Evolution and Biodiversity:

The evolutionary basis of biodiversity and its potential for adaptation to global change

Report of an electronic conference, March 2010

E-Conference organisation:

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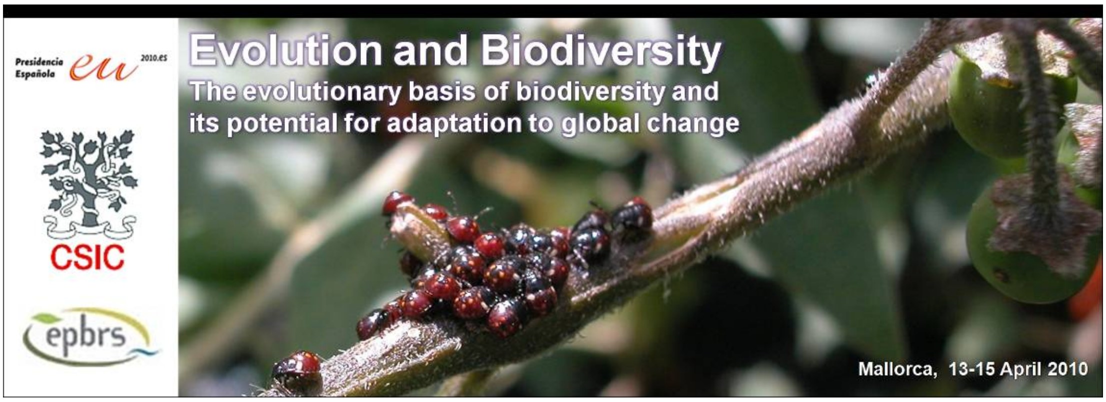
The changing landscape (Peyresq, southern France). Allan Watt, CEH Edinburgh.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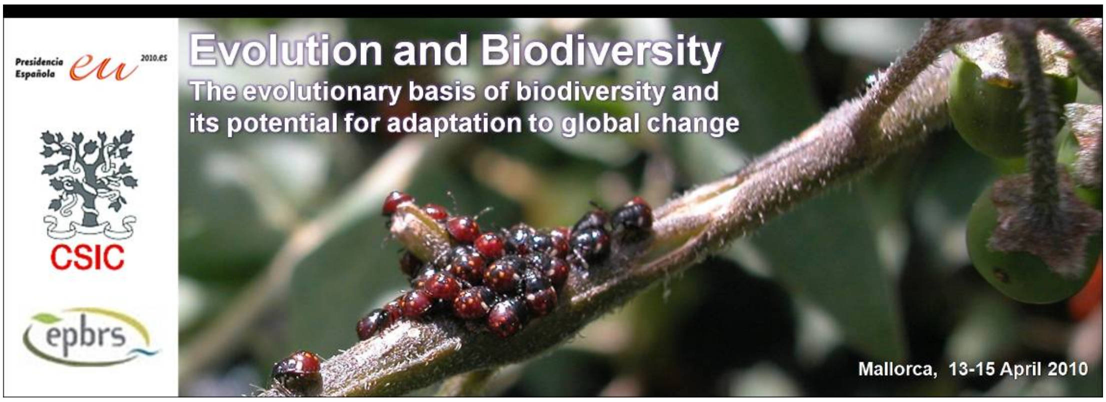
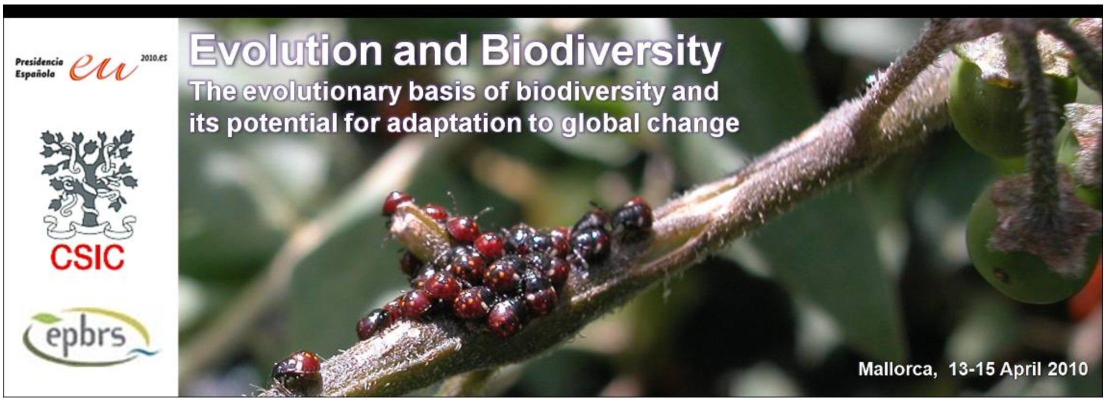


Preface

Research on biodiversity is essential to help the European Union and EU Member States to implement the Convention on Biological Diversity as well as reach the target of halting the loss of biodiversity in Europe by 2010.

