



Sciences biologiques,
Écologie et Environnement
**CONFÉRENCES
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Roscoff (France), 2-6 Avril 2014

**Des virus émergents aux virus pandémiques : interaction entre écologie
des hôtes et évolution virale**

*From emerging to pandemic viruses: interplay between host ecology
and viral evolution*

PRESIDENT : Roland R. REGOES
ETH Zentrum, Zürich, Suisse

VICE-PRESIDENT: Samuel ALIZON
Laboratoire MIVEGEC, CNRS-IRD, Montpellier, France

Rapport sur la conférence

Conference report

Rapport final de la conférence Jacques-Monod :

« Des virus émergents aux virus pandémiques : interaction entre écologie des hôtes et évolution virale »

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Résumé

La conférence “*Des virus émergents aux virus pandémiques : interaction entre écologie des hôtes et évolution virale*” s'est tenue à Roscoff du 2 au 6 avril 2014. Son principal but était de rassembler des experts étudiant l'émergence virus mais utilisant pour ce faire des outils différents et des virus infectant des hôtes différents, allant des Archaea aux plantes et aux animaux.

En plus de nos 28 orateurs invités, nous avons reçu la participation de 71 participants provenant de 14 pays différents (Afrique du Sud, Allemagne, Colombie, Danemark, Espagne, France, Grande Bretagne, Italie, Pays Bas, Pologne, Slovénie, Suède, Suisse, USA), soit trois pays de plus que la précédente édition. Ce succès s'explique aussi en partie par le soutien (en plus de celui du CNRS et de l'INSERM bien sur) d'institutions telles que la FEMS, le REID ou l'IRD. Une autre marque du succès de la conférence a été la participation de l'un des éditeurs de *EMBO journal*. Enfin, signe des temps, une des participantes a ouvert un fil twitter permettant au monde entier de suivre la conférence en direct: <https://twitter.com/search?q=%23vwcl&src=hash&f=realtime>

La plupart des présentations ont été données par des experts du champ et le nombre d'article issues de revues telles que *Science* ou *Nature* était impressionnant. Il y avait une atmosphère très conviviale et de nombreuses discussions purent avoir lieu pendant les pauses, les repas et l'excursion. Nathalie Babic et Alain Paoli ont grandement contribué à la fluidité de la conférence. Les participants ont aussi tous été très impressionnés par la qualité et la diversité des repas et du service à l'hôtel Gulf Stream.

Une des facettes de la conférence qui a contribué à son succès a été qu'elle a rassemblé des scientifiques travaillant sur des systèmes différents avec des approches différentes. Ainsi, beaucoup de collègues travaillant sur les virus animaux n'avaient aucune idée du potentiel qu'offrent les virus de plante pour tester certaines idées. De plus, la plupart des participants ont été ébahis par la diversité virale découverte dans les amibes ou les

archaebactéries. Comme l'a résumé Olivier Pybus au cours d'une des discussions, de nombreux résultats présentés au cours de cette conférence nous ont rendu plus humbles au vu de la spécialisation de nos systèmes et résultats.

La conférence a été divisée en sessions visant plus à capturer des thématiques que des virus en particulier. Les sessions étaient les suivantes :

1. Outbreaks
2. Immunité
3. Virus multi-hôtes
4. Évolution expérimentale
5. Émergence dans la nature
6. Virulence
7. Intra-hôte
8. Dynamiques spatiales
9. Modélisation

Nous avons tâché de maximiser le nombre de présentations et au final avons eu 49 présentations orales dont 11 ont été données par des femmes (22 %), ce qui est mieux que la précédente édition mais toujours non satisfaisant. Au final, 26 orateurs ont donné des contributions de 30 minutes. Parmi ces derniers, 10 provenaient de laboratoires français, 10 d'Europe et 6 du reste du monde. De plus, 23 participants ont pu donner des présentations orales de 15 minutes, toutes d'excellente facture. Nous avons eu deux sessions posters (2 heures chaque, avec 35 posters par session) pour compléter le programme scientifique. La place centrale des sessions posters dans le programme a été très appréciée, ainsi que l'apéritif concomitant, qui a facilité les discussions. Les présentations orales et affichées étaient toutes d'excellente qualité.

