f	Oxford University	UK
4	Mike Boots	m	University of Exeter	UK
4	Hinrich Schulenburg	m	CAU University Kiel	Germany

- Nine out of 26 invited speakers (35%) were females. This is lower than our original target and was due to the cancellation of two female invited speakers (Sarah Reece, Marlene Zuk)
- Nine of the 26 invited speakers (35%) had been at the previous JMC (Sept. 2011).
- Ten invited speakers were from France, 10 from Europe (outside France) and 6 were from outside Europe.

Non-invited contributions

There were a total of 85 (non-invited) contributions. Of those, 29 were from France, 44 were from Europe and 12 were from outside Europe. Roughly a third of these contributions (33%) were from PhD students, the rest were either post-docs or scientists in tenured (and even senior) positions. Slightly over half (55%) of these contributions came from female scientists, a clear indication that we should strive towards a more balanced sex ratio in the invited speaker list for the next conference.

15 of the non-invited contributors were invited to give a short (15 min) talk (see below). We were faced with tough choices when it came to allocate the short talk slots because the average quality of the posters was extremely high.

One of the participants was Holger Breithaupt, the Editor responsible for the Science and Society section of *EMBO Reports*.

Contributed talks by session

The following 15 people were selected based on their abstracts to give 15 minute presentations:

Session	Speaker	Gender	Institution	Country
1	Eleanor Watkins	f	Oxford University	UK
1	Anssi Karvonen	m	Jyväskylä University	Finland
1	Rafal Mostowy	m	Imperial College London	UK
1	David Duneau	m	Cornell University	USA
1	Teppo Hiltunen	m	University of Helsinki	Finland
1	Anna Liisa Laine	f	University of Helsinki	Finland
1	Matthew Aardema	m	Princeton University	USA
2	Lars Råberg	m	Lund University	Sweden
2	Helena Westerdahl	f	Lund University	Sweden
2	Tobias Lenz	m	Harvard University	USA
2	Ann Tate	f	Princeton University	USA
2	Seth Barribeau	m	University of Zurich	Switzerland
2	Edze Westra	m	University of Exeter	UK
3	Nicole Mideo	f	University of Toronto	Canada
3	Thierry Rigaud	m	CNRS Dijon	France

Part 3: Scientific program

Virtually no animals and plants would have evolved had they not been forced to reproduce sexually to offset the negative effects of infectious diseases. In a world without infectious diseases, asexual reproduction would, indeed, prevail. However, with asexual reproduction there is no evolutionary improvement, only genetic degeneration through fatal mutation accumulation. Host parasite-interactions and coevolution are now accepted as the basis of our understanding of animal and plant evolution. Participants to the JMC "Infection Diseases as Drivers of Evolution: The Challenges Ahead" discussed some of the puzzling gaps and burning questions in our knowledge of how pathogens and hosts drive each other's evolution.

Infectious diseases are always ahead in the race with their hosts. There are recently discovered new kinds of genetic devices with potential to create novel virulence mechanisms and to drive the evolution of pathogen diversity. The potential for variation in the expression levels of virulence genes and to what extent such expression levels can be transmitted between generations is a topic of hot debate. Hosts cannot predict what direction infectious diseases will take in the future. The way out of this dilemma may be the evolution and maintenance of a high standing genetic variation in defence genes. Immunogenes are, indeed, usually highly polymorphic. How can such a polymorphism evolve and be maintained? Both theoretical and empirical approaches are essential to solve this puzzle.

Host phenotypes are drastically and rapidly altered by the presence of a pathogen. These host changes may be host driven and aimed at compensating or minimizing the negative effects of the parasite, or parasite driven and be a manipulative strategy of the parasite aimed at maximizing its own survival and transmission. Although establishing the adaptive nature of the phenotypic change is still a challenge, recent advances in the field of epigenetics are providing a mechanistic basis for how such host phenotypic plasticity occurs. The Red Queen hypothesis predicts a co-evolutionary arms race between hosts and their parasites. To avoid losing the race, hosts have to keep renewing their resistance or tolerance mechanisms, which requires that the genes involved are highly polymorphic. Inversely, infectious diseases have to keep diversifying to avoid detection. Support for the Red Queen hypothesis comes from a

variety of sources, many of which were covered in our conference.