The need for co-ordination between researchers, the policy-makers that need research results and the organisations that fund research is reflected in the aims of the European Platform for Biodiversity Research Strategy (EPBRS), a forum of scientists and policy makers representing the EU countries, whose aims are to promote discussion of EU biodiversity research strategies and priorities, to exchange information on national biodiversity activities and to disseminate current best practices and information regarding the scientific understanding of biodiversity conservation.

This is a report of the E-Conference entitled Evolution and Biodiversity: The evolutionary basis of biodiversity and its potential for adaptation to global change preceding the EPBRS meeting to be held under the Spanish EU presidency in Palma, Mallorca, from the 12th-15th April 2010.



Introduction

Joachim Mergeay, E-Conference Chair

We are facing global changes that are unprecedented in the history of humanity, but that we have caused ourselves. We have created a world where the influence of a single species is omnipresent in all realms and ecosystems. Pollution, overexploitation, habitat loss and fragmentation, invasive species and climate change are the main causes of global change, and as a corollary, current biodiversity loss. Jointly they form a multitude of stresses on life on this planet.

The main question is not whether life on earth will adapt to global change, because it will. Life inevitably finds new pathways to cope with change. The issue is rather how this will happen. What does a relatively sudden and massive interference into such ecosystems do with the stability and functioning of these ecosystems, and what is the role of evolution in the responses to global change?

In contrast to the dynamic evolutionary flux that characterizes life, our view on biodiversity and ecosystem functioning has mainly been a static one, trying to conserve biodiversity as it is, and preferably, as it was. Given the pace and magnitude of global change we are imposing onto our world, we need to be able to predict how life will change as a result of our own actions. We will still need the same ecosystem functions and services tomorrow, so we will need to know if and how these will be altered by our actions. That is a serious challenge.

In the "United Nations international year of biodiversity" we should get to the evolutionary sources of biodiversity itself, and rethink biodiversity in all its aspects. We need to understand how evolution shapes diversity, from genes to ecosystems. How diversity originates, how functions originate, and how they are affected by change. How biotic interactions originate and how we can maintain the ecosystem services we badly need in spite of the changes we impose on life.

We live in an era where science policy makers and science funding agencies are focusing more and more on direct applications and short term return-on-investment. But for science to provide solutions to the biodiversity crisis and its associated social and economic consequences, we first need to understand the processes that generate and maintain biodiversity in the face of global change. This was the key issue of this e-conference.

The e-conference covered three main topics, one per week of the e-conference:

Session 1: The evolutionary basis of biodiversity - strategies to manage and preserve evolutionary processes, and their likely impact on biodiversity
This first session focused mostly on the lowest levels of biodiversity (genes and individuals). We started by considering the role of evolution in biodiversity from a human perspective, and then looked in more detail at:

- New genomic techniques and their applications in conservation biology
- The genetic basis of phenotypic evolution
- Non-genetic inheritance mechanisms (epigenetics)
- Genetic and genomic studies of a biodiversity hotspot
- How rapid evolution affects invasive species as well as species in invaded biota

Session 2: Evolutionary responses to global change

This session focused on how populations respond to global change, and how this affects relatively simple biotic interactions. In particular it addressed:

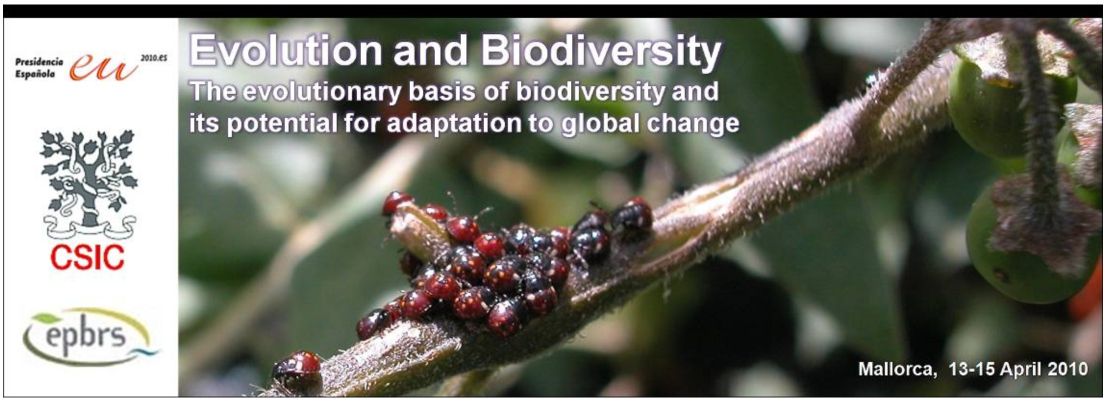
- Landscape-level impacts on ecological and evolutionary change
- Genetic consequences of habitat fragmentation on populations
- Past climate change and the reconstruction of its effects
- Present-day rapid evolutionary responses to climate change, and predicting evolution
- The challenging task of accurately distinguishing evolutionary responses from other confounding factors

Session 3: Evolution in complex systems and co-evolutionary networks: managing complexity in the face of uncertainty