Tous les participants ont été très enthousiastes tout au long de la conférence et, encore une fois, tous semblent avoir beaucoup appris au cours de ces 4 jours. La demande de reconduction d'une conférence sur ce sujet a été unanime.

**Final report from the Jacques Monod Conference entitled:
From emerging to pandemic viruses: interplay between host ecology and virual
evolution
Roscoff, April 2-6, 2014**

Summary

The conference “*From emerging to pandemic viruses: interplay between host ecology and virual evolution*” was held in Roscoff from Apr 2-6, 2014. Its main purpouse was to bring together experts studying virus emergence using different tools and different model hosts, ranging from Archaea to plants and humans.

Overall, in addition to our 28 speakers, we had 71 participants from 14 different countries (Colombia, Denmark, Italy, France, Germany, Poland, Spain, Switzerland, The Netherlands, Slovenia, South Africa, Sweden, the UK, USA). This is 3 more countries than the first CJM on this topic. Part of this success was thanks to the support from institutions such as the FEMS, the REID or the IRD. Another illustration of the success of the conference was the participation of an editor of the *EMBO journal*. Note also that one of the participants opened a twitter feed so that the conference could be followed throughout the world: <https://twitter.com/search?q=%23vwcl&src=hash&f=realtime>

Many of the presentations were given by experts in the field and the number of *Science* and *Nature papers* presented was impressive. There was an extremely good atmosphere and lots of discussions took place during the breaks, the meals and the excursion. Nathalie Babic and Alain Paoli helped a lot to make everything happen smoothly. The participants were also very impressed by the quality of the catering at the Gulf Stream hotel: meals were not only excellent but taxonomically very diverse.

One of the key aspects of the meeting that made it so successful was that it brought together scientists woirking on different systems. For instance, many colleagues working on animal viruses had little idea about the potentialities opened by plant viruses to test hypotheses experimentally. Furthermore, most of the participants were stunned about the extreme viral diversity found in amoeba or in Archaea living in extreme geothermical conditions. As Dr. Olivier Pybus put it during one of the discussions, many of the results presented by other colleagues were humbling in that they made us realise at how

specialised our systems and our results are.

This conference was divided into sessions that tried to gather different type of approaches and different type of viruses. More specifically, we had the following sessions:

1. Outbreaks
2. Immunity
3. Multi-host viruses
4. Experimental evolution
5. Emergence in the wild
6. Virulence
7. Within-host
8. Spatial dynamics
9. Modelling

We tried to maximise the number of contributed talks and overall managed to have 49 oral presentations. Amongst these, 11 were given by women (22 %), which is better than the previous edition but still unsatisfying. A total of 26 speakers were invited to give 30' full talks. Of these, 10 come from French laboratories, 10 from other European laboratories and 6 from outside Europe. In addition, 23 applicants gave 15' oral presentations. Selection was based on the originality and novelty of their abstracts. We had two poster sessions (2 hours each, with 35 posters per session) completed the scientific program. The poster sessions were particularly appreciated because of their central place in the program and also because of the apero, which made the discussions easier. The oral and poster presentations were of outstanding quality. Participants all seemed extremely happy with the conference and, again, a lot of them seem to have discovered whole new approaches and viral diversity.

Scientific report

Introduction was given by the chairperson, Roland R. REGOES. In addition to thanking the CNRS and INSERM and all the staff of the Jacques Monod conferences, he also thanked our generous sponsors, especially the Federation of European Microbiology Societies (FEMS), who allowed several young microbiologists to attend the conference, but also the IRD, the ESV and the REID.

Session 1. Outbreaks

The goal of this session was to understand the origin of outbreaks, i.e. rapid emergence of infectious diseases in population. Andrew CUNNINGHAM (Zoological society, London, UK) opened the session by focusing on a bat species (*Eidolon helvum*), which is known to be a reservoir for many viruses, some of which can infect humans. His view though is more that of a conservation biologist, which brings a different light to the emergence problem. His results based on two bat viruses, Lagos bat virus and hendra virus showed the importance of the ecology of the host (e.g. population structure). He also presented experiments of virus injection in bats to understand the pathology of the infection.