Session I The ever-changing diversity of infectious diseases as a complex challenge for host evolution /La diversification incessante des maladies infectieuses comme challenge à l'évolution de l'hôte

The first session discussed parasitic diversity and variability as a very complex selection regime that host counter-adaptations have to track. Joanne Webster focussed on evolving and emerging zoonotic schistosome species, discussing the implications of such dynamics on host morbidity, transmission potential and control. Andy Dobson analysed the fast evolutionary dynamics and host responses to a new avian pathogen. Paul Schmid-Hempel addressed the question of to what extent microbiota, infectious disease agents, and the host genetic background interact and evolve. Multiple infections are the rule rather than the exception and thus a great challenge for any immune system. Samuel Alizon stressed the differences between co-infections by closely related or by unrelated parasite strains. Karen McCoy showed that host characteristics at the individual, population and community scales determine the evolutionary pathway of a parasite: the evolution of vector host races can cascade down to alter the evolutionary pathway of the microparasites they harbour.

Session II Host diversity through standing genetic variation as an evolutionary response to infection / Variabilité génétique et diversité d'hôtes comme réponse évolutive aux infections

This session was devoted to host plasticity through standing genetic variation, i.e. polymorphic immune genes that allow for fast host responses to quickly changing infectious diseases at the population level. Scott Edwards demonstrated the prominent role for standing variation in the rapid adaptation of House Finches to a novel bacterial pathogen *Mycoplasma gallisepticum* in North America. Camille Bonneaud continued by showing how fast resistance evolved in the finch population. She demonstrated also the evolution of virulence in the bacterial pathogen over the course of the new invasion. Nathalie Charbonnel presented another example of immunogene variability at the population level. She investigated the interplay between immune gene polymorphism in bank vole populations and the epidemiology of Puumala hantavirus, the agent of nephropathia epidemica in humans. Humans and other vertebrates use olfactory cues by which potential partners reveal their mix of polymorphic MHC immunogenes for mate choice. Choice aims at an optimal MHC diversity in the offspring which provides a maximal resistance against a variety of pathogens as pointed out by Manfred Milinski. The natural odour signal consists of 9mer peptides transported by the sender's MHC molecules. Dan Bolnick showed that a stickleback's individual set of MHC immunogenes determines both its (beneficial)symbiotic gut microbe community and its (harmful) parasitic helminth community composition. The long-standing puzzle of individual gut microbe composition finds its explanation in the polymorphic MHC immunogenes. Brian Lazzaro suggested that balancing selection driven by changing parasite pressure led to convergent evolution of antimicrobial peptides, which he argues evolve under a "trench warfare model" with selection pressures fluctuating over time and space. Yannick Moret pointed out that trans-generational immune priming corresponds to a plastic change in levels of immune defence of organisms as a result of the immunological experience of their parents, which is adaptive when offspring are exposed to the same parasites their parents suffered from.

Session III *Phenotypic plasticity both as a host response to infection and as a parasite strategy /La plasticité phénotypique : à la fois réponse de l'hôtes à l'infection et stratégie parasitaire*