This session aimed mostly at understanding evolutionary dynamics in communities and ecosystems, and the feedbacks between ecological and evolutionary processes. In particular it focused on:

- How we should tackle the interaction between ecology and evolution at various levels of biotic organisation
- How we can learn from non-biological complex networks to better understand the evolution of biotic complexity, and try to find general patterns into complex multi-species interactions
- How ecological processes influence evolution and vice-versa
- Coevolution in complex environments
- The theory of geographic mosaic of coevolution
- How to manage biotic complexity in the face of uncertainty

The keynote contributors to this e-conference were globally distributed, and came from a wide gamut of scientific backgrounds, including social, life and environmental sciences, with geneticists, ecologists, evolutionary biologists, palaeontologists and philosophers. We hoped to bring a broad and interdisciplinary view on evolutionary research, with new ideas, challenging perspectives and urgent research needs. Above all, we hoped this e-conference would be intellectually stimulating, interesting and fun.



Summary of contributions

Joachim Mergeay and Fiona Grant

Summary for week 1: 'The evolutionary basis of biodiversity'

The evolutionary basis of biodiversity was discussed in the first week of the e-conference. A central question inherent to this topic was what should motivate society to conserve biodiversity. Stefaan Blancke and Felix Rauschmayer put forward the need to conserve biodiversity for moral reasons. Stefaan Blancke also emphasised the need to conserve biodiversity for the ecosystem services that it provided to human society. François Bonhomme, however, argued that there was a risk that the latter view would dominate science policy and political and economic decisions.

As mentioned in Stefaan Blancke's keynote, viewing biodiversity in evolutionary terms was a step forward with regards to the rather static view that had dominated our perspective in the past. This view had also led to a fixed systematic view on biodiversity that was rightly questioned by Pierre-Henri Gouyon, thereby honouring again the legacy of Charles Darwin. We have long thought of evolution as an extremely slow process, and have too often only regarded it on a macro-evolutionary scale: the origination of a new species and the loss of species through extinction. Nevertheless, the rate of species loss greatly exceeds that of the origination of new species. We cannot solve or compensate for the loss of species that we have caused in the past, and rapid evolutionary responses are not going to help in any way, as argued by François Bonhomme. In addition, many other species are facing extinction, and may purely survive temporarily on extinction debts. Can we use evolutionary processes and principles to save them from extinction?

Maybe we can, but as indicated by Pierre-Henri Gouyon, we are only fighting the symptoms because the underlying evolutionary processes that constantly create new evolutionary variants are disrupted and disturbed. However, one can argue that in general genetic variation (instead of creation of new variation) is more important for short term evolutionary changes (Frankham et al., 2009), which puts the focus again on the conservation of present-day genetic variation for safekeeping evolutionary potential.

Joop Ouborg highlighted the promise of genomic tools in the study of biological conservation. He argued that the development of new genomic techniques could make it possible to progress from the correlative and retrospective inferences of conservation genetics, based on neutral genetic markers, to a causal, mechanistic and prospective understanding, based on functionally important genetic variation, in a conservation genomic approach. These approaches could be used to investigate in non-model organisms and in organisms that could not be subjected to experimental approaches the functional genetic basis of adaptation, of inbreeding depression, genetic drift and so on.

Some caveats and questions were raised by Joachim Mergeay, who warned against the oversimplification of underlying genetic processes. Some of his questions were answered in the next keynote contribution, by Virginie Orgogozo. In her essay on the genetic basis of evolution, she focused on two observations: Firstly, the variation between species was driven mostly by a subset of the variation within species, because within species variation was often caused by loss of function of a gene due to mutations in that same gene, whereas across species (the evolutionary changes that were eventually conserved) this was more often due to differences in regulatory elements. Secondly, mutations contributing to phenotypic variation were often homologous across species, and tended to affect selected genes. She argued that the rapid progress in molecular biology gave us hope that we might soon be able to draw a list of sensible candidate genes for many phenotypic traits.

This could give the impression that knowing and understanding the genetics of evolutionary changes could allow us to predict these evolutionary changes. Already in the opening statement of the e-conference it was mentioned that we needed to be able to predict evolutionary responses to global change. Ferdinando Boero argued that genetics alone could never be used to make any kind of predictions if we did not know the ultimate causes of change, which were ecological. This therefore required a much better understanding of the underlying ecological processes to understand evolutionary changes. But even then, he argued, we would only ever be able to reconstruct past evolutionary responses. Eventually, ecological processes and biotic interactions, except in the simplest systems, were likely to be too complex to allow for any sound evolutionary predictions, according to Ferdinando Boero.

Russel Bonduriansky emphasized in his keynote the role of non-genetic inheritance in adaptation. These could be acquired through learning processes, phenotypic plasticity, and through epigenetic inheritance. Especially the latter were novel, and although genomic tools could increase our understanding of the role of epigenetics (silencing of functional genes through methylation of Cytosine bases), we needed ecological studies to complement our knowledge of epigenetics in laboratory conditions.