His presentation was followed by that of Katie HAMPSON (Institute for Biodiversity, Glasgow, UK), who presented work on contact tracing of rabies outbreaks in Africa. The talk contrasted with the previous one because it focused on a human disease, which causes many deaths in Africa. What was particularly striking is that thanks to field work and interviews with dog owners and community members, she was able to infer the range of dispersal for thousands of rabid dogs. She also showed that the phylogeographical patterns differ for domestic dogs in the USA and in Tanzania.

Jamie LLOYD-SMITH (UCLA, USA) then presented some more theoretical work on how to model and predict disease outbreaks. He focused particularly on what he called "stuttering chains", i.e. pathogens that do not spread enough to generate large outbreaks but can nevertheless cause several cases. There is also a risk that during these limited outbreaks they mutate into more adapted strains. He gave a particularly clear presentation, which was well appreciated even from medical doctors like Antoin GESSAIN (Institut Pasteur, Paris), who gave a much more applied presentation on "hunting" for human viruses in Africa.

In between, we had a presentation from Darren MARTIN (University of Cape Town, South Africa) on a plant virus, which is known for its small genome size. By combining field data, phylogenetics and experimental approaches, his team was able to track the origin of the outbreak since 1863. What was striking was that the estimations obtained using the different methods coincided.

Finally, we ended the session by an original presentation from Eduardo CASTRO-NALLAR (George Washington University, Ashburn, USA), who talked about an outbreak of a novel virus infecting salmon in Chile. In addition to its applied aspect, it raised technical issues because conventional methods (PCR or cell culture) did not allow to isolate the virus.

Overall, this session provided us with examples of outbreaks on different types of hosts. It also showed how different approaches can be used to monitor and understand these outbreaks, from interviews in the field to experiments in the lab or mathematical models.

Session 2. Immunity

Part of what explains viral outbreaks is the immunity of the host population. To introduce this session, we had two talks by Sarah COBEY (University of Chicago, USA) and Michiel VAN BOVEN (National Institute for Health and the Environment, Bilthoven, The Netherlands) on influenza, which is arguably one of the systems where the role of immunity is most intensively studied. The two speakers emphasized the importance of cross-protective antibodies, which are the focus of many recent studies because they might allow to develop vaccines that are protective for longer than a single season. While Sarah Cobey focused on the population biology of B-cell responses in germinal centers, Michiel van Boven showed how the population immunity patterns vary with time.

We then switched to a completely different system with Nathalie Charbonnel (CBGP, Montpellier), who presented results on hantaviruses infecting rodents in the wild. These viruses are closely monitored because they can be transmitted to humans and cause virulent infections. What is striking is that these viruses, pumalaviruses, are virulent in humans although they do not replicate in them at a high rate. This raises many issues regarding the two strategies hosts have to face infections, i.e. to resist or to tolerate. Roland REGOES (ETH Zürich, Switzerland) followed on this idea of resistance vs. tolerance but focusing on HIV in humans. Analysing data from the Swiss HIV Cohort Study he was able

to detect an association of tolerance with HLA-B, showing that individuals who are homozygous are less tolerant than those who are heterozygous.

Paul TURNER (Yale University, USA) moved on to experimental aspects and showed how using the Vesicular Stomatoc Virus (VSV) it is possible to test the effect of host immunity. To this end, they performed evolutionary experiments, i.e. adapted the virus to one type of cell line through serial passage experiments and then tested its fitness in other cell lines.

Finally, the session was closed by Peter MARKOV (Department of Zoology, Oxford, UCL), who presented results on the adaptation of hepatitis C virus to host HLA. His main result was that there is some adaptation, such suggesting that the virus can be pre-adapted locally.

This session allowed us to explore the importance of host immunity in viral outbreaks. It had some unexpected discussion. For instance, Paul TURNER's talk raised several issues about the adaptiveness for viruses to be oncogenic because several of the cell lines he used for his experiment were derived from tumours.