This session was devoted to cases where both the parasite strategy and the host response are plastic. Christoph Grunau argued that including epigenetic inheritance into the theory of adaptation explains seemingly contradictory findings. He supports this idea by using recent results from the human body fluke *Schistosoma mansoni* that demonstrate that adaptive phenotypic changes can be entirely based on epigenetic modifications. David Schneider presented a model describing bacterial growth, immune induction and damage production as having sigmoid kinetics. The model can be applied from insects to mice and humans and shows that resilient hosts trace a looping pattern through a multidimensional disease space before they return to health. Andrea Graham studied the within-host dynamics of optimal defence: how infectious diseases drive the evolution of immune systems, which arguably are among the ultimate examples of phenotypically plastic traits. Using the intestinal nematode *Heligmosomoides polygyrus* and different strains of inbred mice, Gabriele Sorci studied the delicate balance between a too weak and too strong inflammatory response as a host response to invading pathogens. An overzealous response may incur devastating effects on host homeostasis and fitness. Tatiana Giraud presented one of the few studies to have empirically verified theoretical expectations for castrating parasites, showing in particular that castrated hosts live longer, and that multiple infections increase virulence, here in term of non-recovery, resources uptake and host castration. Coinfections are particularly relevant when the host is a vector of diseases, because multiple infections can have drastic consequences for parasite transmission at both the ecological and evolutionary time scales. Ana Rivero presented such consequences for malaria transmission from *Plasmodium-Wolbachia* coinfections in mosquitoes. She showed that *Wolbachia* infected mosquitoes are better vectors of malaria than *Wolbachia*-free ones which may hamper the prospects for using *Wolbachia* as a disease control method. Sylvain Gandon used evolutionary epidemiology theory to predict how malaria may manipulate the host choice behaviour of mosquitoes, invest in dormancy strategies in seasonal environments and respond plastically to the presence of mosquitoes. Julien Varaldi discussed how inherited viruses can manipulate the behaviour of their parasitoid host to induce super parasitism. Only the virus directly benefits from this behaviour, being ahead in the race.

Session IV *The Red Queen's moving equilibrium – is it inevitable? /L'équilibre instable de la Reine Rouge - est-il inévitable ?*

The Red Queen told Alice in Wonderland «Now, here, you see, it takes all the running you can do, to keep in the same place» (*Through the Looking Glass*, Lewis Carroll, 1871). Both parasites and hosts need to keep running to avoid losing the (arms) race. Dieter Ebert studied the population genetics of red queen dynamics by analysing the genetic architecture of host-parasite interactions to test predictions and assumptions of host-parasite coevolution. Christophe Eizaguirre showed that the host-parasite arms race can end in local adaptation of either one or both partners having important consequences for species formation. For example, parasites can exert diverging selection on host populations utilizing different niches until new species are formed. The dynamical changes in bacterial abundance and densities within eukaryotic hosts over time are an important factor for the understanding of both disease progression over time and stability of the host-associated microbiota. Britt Koskella studied the potential role that bacteriophage viruses might play in shaping these communities over both ecological and evolutionary timescales. Sunetra Gupta pointed to one of the greatest challenges to the control of infectious diseases – the degree of antigenic diversity exhibited by many pathogen populations. She presented a multi-locus model for pathogen evolution that

resolves the paradox that many of these populations exist, either stably or unstably, as discrete antigenic types, which may then circulate as independently transmitted strains with their own particular virulence characteristics. Mike Boots, another theorist, discussed a series of models that examine how epidemiological feedbacks and the characteristics of the interaction between host types and parasites strains determine the coevolution of host-parasite diversity. The theory shows that epidemiological feedbacks can generate diversity, but this is usually limited to dimorphism. Finally, Hinrich Schulenburg showed that antagonistic interactions between host (*C. elegans*) and pathogen (*Bacillus thuringiensis*) can produce very high selection intensities. In experiments coevolution caused multiple phenotypic changes, increased genetic diversity and increased local adaptation in both antagonists consistent with negative frequency-dependent dynamics.

Part 4: Final comments and future outlook

This conference was planned to support excellent and innovative research in the field of infectious diseases as drivers of evolution, with a special focus on parasite exploitation strategies but also as a consequence on host defences as counter-strategies. One of the goals of this conference was to bridge the gap between functional evolutionary ecological approaches and genetic / epigenetic research. We also wished to bring together students with various backgrounds to induce discussion and potentially collaboration among them. We believe that these goals were achieved. Undoubtedly, the strength of the conference was to see that attendees indeed had very fruitful discussions and interactions. The conference also allowed younger people to obtain an overview over this rapidly growing field.

Depicted by the cutting edge and largely unpublished research presented at the conference, a conceptual framework is beginning to emerge which allows us to better understand the way in which parasites and hosts drive each other's evolution.