Another way to understand circumstances that resulted in rapid evolutionary change was by studying biological invasions, which was addressed in Richard Shine's keynote contribution. He explained that invasive species were themselves subjected to new selection pressures, including intraspecific competition in an invasion front of cane toads that led to differences in dispersal rates among invasive cane toads. Secondly, invasions were good laboratories to study responses of species to selection pressures from exotic species. The invasion of cane toads in Australia showed that different species tended to react differently to cane toads: some by phenotypic evolution, physiology (resistance to toxins), behaviour, but also by non-genetic mechanisms, such as learning not to eat toads. This again highlighted the unpredictable nature of evolutionary responses mentioned by Ferdinando Boero. With regards to management of invasive species, it showed that management itself should include the possibility of evolutionary responses.

Eviatar Nevo wrote a fascinating keynote about hotspots of evolutionary changes, located in so-called evolutionary canyons in Israel. Using an integral approach that included detailed studies of ecology, physiology, geography, genetics and genomics, and over a wide range of taxa, his research revealed a number of generalities of evolution on both micro- and macro-evolution driven by microscale differences.

In the final keynote of the week, Timo Vuorisalo focused on the legal instruments for the conservation of biodiversity in Europe, such as the Habitats Directive, the Natura 2000 network and the Convention on Biological Diversity. He highlighted the lack of a European long-term perspective on the preservation of evolutionary potential, and on the lack of separate management for different evolutionary significant units. Although this may be intended in the term "genetic isolation" of the Habitats Directive, genetic isolation was not necessarily a result of functional evolutionary adaptations, because genetic drift and inbreeding could also lead to strong genetic isolation, cases in which further isolation should be avoided. Elena Bukvareva further commented on the conservation of evolutionary potential in Europe, with a focus on the different roles of intraspecific and interspecific biodiversity in relation to environmental stability. She argued that we should not necessarily focus on maximizing biodiversity, but rather on optimal levels, and explained the principles underlying this concept.

Summary for week 2: 'Evolutionary responses to anthropogenic pressures'

Hans Van Dyck opened discussion by outlining the importance of incorporating evolutionary dimensions in conservation management strategies and called for a better insight and understanding of patterns underlying evolutionary processes. Hans-Peter Grossart agreed with these points and emphasized the need to take the complex interrelationships between organisms, populations and ecosystems into account when trying to understand evolutionary processes and changes in biodiversity.

Kuke Bijlsma outlined a major threat for the persistence of biodiversity: fragmentation. He argued that from a population genetics perspective, fragmentation of populations resulted in small, isolated populations that were subject to genetic drift and inbreeding and that these processes tended to cause decreased fitness, decreased tolerance to environmental stress and impeded adaptive responses to changing and stressful environmental conditions. On the other hand, Ferdinando Boero suggested that fragmentation was not necessarily detrimental to biodiversity; he argued that fragmented populations were conducive to evolutionary change, in both an anagenetic and cladogenetic fashion. Similarly, Francois Bonhomme agreed that it was possible for fragmentation to, on occasion, promote local adaptation and the rise of evolutionary novelties. Pablo Goicoechea developed these ideas further, highlighting that the scale of fragmentation was an important factor to consider, as was the species and the mobility of its gametes.

Discussion then ensued on the topic of John Stewart's keynote contribution: evolutionary processes during past Quaternary climatic cycles. He outlined that ecological community make-up was affected by climate change in the Quaternary and that this was probably both the cause of, and caused by, evolutionary processes such as species evolution, adaptation and extinction of species and populations. Jan Jansen agreed with this and highlighted the need to also study evolutionary processes that were triggered by historic land use practices in socio-economic and political-administrative settings. Martin Sharman responded with a very provocative contribution, which sparked a great deal of debate around the issue of the burden human-kind impose on our planet. Gernot Gloeckner and Balint Czucz agreed with Martin Sharman, but Balint reasoned that ecologists had an important role in communicating to society about how to create resilient systems. Martin Sharman called for future research on understanding how we could stop the loss of biodiversity. Arturo Arino stressed the importance of assessing what biodiversity was being lost and how it was being lost in order to be able to attempt to establish a sustainable relationship with the world we live in.

Joachim Mergeay advised that the role of biologists was to clearly document and study the loss of biodiversity, and to come up with scientific evidence for the role of biodiversity in ecosystem services and ecosystem resilience to disturbance. Rasmus Ejrnaes agreed with this, but also highlighted that while optimal resource exploitation could conserve ecosystem services, it could also lead to the loss of biodiversity; he used the examples of managed forests and organic farming. Ferdinando Boero warned that to solve the biodiversity problems imposed by global change, it was necessary to tackle the ultimate causes (i.e. human overpopulation) rather than focussing only on proximate causes. He also argued that ecosystem goods and services were provided by few species, when compared to the whole of biodiversity. He argued, therefore, that it was not enough just to concentrate on preserving 'useful' species, but that there was a need to make politicians understand that the economic values of biodiversity were not the only reason to preserve it. This view also shared by Pablo Goicoechea.