Session 3. Multi-host viruses

Many viruses are able to exploit several hosts and this is often at the root of emergence. Exploiting multiple hosts is a characteristic of arboviruses, which are viruses transmitted by vectors. The first presentation of this session by Scott WEAVER (University of Texas Medical Branch, USA) was on Chikungunya virus, a human virus that is transmitted by *Aedes* mosquitoes and has many similarities with dengue virus in terms its mode of transmission, its molecular genetics, and its pathology in the human host. This presentation was extremely timely because there is an ongoing outbreak of Chikungunya in French Guyana. In the study presented, detailed fitness measures of the old and new epidemic strains were taken, which allowed to recapitulate the population genetic history of the recent emergence event.

Frank JIGGINS (Cambridge University, UK) adopted a more conceptual approach by infecting 51 different species of Drosophilidae with three host specific viruses (sigma viruses). He showed that phylogenetic proximity between host explains infection patterns. In other words, he proved that viruses can more easily infect hosts that are phylogenetically more related.

Finally, Louis LAMBRECHTS (Institut Pasteur, Paris) analysed genotype × genotype

interactions between dengue virus and its *Aedes* vector. His conclusion is that there can be strong interactions and that results based on either one mosquito genotype or one virus genotype should be interpreted with care as they could yield different results for different interactions.

Session 4. Experimental evolution

One of the advantages of working on viruses is that they have a short generation time and, to quote another evolutionary biologist, we can have the “Beagle in a bottle” (the Beagle being the name of the boat on which Darwin went to the Galapagos islands).

The sessions was opened by a brilliant talk from Bruce LEVIN (Emory University, USA) on the CRISPR system, which is presented as an adaptive immune system of bacteria. He presented a mathematical model on the evolution of the system as well as new results showing that bacteria can lose the CRISPR system in conditions where DNA exchanges are very adaptive (e.g. in the presence of antibiotics).

We then had a presentation by Marco VIGNUZZI (Institut Pasteur, Paris) who showed how next generation sequencing tools can be used to analyse evolutionary experiments. His work focused on the spread of chikungunya virus within its host and showed how the emergence of more adapted mutants can be monitored in each organ of the mosquito.

The session was completed with a presentation of Santiago ELENA (University of Valencia, Spain) on experimental evolution using plant viruses. One of the key results was obtained by evolving the tobacco etch potyvirus on two different plants separately or alternating between host plants. He showed that in the treatment where the virus alternated hosts it became more generalist.

Session 5. Outbreaks in the wild

This session was perhaps the most humbling for most participants because it revealed how little we currently know about viral diversity. David PRANGISHVILI (Institut Pasteur, Paris) first presented what his group has found on viruses living in extreme geothermal environments (temperatures above 80°C). What was fascinating was not the diversity of viruses per se but also the wide variety of shape these viruses can take. Since they need to adapt to these extreme environments, the viruses have developed unique adaptations that are still only partially understood.

We then had another timely talk by Lena WILFERT (University of Exeter, UK) on the

role of viruses in the decline of pollinators. She showed that bumblebees, which are currently spreading in South America and causing the decline of other pollinators could actually be mediated by a viral infection.

Also using data from South America, Daniel STREICKER (University of Glasgow, UK) showed some very original results on how rabies virus spreads in bat populations. By using comparative genomics between the virus and the host they showed that the dispersal was mainly due to the males, which has obvious implications in controlling the disease.

Nathalie SIMON (Station Biologique de Roscoff, France) then presented some very clear and clean results on the dynamics of viruses infecting *Micromonas* algae in the English channel. She showed how these viruses have a key role in the ecosystem and also how the data allows to analyse the interaction between the host and the virus dynamics. Her team was also able to assess the specificity of viruses by performing cross-infections.

Jonas WALDENSTRÖM (Linnaeus University, Sweden) ended the day with a presentation on influenza circulating in wild duck populations. What was particularly original in his work is the experimental set up they have devised with a very large cage to trap individuals and, inside this large cage, a smaller cage with “resident” ducks. The latter can easily be monitored and they allow the researchers to know what viral serotypes circulate. Overall, they have now accumulated more than 12 years of data with 30000 samples.