In the next few years recent advances in the genotyping, transcriptomic, and bioinformatic technology are likely to drive a leap forward in the field of host-parasite interactions by allowing to address long standing questions in the field such as whether host genetic diversity affects disease spread, or how are host resistance polymorphisms maintained in diffusely interacting (as opposed to tightly coevolving) host-parasite combinations. We also expect the field of epigenetics, still largely confined to particular fields of biology, to be widely applied to the field of host-parasite interactions, providing key insights about the role of epigenetic modifications such as DNA methylation and histone de-acetylation as a source of fast-acting and readily available non-genetic variation that can be directly shaped by pathogen pressure.

Another major topic, which is likely to come up in the near future, is the role of biotic and abiotic (habitat fragmentation, global change) factors in driving infectious disease epidemiology and evolution. In particular, many studies are escaping the "one-host one-parasite" paradigm to acknowledge the complexity of multiple parasites per host, and multiple hosts per parasite. This view is being further widened in efforts to adopt a community ecology approach that acknowledges that host-parasite interactions are embedded in a larger food web that includes third party actors such as host plants, or predators.

Finally, it is now clear that microbiota play a key role in the susceptibility of hosts and vectors to pathogens. In the next few years we hope we will advance in our understanding of how important this may be relative to host genetics and the environment.

What next?

At the General Discussion, which despite taking place on the last day and after the conference dinner was attended by virtually all participants, there was an unanimous decision to apply for a follow up conference in 2017. One of the issues highlighted by all participants is that these Jacques Monod Conferences (this was the 4th such JMCs on the ecology and evolution of host-parasite interactions, the previous ones having taken place in 2004, 2007 and 2011) are **unique in the field**. Indeed no other conference in Europe or North America spans the whole field of host-parasite interactions. The breadth of approaches (molecular, phenotypic, genetic, épigenetic, theoretical), model systems (everything from bacteria-virus to human-helminth interactions) and subjects (from plant-pathogen coevolution to evolutionary medicine) provide a unique snapshot of the latest advances in the field as a whole that cannot be found anywhere else.

Consequently, it was agreed that the current Vice-President (Ana Rivero, CNRS - Montpellier) will take over the presidency for the next conference and the participants unanimously elected Andrea Graham (Princeton, USA) to act as the next vice-president. The complementary profiles of Rivero (www.anarivero.fr) and Graham (<http://algraham.princeton.edu/>) will be a great asset for the organisation of the next conference and are likely to have as enthusiastic a reception as that of previous conferences.

Annex 1: Detailed program

Sunday, September 7 / *Dimanche 7 Septembre*

08:30 – 08:45: Manfred MILINSKI (*Ploen, Germany*) and **Ana RIVERO** (*Montpellier, France*)

Welcome and opening / *Accueil et ouverture*

SESSION I—The ever-changing diversity of infectious diseases as a complex challenge for host evolution / *La diversification incessante des maladies infectieuses comme challenge à l'évolution de l'hôte*

CHAIRPERSON: Manfred Milinski

08:45 – 09:15 Joanne WEBSTER (*London, United Kingdom*)

Schistosome evolution in a changing world / *Evolution des schistosomes dans un monde changeant*

09:15 - 09:45 Andy DOBSON (*Princeton, U.S.A.*)

The eye of the finch: evolutionary dynamics and host responses of an emerging avian pathogen /

L'oeil du pinson: dynamique évolutive et réponses de l'hôte chez un agent pathogène aviaire émergent

09:45 – 10:15 Paul SCHMID-HEMPEL (*Zürich, Switzerland*)

Infection, expression, microbiota - the mechanics and evolution of specificity / *Infection, expression, microbiome - mécanique et évolution de la spécificité*

10:15 – 10:30 Eleanor WATKINS (*Oxford, United Kingdom*)

Multivalent pneumococcal vaccines can increase the transmissibility and virulence of non-vaccine strains / *Les vaccins anti-pneumococciques polyvalents peuvent augmenter la transmissibilité et la virulence des souches non vaccinales*

10:30-11:00 Coffee break – *Pause café*

11:00 – 11:30 Samuel ALIZON (*Montpellier, France*)