Luisa Orsini and Joachim Mergeay gave examples of how neutral and selective variation in natural populations along extended time axes could be used to unravel patterns of adaptation to global change. They highlighted the value of dormant propagules as a way to reconstruct past evolutionary changes. On a similar topic, Katalin Török, Gabriella Kutta and Geza Kosa used the Pannonian seed bank as an example of conserving the genetic basis of evolution of vascular plants. Viktor Kotolupov stated that all biological systems had common characteristics within the framework in which they evolved. An example of a biological system was given by Adrianna Vella and Noel Vella, who presented a case study as an example of how genetic diversity influenced fish evolution and conservation in the Mediterranean.

Mark Visser emphasized the importance of assessing the adaptation potential of two major climate change induced shifts: changes in phenology and range shifts. He argued that the rate of adaptation was mainly set by the rate of micro-evolutionary responses. Pablo Goicoechea suggested Mark Visser's contribution showed a good way to link climate change with biodiversity loss, and he further argued that micro-evolutionary responses would be driven by standing genetic variation (instead of by new mutations), thereby highlighting the importance of genetically diverse populations with high evolutionary potential. Equally, Vladimir Vershinin argued that as a result of this it was the pre-adaptive features of species and populations that played a critical role in their survival. Similarly, Stefan Schindler and colleagues highlighted the need to further investigate the plasticity and evolutionary potential of plant and animal species. Their contribution summarized the results of the 2nd annual meeting of the Austrian Platform for Biodiversity Research (BDFA) and highlighted key areas for future research on evolutionary responses to anthropogenic pressures. On the same topic, Sabine Hille focussed on the importance of gaining a better understanding of species life history traits and their ability to respond to phenology shifts in food abundance as a result of climate change.

Francisco Rodriguez-Trellez looked at our current understanding of genetic responses to recent climate change. He focussed his contribution on previous studies carried out on the fruit fly Drosophila. He highlighted the need for a causal link (instead of a mere correlation) to be established between climate and certain genetic traits such as chromosomal inversions, and the need to gain a better understanding of the genetic architecture underpinning the 'climate-sensing' character set.

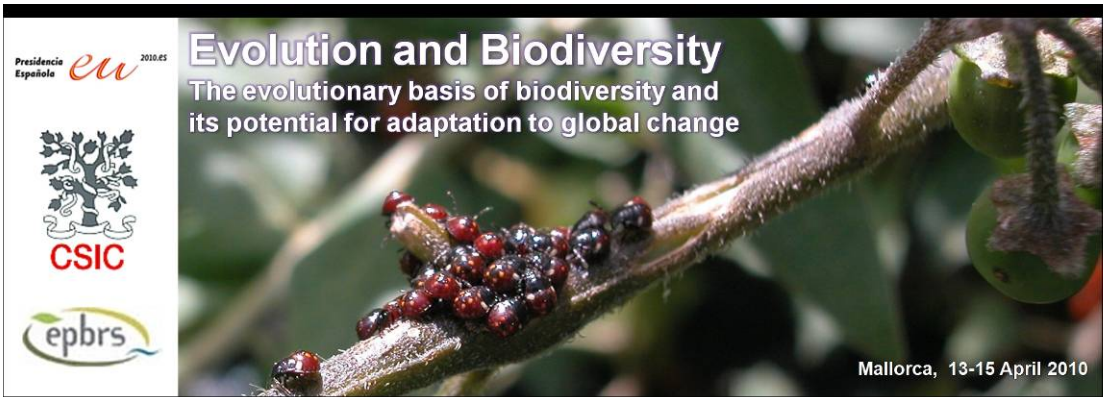
Summary for week 3: 'Evolution in complex systems and co-evolutionary networks'

The week started with a keynote from Andrew Hendry, who examined the interactions between ecology and evolution in contemporary time. He outlined three examples at the population, community and ecosystem level and highlighted the need to further understand how contemporary phenotypic changes influence ecological variables on similar time frames. In response, Martin Sharman proposed that future research was required to gain a better understanding of the evidence for and against critical transitions in ecosystems and to characterise the tipping points. Simona Mihailescu used the Romanian Natura 2000 network as a case study for maintaining biodiversity in complex ecosystems. She called for future research to evaluate the impact of human activities on species, habitats, landscapes and ecosystems. Peter Bridgewater questioned how useful protected areas were for evolutionary potential. He considered the possibility that protected areas may lead to the decay of complex systems, while evolution was forced to continue in urban systems. Andreas Tribsch and colleagues provided another detailed list of research recommendations, which came out of the 2nd annual meeting of the Austrian Platform for Biodiversity Research, focussed on this week's topic of evolution in complex systems and co-evolutionary networks.