The session continued on the next day with an impressive talk by Jean-Michel CLAVERIE (Institut Microbiologie de la Méditerranée, Marseille), who gave an overview on the work he and his team have been doing to find “giant” viruses. What was particularly humbling for the audience is that for instance in the last pandoraviruses they have discovered and which has a genome of 2.5 Mb with 2500 genes, more than 94% of these genes do not match with anything we currently know.

From a more applied perspective, Lise FREZAL (Institut de Biologie de l'ENS, Paris) introduced us to the new host-parasite system the team of her supervisor Marie-Anne Félix has been setting up. It involves the worm *Caenorhabditis briggsae* and its natural pathogens Santeuil and Le Blanc viruses. What is particularly important here is the fact that these viruses are natural parasites of the host because most of the time work on *Caenorhabditis* feeds on bacteria that are found in the soil but there is no evidence that they infect the worm *in natura*. A very appealing feature of this system is that it allows for

coevolution since the generation time of the worm is in the order of 3 days.

Session 6. Virulence

By definition, viruses have to exploit a host and it makes a lot of sense to investigate how the harm a virus does to its host evolves.

We had two talks on this topic that were based on Human Immunodeficiency Virus because this is one of the most studied viruses and because there have been several new results lately. Eric ARTS (Case Western Reserve University, Canada) presented some of the work he has been conducting in the field on comparing the virulence of HIV subtypes. He also presented the results of original experiments designed to determine whether any virus can pass the genital epithelial tissue barrier, or if there is a selection of particular viral genotypes. Quite surprisingly, they show that viruses isolated from chronic infections are less able to cross the tissue than viruses from acute infections. There is also a pronounced difference between viruses from different subtypes. The second talk was from Christophe FRASER (Imperial College of London, UK) and it presented the result of several results that have led to a recent review in *Science*. All these point to an underestimated effect of the virus genetics on the virulence of HIV infections.

Eckard WIMMER (Stony Brooks University, USA) also presented results published in *Science* that dealt with codon *pair* bias. This phenomenon is much less known than codon usage bias and it is due to the fact that there are very few G following C in the DNA sequence. Performing sequence deoptimisation and optimisation on polioviruses has quantifiable effects on virus fitness. This could also be the basis for the development of new vaccines since codon deoptimisation is a way to generate attenuated viruses without altering the epitopes they present to the immune system.

We also had two contributed talks in this session. Rémy FROISSART (BGPI, Montpellier) presented results obtained on the evolution of virulence of the Cauliflower mosaic virus. What was very nice is that they were able to investigate not only the viral accumulation in the host but also the epidemiological parameters (host disease-induced mortality and transmission rate). Also, these results were obtained in two different hosts. They find a trade-off between the intensity of transmission and the duration of the infection in two different host plant species. They also show that viral accumulation is correlated with the other. However, they do not find any correlation between the virulence in the two hosts. Ben LONGDON (University of Cambridge, UK) analysed the virulence of a natural

Drosophila virus in 53 species of *Drosophilidae*. He found that there was a strong phylogenetic signal, which means that individuals from host species that are related tend to exhibit the same virulence when infected. However, there was no effect of the distance between a given species and the species on which the virus evolved on the virulence.

Session 7. Within-host

Viruses evolve so rapidly that many of the questions on emergence we asked could be asked over the course of a single infection. This idea was illustrated with a fascinating talk from Stéphane BLANC (BGPI, Montpellier) on multipartite viruses. These viruses are unique in that they are fragmented (as influenza viruses) but each virus capsid only contains a single fragment (whereas for influenza all the fragments are in each capsid). Even more astonishingly, the relative frequency of each fragment in the host is very constrained and, when seeded with an equal ratio of each fragments, infections seem to converge towards an optimal formula. This formula is different when the virus infects another host plant. It is also different in the aphid vector during the transmission. This talk was one that generated a lot of discussion across fields.

We then had a very clear talk by Yves GAUDIN (Laboratoire de Virologie structurale, Gif sur Yvette) on the way rhabdoviruses enter the host cells. Using electron microscopy and tomography, it is possible to show how the change in pH from the external to the intra-cellular environment induces a conformational change in the structure of membrane glycoproteins involved in the cell fusion. This talk was interesting because it provided the audience with an overview of an aspect of virology that is often overlooked in evolutionary biology that is the mechanistic bases of host-virus interactions.