Multiple infections and virulence evolution / *Infections multiples et évolution de la virulence*

11:30 – 11:45 Anssi KARVONEN (*Jyväskylä, Finland*)

Interactions among co-infecting bacterial strains and fluke genotypes shape disease virulence / *Effet des co-infections entre souches bactériennes et genotypes de la douve sur la virulence.*

11:45 – 12:00 Raffal MOSTOWY (*London, United Kingdom*)

The impact of recombination on the emergence of novel pneumococcal serotypes / *L'impact de la recombinaison sur l'émergence de nouveaux sérotypes pneumococciques*

12:00 – 12:15 David DUNEAU (*Ithaca, U.S.A*)

Host sexual dimorphism and its consequences for parasite evolution / *Dimorphisme sexuel de l'hôte et conséquences pour l'évolution des parasites*

12:15 – 12:30 Teppo HILTUNEN (*Helsinki, Finland*)

The key role of viral parasites on eco-evolutionary dynamics in toxic cyanobacterial populations / *Le rôle des parasites viraux sur la dynamique éco-évolutive des populations de cyanobactéries toxiques*

12 :30-12 :45 Anna-Liisa LAINE (*Helsinki, Finland*)

Ecological and evolutionary effects of fragmentation on infectious disease dynamics / *Effets écologiques et évolutifs de la fragmentation sur la dynamique des maladies infectieuses*

13:00-14:15 Lunch at the Conference Centre (Gulf Stream Hotel) / Déjeuner au Centre de Conférence (Hôtel Gulf Stream)

CHAIRPERSON: Ana Rivero

14:30 – 15:00 Karen MCCOY (*Montpellier, France*)

Hosts as drivers of parasite diversity: host specialization and the circulation of vector borne disease agents / *Hôtes en tant que moteurs de la diversité des parasites: spécialisation de l'hôte et la circulation de pathogènes à transmission vectorielle*

15:00 – 15:15 Matthew AARDEMA (*Princeton, U.S.A.*)

Divergent demographic histories of host-adapted populations of the tick-borne infectious bacteria, *Anaplasma phagocytophilum* / *Histoires démographiques divergentes des bactéries infectieuses transmises par les tiques, Anaplasma phagocytophilum*

SESSION II —Host diversity through standing genetic variation as an evolutionary response to infection / Variabilité génétique et diversité d'hôtes comme réponse évolutive aux infections

CHAIRPERSON: Ana Rivero

15:15 – 15:45 Scott EDWARDS (*Cambridge, U.S.A.*)

Population genomics and transcriptomics of adaptation of House Finches (*Haemorhous mexicanus*) to a rapidly evolving bacterial pathogen / *Génomique et transcriptomique de l'adaptation du Roselin Familier (Haemorhous mexicanus) à une bactérie pathogène à évolution rapide*

15:45 – 16:00 Lars RABERG (*Lund, Sweden*)

Toll-like receptors: genetic diversity and association with infection status / *Les récepteurs de type Toll: diversité génétique et association avec l'infection*

16:00-16:30 Coffee break – Pause café

16:30 – 17:00 Camille BONNEAUD (*Exeter, United Kingdom*)

Evolution of host resistance and pathogen virulence following an emerging infectious disease outbreak / *Evolution de la résistance de l'hôte et de la virulence du pathogène suite aux épidémies de maladies émergentes*

17:30-19:15 POSTER SESSION I (*CNRS-Hotel de France building*)

Communications par affiches – session I (Bâtiment CNRS-Hôtel de France)

19 :15 Free evening – Soirée libre

Monday, September 8 / Lundi 8 Septembre

SESSION II —Host diversity through standing genetic variation as an evolutionary response to infection (continued) / Variabilité génétique et diversité d'hôtes comme réponse évolutive aux infections (suite)

CHAIRPERSON: Thierry Rigaud

08:30 – 09:00 Nathalie CHARBONNEL (Montpellier, France)

Immune gene variability in bank vole populations with contrasted exposition to Puumala hantavirus / *Variabilité génétique immunitaire chez les populations de campagnols exposées aux hantavirus Puumala*

09:00 – 09:30 Manfred MILINSKI (Ploen, Germany)

Olfactory signalling of immunogenetics for mate choice / *Signalisation olfactive de l'immunogénétique pour le choix du partenaire*

09:30 – 10:00 Dan BOLNICK (Austin, U.S.A.)