Pedro Jordano introduced the topic of multi-species interactions; he argued that they were the key to understanding evolution and the consequences of species losses in order to ensure the persistence of the whole ecosystem network. Luis Santamaria and Miguel Rodriguez-Girones highlighted the need to understand the labile nature of multi-species interactions and to predict their dynamics. They argued that pollination and dispersal networks should be used as a model to investigate co-evolutionary responses to landscape and climate change. In response to this contribution, Ferdinando Boero stressed the need for further knowledge on species interactions and emphasised that the intricacies of both positive and negative interactions required detailed knowledge of species natural history. Edit Kovacs-Lang emphasised the importance of studying functional diversity to gain a better understanding of the functioning of complex biological systems.

The topic of metacommunities was covered by Mark Urban who highlighted the need for future theoretical models to incorporate multi-species interactions in order to be able to assess species responses to climate change. Luc De Meester continued this discussion by outlining the concept of evolution in metacommunities as an integration of evolution, community ecology and space. He highlighted how eco-evolutionary dynamics could impact on species composition and trait changes across environmental gradients in space and time. Rasmus Ejrnaes and Hans Henrik Bruun outlined their hypothesis of the community-level birth rate (CBR) in the process of evolution in plant communities and highlighted its importance for the build-up of species over time during the assembly of a community and for the build-up of the species pool by migration and speciation. Yiannis Matsinos summarised the concept of Population Viability Analysis (PVA) as a management tool used in conservation biology to evaluate risk of extinction. He examined how the role of uncertainty on extinction probability affected PVA predictions.

The week ended with two keynote contributions that focussed on the ‘Geographic mosaic of co-evolution’ framework. Michael Hochberg examined co-evolutionary patterns and processes and called for future research to establish how complex environments affected genetic and species biodiversity in tightly and loosely coupled interactions and networks. John Thompson highlighted the importance of developing a science of applied co-evolutionary biology and emphasised the need to gain a better understanding of the ecological underpinnings of the co-evolutionary process. On a similar topic, Tiiu and Kalevi Kull summarised the development of contemporary research on coevolution, focussing on the concept of consortium.



Research priorities

Fiona Grant, Joachim Mergeay & Juliette Young

1. Research needs to evaluate the evolutionary basis of biodiversity:

Genetic techniques and mechanisms:

- Gain a better understanding of genetic and genomic processes underlying biodiversity dynamics, functional genetic variation and adaptation
- Investigate the role of genetic versus non-genetic and epigenetic mechanisms in phenotypic change and evolution
- Further understand how non-genetic inheritance might contribute to adaptation in rapidly changing environments
- Better understand the genetic basis of phenotypic change by including genomic techniques in non-model organisms
- Further understand why inversion frequencies change directionally in the long-term

Biological invasions:

- Better understand evolutionary responses to disturbance using biological invasions as natural laboratories
- Further understand the role of phenotypic plasticity versus rapid evolution in invasive species
- Further understand the circumstances that result in rapid evolutionary change in some species, but not others using biological invasions as natural laboratories
- Assess the evolutionary potential of alien and native hybrids and the consequences of introgression of natives and taxonomically related aliens into gene pools of native species

Management and preservation of evolutionary processes:

- Assess the minimum viable population size needed in order to make conservation status nationally favourable
- Further explore the evolutionary potential of refugial populations and populations along environmental gradients by analysing functional genetic variation
- Chart the phylogenetic distribution and inter-taxon variation in trans-generational responses to factors such as temperature
- Further understand how trans-generational responses might contribute to population growth and persistence
- Investigate the role and potential of evolutionary change in specialist versus generalist species

2. Research needs to assess the evolutionary responses to anthropogenic pressures:

Response to global change:

- Interpret patterns of change and understand the ultimate and proximate mechanisms behind these patterns

- Further understand the relationship between evolution at the species level driven by global change and the cascading effects of this evolutionary change on communities and ecosystems
- Better understand impacts of global change on future biota by studying non-analogue past communities
- Further understand the relationship between ecological and evolutionary change in response to environmental change using long-term monitoring data (time series, paleogenetics, museum specimens)
- Understand how individualistic responses to climate change alter species distributions and food web structure
- Further study the adaptability of species to different climate regimes in a given study area
- Further understand shifts in species phenology as a result of environmental change

<u>Anthropogenic pressures:</u>

- Identify evolutionary processes and selection regimes in urban environments
- Further understand the factors that affect ecosystem resilience, resource constraints and their internal dynamics
- Identify critical transitions in ecosystems, and characterise, where possible, the tipping points
- Further develop models to study the persistence of biodiversity under anthropogenic stress, taking into account the genetic consequences of population fragmentation
- Investigate the plasticity and evolutionary potential of organisms in relation to changes in land use

<u>Fragmentation:</u>

- Assess the role of fragmentation in reducing or enhancing evolutionary responses
- Further understand the consequences of changes in population fragmentation on gene flow and genetic drift
- Further understand the adaptation plasticity of populations that are genetically eroded due to habitat fragmentation