The final talk in the session (unfortunately Moncef BENKIRANE has to cancel at the last minute for health issues) was from Marine COMBE (University of Valencia) who presented original work on measuring viral mutation rates at the cellular level for VSV.

Session 7. Spatial spread

Due to their rapid evolution, viruses have been the basis of many studies attempting to infer geographical spread. This is because by analysing their genome one can infer transmission patterns. The first talk was given by a world expert in phylogeography, Oliver PYBUS (University of Oxford, UK). He presented recent results obtained in

analysing the spread of West Nile Virus in the US. What was most striking was the importance of (rare) long distance dispersal events to explain the phylogeographical patterns observed.

Gerald HECKEL (University of Bern, Switzerland) then presented his investigations on the distribution of hantavirus in Germany during a contributed talk. He showed that host structure and virus structure seemed to differ at a small scale. He also showed that inference using a Bayesian skyline model revealed a constant population size. As pointed out by Dr. Pybus, such a pattern is often an indicator of an underlying structure in the data.

The second long talk in the session was given by Britt KOSKELLA (University of Exeter, UK) and contrasted with the previous one in that she provided experimental evidence for coevolutionary dynamics in time and space. More precisely, she investigated the ability of viruses to infect bacterial communities depending on whether these communities originated from the same leaf of the same tree or from another leaf or from a different tree. She also performed time shift experiments by infecting bacterial communities sampled early in the season by viruses sampled late in the season and *vice versa*. She showed no adaptation at the tree level but adaptation at the between-tree level.

Sébastien LION (CEFE, Montpellier) presented a mixture of experimental and theoretical results. He showed how the viscosity of the bacteria culture medium affects the competition between an avirulence and a virulent phage. Consistently with model predictions, the less the environment is structured, the more the virulent strain has an advantage. He also showed that increasing spatial structure in the population favours bacterial suicide, i.e. the fact that bacteria would die before producing any phages. This again is what kin selection theory predicts as a result of medium viscosity.

The next short talk was given by Henrik SALJE (John Hopkins School of Public Health, Baltimore, USA) on analysing the geographical spread of dengue virus in Vietnam. He found very strong structuring of the epidemics with dengue cases clustering at a range of 1.5 km on average. He also showed an increase of heterotopic cases over time, consistent with the hypothesis that virulence in dengue infections can be driven by re-infection by a different genotype.

Pauline BERNARDO (BGPI, Montpellier) introduced a new approach that combines metagenomics and geography to look for new viruses as a function of the landscape. She applied her method in wild and cultivated plants in Camargue (France) and in Western

Cape region (South Africa). This allowed her to detect two new geminivirus species that could be emerging as agricultural pests.

The final talk of the session was contributed by Simon FROST (University of Cambridge, UK) who presented a phylogeny-based method to infer the number of host jumps from a pathogen. One originality is that he allowed for bi-directional jumps, as can be expected if there is spatial structure. This way, he shows that the mode of spread, i.e. whether infected individuals themselves move or if it is only the pathogen that is spread from one population to the next, affects phylogeny structure.

Overall, the spatial structure session provided us with a nice overview of complementary methods to analyse and predict emerging virus spread.

Session 8. Modelling

This session was perhaps the only one that was a little bit specialised. The intention was also to illustrate the diversity of methods to analyse viral outbreaks.

Samuel ALIZON (MIVEGEC, Montpellier) presented a very recent model on estimating the probability of emergence of a new pandemic strain from a weakly adapted strain, through a process known as evolutionary emergence. His result was that the ongoing spread of the first strain can strongly impede the emergence of the mutated (pandemic) strain. By applying this model to the chikungunya virus outbreak in La Réunion in 2005-2006, he was able to show that current estimates of evolutionary emergence could be overestimated by at least one order of magnitude.

Claude LOVERDO (Laboratoire Jean Perrin, Paris) also modelled virus emergence but by looking at a different scale. The idea is that the virus first needs to emerge within a host before being able to emerge at the host population level. What was particularly challenging is that she managed to link these different levels of selection for the virus.