Stickleback MHC class II genotype modifies both symbiotic gut microbe community and helminth

parasite community composition / *Le CMH de classe II modifie la composition des communautés symbiotiques intestinales et des helminthes parasites chez l'épinoche*

10:00 – 10:15 Helena WESTERDAHL (Lund, Sweden)

Unique peptide-binding motifs of songbird MHC molecules / *Motifs de liaison peptidique uniques chez le CMH des oiseaux*

10:15 – 10:30 Tobias LENZ (Boston, U.S.A.)

Costs and benefits of parasite-mediated balancing selection: The example of the MHC / *Coûts et bénéfices de la sélection balancée induite par les parasites: l'exemple du CMH*

10:30-11:00 Coffee break – Pause café

11:00 – 11:30 Brian LAZZARO (Ithaca, U.S.A.)

Balancing selection and convergent evolution in an antimicrobial peptide / *Sélection balancée et évolution convergente d'un peptide antimicrobien*

11:30 – 12:00 Yanick MORET (Dijon, France)

Evolutionary ecology and mechanisms of transgenerational immune priming in insects / *Ecologie évolutive et mécanismes de l'immunité transgénérationnelle chez les insectes*

12:30 – 12:45 Ann TATE (Princeton, U.S.A.)

Trans-generational immune priming increases resistance and tolerance to infection through the

temporal interplay of host immunity and pathogen virulence factors / *L'immunitaire transgénérationnelle augmente la résistance et la tolérance à l'infection par le biais de l'interaction temporelle entre virulence du pathogène et immunité de l'hôte*

12:15 – 12:30 Seth BARRIBEAU (Zürich, Switzerland)

Constitutive protection, mismatch, and the role of small RNA in transgenerational immune memory in the bumblebee *Bombus terrestris* / *Protection constitutive, mésappariement, et le rôle des petits ARN dans la mémoire immunitaire transgénérationnelle chez le bourdon *Bombus terrestris**

12:30 – 12:45 Edze WESTRA (Exeter, United Kingdom)

Costs and benefits of bacterial adaptive immunity systems / *Coûts et bénéfices des l'immunité adaptative chez les bactéries*

13:00-14:00 Lunch at the Conference Centre (Gulf Stream Hotel) / Déjeuner au Centre de Conférence (Hôtel Gulf Stream)

13:30-17:00 Boat trip to Batz Island – Excursion à l'île de Batz

18:00-19:45 POSTER SESSION II (CNRS-Hotel de France building)

Communications par affiches – session I (Bâtiment CNRS-Hôtel de France)

20:00-21:30 Dinner at the Conference Centre (Gulf Stream Hotel)

Dîner au Centre de Conférence (Hôtel Gulf Stream)

Tuesday, September 9 / Mardi 9 Septembre

SESSION III —Phenotypic plasticity both as a host response to infection and as a parasite strategy / La plasticité phénotypique : à la fois réponse des hôtes à l'infection et stratégie parasitaire

CHAIRPERSON: Dieter Ebert

08:30-09:00 Christophe GRUNAU (Perpignan, France)

Darwin's Pangenens and Jollos' Dauermodifikation - myth or reality? Lessons from the human parasite *Schistosoma mansoni* / *Les pangens de Darwin et les Dauermodifikationen de Jollos - mythe ou réalité? Leçons tirées du parasite humain Schistosoma mansoni*

09:30 – 09:30 David SCHNEIDER (Stanford, U.S.A.)

Determining the shape of disease space / *Détermination de la forme de la spatialité des maladies*

09:00 – 09:30 Andrea GRAHAM (Princeton, U.S.A.)