<u>Plastic and evolutionary adaptation:</u>

- Identify evolutionary significant units, including phylogeographical methods
- Assess the impact of evolutionary change on phenotypic change and/or phenotypic plasticity
- Further understand neutral and selective variation in natural populations along extended time axes (paleogenetics, time series, museum specimens) to explore patterns of adaptation
- Determine nature conservation units, especially with regards to inbreeding and disruption to local adaptation and enhanced evolutionary potential
- Understand the effect of functional redundancy in ecosystems on the rate of adaptation in populations, and ecosystem resilience
- Further understand the genetic architecture underpinning the ‘climate-sensing’ character set of Drosophila
- Better quantify immigration and adaptation rates in local populations using neutral and genomic markers

3. Research needs to identify evolution in complex systems and co-evolutionary networks:

<u>Multi-species interactions:</u>

- Further develop theoretical models that incorporate multi-species interactions, regional dispersal and evolutionary dynamics
- Establish how complex environments affect genetic and species biodiversity in tightly and loosely coupled interactions and networks
- Quantify metacommunity structure of organisms across landscapes
- Further understand the labile nature of multi-species interactions and the processes that govern them

- Establish which factors drive the assembly and structure of mutualistic interaction networks
- Further understand interrelationships between organisms and populations/ networks, particularly those that are disrupted by anthropogenic actions

Co-evolution:

- Understand the generalities of coevolution in complex multi-species networks with the use of models
- Develop models of the distribution of co-evolutionary networks and its comparison with single species responses
- Further understand the ecological underpinnings of the co-evolutionary process
- Better understand how mega-diverse assemblages co-evolve
- Further understand cryptic co-evolutionary networks in order to establish loose mutualism from symbiosis and true co-evolution

Traits:

- Understand the evolution of quantitative traits across natural landscapes
- Assess trait selection in populations under depressed reproduction
- Establish whether communities and ecosystems are indirectly affected as a result of changes in population dynamics, or directly affected by the evolution of traits.

Complex systems:

- Understand how complex self-organising systems interact with ecosystems
- Determine when true feedbacks occur between ecological processes and evolution
- Further understand how feedbacks between ecology and evolution change biota across all hierarchical levels of biological organisation
- Further develop climate envelope models to explicitly take dispersal limitation into account
- Further understand the role of structural and functional diversity in the performance of complex biological systems
- Further understand the role of community-level birth rate in order to assess the impact of communities and environments on evolution
- Further understand how contemporary phenotypic changes influence ecological variables on similar time frames (evo to eco)

4. In order to achieve the above research needs the following enabling actions are necessary:

General:

- Improve knowledge of the natural history of populations, species, communities and ecosystems
- Acknowledge that biodiversity in all its aspects is too complex to allow for detailed predictions about future biodiversity change
- Gain long-term datasets
- Adopt a multi-disciplinary approach to research

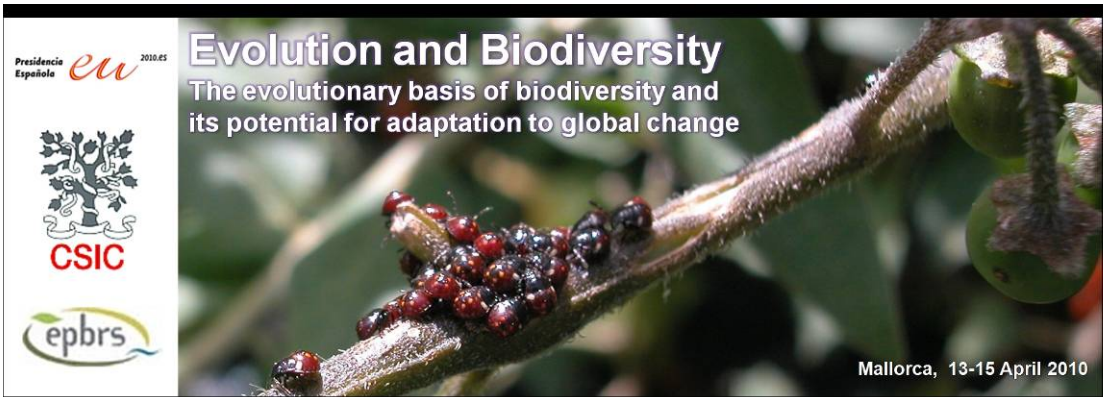
Communication and education:

- Translate evolutionary insights into workable formats and language for policy makers and conservation practitioners
- Develop open-access databases of evolutionary and genetic research
- Improve university education in the basics of ‘organism biology’, namely identifying species, monitoring, biology of species, animal behaviour etc
- Explain and encourage valuation of biodiversity that transcends the ecosystem services argument

Conservation management strategies:

- Incorporate an evolutionary perspective and take into consideration adaptive genetic processes
- Target not only extant diversity, but also the processes and environments promoting a high community-level birth rate

- Protect communities with optimal natural diversity, i.e. natural communities with low diversity may be as important as those with high diversity
- The nature protection strategy should take into account both species and intra-species diversity as an interconnected system
- Use data on genetic diversity of multiple species in order to systematically design conservation areas and compare the resulting conservation networks with existing ones
- Focus on endemic and IUCN listed species as these are often located in refugia and will lead to data for targeted conservation efforts regarding these species