Sebastian Bonhoeffer (ETH Zürich) then gave a detailed presentation of the work his group has been doing on the molecular bases of HIV fitness and drug resistance over the last 5 years. For instance, they were able to analyse more than 70,000 virus sequences for which the phenotype (growth rate) are known, which allowed them to build an algorithm that predicts virus replicative capacity *in vitro* from its RNA sequence. Thanks to this computational method, they could show that the replicative capacity seems to increase over the course of an infection.

Sylvain GANDON (CEFE, Montpellier) presented theoretical results on the evolution

of plasticity, i.e. on the ability of pathogens to exhibit different behaviour depending on the environment they face. By applying these models to bacteriophages, he showed that there is a great diversity of cues pathogens can use to adapt their strategies. Accounting for this plasticity is essential to better understand pathogen spread.

Tanja STADLER (ETH Zurich, Switzerland) then showed some very elegant mathematical work to analyse phylogenies. In particular, she extended some of her previous models that allow to infer the transmission rate and the duration of an infection by analysing phylogenies built using virus sequences sampled in different patients.

The final talk was very well received in spite of a very rich program. Gael THEBAUT (BGPI, Montpellier) presented the analysis of an epidemic involving two strains of *Tomato leaf curl virus* that has been going on in La Réunion island. The originality of the model is that it was complemented with experiments in the lab, which allowed them to calibrate their model, especially with regards to co-infection parameters. The main result was that one of the virus strains benefits from the co-infection, which allows it to persist in the population. This is a rare case of unilateral facilitation.

Conclusion and recommendations

This was the second Jacques Monod conference organised on virus emergence. As the first one, it was undeniably a success. There are some indicators that reveal that the conference is also establishing itself in the field. First, we were delighted to have one of the editors of the EMBO journal attending the conference. Second, we were also delighted to expand the audience to more molecular virologists and even very famous ones as Eckard Wimmer. Another noteworthy point is that the number of countries represented has increased since the last time (14 instead of 11), with several participants coming from far away (USA, Colombia, Poland) only to present a poster. Finally, we were able to attract significant funding from the FEMS, which greatly facilitated the presence of PhD students.

All the discussions with the participants lead us to think that this conference was a true success. Some of the comments and emails we received from senior scientists after the conference include statements such as:

"This is truly one of the few best conferences I went to."

"I am thrilled when I remember the many exciting talks given during the sessions. Your and

Natalie's hospitality was exceptional. And so were weather and food!"

"Great meeting!"

"The meeting was on the better side of awesome."

In terms of the recommendations for the next conferences, although it is extremely painful for the organisers to only attribute posters to brilliant scientists, who submit excellent posters, it would be preferable to decrease the number of talks in order to favour discussions. Adding discussion sections *per se* is often disappointing but what seemed to be a good suggestion was to increase the duration of the coffee breaks (e.g. to 1 hour) in order to allow for much more flexibility in the questions. The afternoon excursion to Batz island provided room for extended discussion in addition to an opportunity for physical exercise, and should definitely be maintained. The 2 hours poster sessions were very appreciated and we have seen much more discussions and participation taking place there than at any conference. Finally, from a program perspective, what could be interesting for a future edition would be to increase slightly the representation of molecular virologists amongst the invited speakers. (With Paul Turner as the next vice chairperson this goal will be easily accomplished.) All those who were present were definitely thrilled to discover new techniques and new approaches. Finally, we should also coordinate with the organising committee to avoid having two conferences on related topics the same year. This seems to have dissuaded several colleagues from applying.

In addition to the ideal location (and many participants insisted on that we conveyed warm felicitations to the chef for making such tasty and varied meals), what the participants seemed to have enjoyed most is the gathering between researchers working on different types of viruses. This conference is one of the very few worldwide that really allows virologists to expand their view of the field. Given the success of the conference, the participants were unanimously in favour of reconducting the conference. As a replacement for our chairperson (Dr. Regoes), the participants elected Paul TURNER (Yale University, USA) to assist the current vice-chairperson (Samuel ALIZON).