The within-host dynamics of optimal defense / *La dynamique intra-hôte des défenses optimales*

10:00 – 10:30 Gabriele SORCI (Dijon, France)

Host and parasite (mal)adaptation to an inflammatory environment / *(Mal)adaptation de l'hôte et du parasite à un environnement inflammatoire*

10:30-11:00 Coffee break– Pause café

11:00 – 11:30 Tatiana GIRAUD (Paris, France)

Influence of multiple infection and relatedness on virulence: experimental evidence from a castrating fungal plant parasite / *Influence de l'infection multiple de l'apparement sur la virulence: le cas d'un parasite fongique castrateur de plantes*

11:30 – 12:00 Ana RIVERO (Montpellier, France)

Plasmodium-Wolbachia coinfections in mosquitoes: consequences for malaria transmission / *Coinfections Plasmodium-Wolbachia chez les moustiques: conséquences pour la transmission de la Malaria*

12:00 – 12:30 Sylvain GANDON (Montpellier, France)

Malaria transmission: vector behaviour, dormancy and plasticity / *Transmission de la malaria: comportement vectoriel, dormance et plasticité*

12:30 – 12:45 Nicole MIDEO (Toronto, Canada)

Clocks and pox: evolutionary ecology of circadian rhythms in malaria infections / *Ecologie évolutive des rythmes circadiens chez la malaria*

13:00 – 14:15 Lunch at the Conference Centre (Gulf Stream Hotel) / Déjeuner au Centre de Conférence (Hôtel Gulf Stream)

14:30 – 15:00 Julien VARALDI (Lyon, France)

Inherited viruses as key players in host-parasitoid interactions / *Les virus à transmission verticale sont des acteurs clés dans les interactions hôte-parasite*

15:00 – 15:15 Thierry RIGAUD (*Dijon, France*)

A ‘manipulative’ parasite modulates the vulnerability to predation of its intermediate host, but alters the host’s food intake / *Un parasite ‘manipulateur’ module la vulnérabilité de son hôte intermédiaire à la prédation et modifie également sa prise de nourriture*

SESSION IV—The Red Queen’s moving equilibrium – is it inevitable? / *L’équilibre instable de la Reine Rouge - est-il inévitable ?*

CHAIRPERSON: Gabriele Sorci

15:15– 15:45 Dieter EBERT (*Basel, Switzerland*)

The population genetics of red queen dynamics / *La génétique des populations et la dynamique de la reine rouge*

15:45 – 16:15 Christophe EIZAGUIRRE (*London, United Kingdom*)

Host-parasite and ecological speciation: when should we expect divergent selection? / *Interactions hôte-parasite et spéciation écologique: quand est-ce que l'on s'attend à de la sélection divergente?*

16:15-16:45 Coffee break – Pause café

16:45 – 17:15 Britt KOSKELLA (*Exeter, United Kingdom*)

Examining coevolution in a complex microbial community: tests of reciprocal adaptation, specificity and diversity over space and time / *Coévolution dans une communauté microbienne complexe: tests de l'adaptation réciproque, de la spécificité et de la diversité dans l'espace et dans le temps*

17:15 – 17:45 Sunetra GUPTA (*Oxford, United Kingdom*)

The role of immunity in host pathogen coevolution / *Le rôle de l'immunité dans la coévolution hôte-parasite*

17:45 – 18:15 Mike BOOTS (*Exeter, United Kingdom*)

How specificity and epidemiology drive the coevolution of static trait diversity in hosts and parasites / *Comment la spécificité et l'épidémiologie déterminent la coévolution de la diversité des traits chez les hôtes et les parasites.*

18:15 – 18:45 Hinrich SCHULENBURG (*Kiel, Germany*)

Lessons from *C. elegans* as a model host: fast and complex adaptations during host-pathogen coevolution / *C elegans comme hôte modèle: adaptations rapides et complexes contre les microbes infectieux*

19:30-20:00 Drinks – Apéritif

20:00-23:00 Banquet at the Conference Centre (Gulf Stream Hotel) / Banquet au Centre de Conférence (Hôtel Gulf Stream)

Wednesday, September 10 / Mercredi 10 Septembre

09:30-10:30 Ana RIVERO (*Montpellier, France*)

General discussion – Discussion générale

10:30 End of the conference