List of contributions

Title of contribution	Author(s)
Session I: The evolutionary basis of biodiversity	
Opening statement	Joachim Mergeay
Human perspectives on biodiversity	Stefaan Blancke
RE: Human perspectives on biodiversity	Francois Bonhomme
RE: Human perspectives on biodiversity	Joachim Mergeay
RE: Human perspectives on biodiversity	Pierre-Henri Gouyon
RE: Human perspectives on biodiversity	Felix Rauschmayer
RE: Human perspectives on biodiversity	Ferdinando Boero
RE: Human perspectives on biodiversity	Joachim Mergeay
RE: Human perspectives on biodiversity	Ferdinando Boero
RE: Human perspectives on biodiversity	Bernard Kaufmann
Towards a mechanistic understanding of biodiversity dynamics	Joop Ouborg
RE: Towards a mechanistic understanding of biodiversity dynamics	Joachim Mergeay
The genetic basis of phenotypic evolution: important results for biodiversity management	Virginie Orgogozo
Non-genetic inheritance and environmental change	Russel Bonduriansky
Biological invasions and evolution	Richard Shine
Research of evolution in action across life at 'evolution canyons'	Eviatar Nevo
Conserving evolutionary potential in Europe	Timo Vuorisalo
RE: Conserving evolutionary potential in Europe	Elena Bukvareva
Preserving ongoing evolutionary processes	Andreas Tribsch et al.
Session II: Evolutionary responses to anthropogenic pressures	
Changing organisms in changing anthropogenic landscapes	Hans Van Dyck
RE: Changing organisms in changing anthropogenic landscapes	Vladimir Vershinin
RE: Changing organisms in changing anthropogenic landscapes	Ferdinando Boero
RE: Changing organisms in changing anthropogenic	Pablo Goicoechea

Title of contribution	Author(s)
landscapes	
RE: Changing organisms in changing anthropogenic landscapes	Hans-Peter Grossart
RE: Changing organisms in changing anthropogenic landscapes	Ferdinando Boero
RE: Changing organisms in changing anthropogenic landscapes	Vladimir Vershinin
Fragmentation does impair adaptive responses to environmental stress	Kuke Bijlsma
RE: Fragmentation does impair adaptive responses to environmental stress	Ferdinando Boero
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Understanding evolutionary processes during past Quaternary climatic cycles: Can it be applied to the future?	John Stewart
RE: Understanding evolutionary processes during past Quaternary climatic cycles	Martin Sharman
RE: Understanding evolutionary processes during past Quaternary climatic cycles	Gernot Gloeckner
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RE: Understanding evolutionary processes during past Quaternary climatic cycles	Ferdinando Boero
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Resurrection ecology, zombie biology, paleogenetics and genomics: reconstructing evolutionary responses of natural populations to past selection pressures	Luisa Orsini and Joachim Mergeay
RE: Resurrection ecology, zombie biology, paleogenetics and genomics	Katalin Torok et al.
RE: Resurrection ecology, zombie biology, paleogenetics and genomics	Nina Katrich
Keeping up with a warming world; the importance of the rate of adaptation to climate change	Marcel Visser

Title of contribution	**Author(s)**
RE: Keeping up with a warming world; the importance of the rate of adaptation to climate change	Pablo Goicochea
Evolutionary processes under global change	Sabine Hille, et al.
Evolutionary potential of animal taxa to adapt and survive climate change	Sabine Hille
RE: Evolutionary potential of animal taxa to adapt and survive climate change	Viktor Kotolupov
RE: Evolutionary potential of animal taxa to adapt and survive climate change	Adrianna Vella and Noel Vella
Measuring evolutionary responses to global climate warming	Francisco Rodrguez-Trellez
Session III: Evolution in complex systems and co-evolutionary networks	
Eco-evolutionary dynamics: interactions between ecology and evolution in contemporary time	Andrew Hendry
RE: Eco-evolutionary dynamics	Simona Mihailescu
RE: Eco-evolutionary dynamics	Martin Sharman
RE: Eco-evolutionary dynamics	Peter Bridgewater
RE: Eco-evolutionary dynamics	Martin Sharman
Multi-species interactions	Pedro Jordano
RE: Multi-species interactions	Edit Kovacs-Lang
RE: Multi-species interactions	Tiiu Kull and Kalevi Kull
RE: Multi-species interactions	Andreas Tribsch et al.
RE: Multi-species interactions	Eva Barreno
Introducing space and time in multi-species networks	Luis Santamaria and Miguel Rodriguez-Girones
RE: Introducing space and time in multi-species networks	Ferdinando Boero
Evolution in metacommunities: eco-evolutionary dynamics in space	Mark Urban
Evolution in metacommunities and global change	Luc De Meester
Evolution takes place in communities	Rasmus Ejrnaes and Hans Henrik Bruun
Assessing conservation risks under uncertainty	Yiannis Matsinos
Coevolution in complex environments	Michael Hochberg
The geographic mosaic of coevolution	John Thompson