



ESF - Science Meeting - Final Report

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APPLICATION DATA

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SCIENCE MEETING

Reference Number : **649**
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ESF ACTIVITY

Unit(s) : **LESC**
Activity Title : **Integrating population genetics and conservation biology: Merging theoretical, experimental and applied approaches**
Activity Acronym : **CONGEN**

PROJECT

Science Meeting : **Workshop**
Title of Science Meeting : **Integrating population genetics and conservation biology: Merging theoretical, experimental and applied approaches: An explorative workshop of ConGen**
Location : **Potsdam, Germany**
Date of Science Meeting : **22/04/2005 - 24/04/2005**
Convenor Name : **Professor Ralph Tiedemann, Potsdam, Germany**

BUDGET

Total estimated Expenditure : **21000 €**
ESF Grant requested : **21000 €**
Co-sponsorship Income : **0 €**

BUDGET GRANTED

ESF Grant FUNDING : **21000 €**

ACTUAL EXPENDITURE

Travel : **7166,21 €**
Accommodation : **3212 €**
Meals (lunch and dinner) : **1302,31 €**
Local administrative costs * : **43,57 €**
TOTAL EXPENDITURE : 11724,09 €

* includes: *administrative and technical assistance, printing, photocopying, telephone, fax, email, etc. Additional support for schools may be considered*

Final Report for ESF-Workshop 649

Integrating population genetics and conservation biology: Merging theoretical, experimental and applied approaches

Potsdam, Germany, 22nd-23rd April 2005

compiled by Ralph Tiedemann, University of Potsdam

1) Summary

At this ESF-workshop, the present state-of-the-art of the conservation genetics field was discussed. The discussion was initiated by eight talks of invited experts, followed by topic discussions. The final discussion summarized the current state of conservation genetics. Despite the recent advances of the conservation genetics related-disciplines and the increasing role that conservation genetics is having in conservation biology, several areas have been identified where our knowledge is still insufficient. Topics specifically mentioned include (1) the need of standardization in conservation genetics methods, (2) integration of demographic and genetic data, (3) effects of biodiversity on population stability, (4) the use of non-neutral (fitness-related) markers and microarrays techniques in conservation genetics, and (5) the role of phenotypic plasticity. These issues need to be addressed before we can start to approach conservation genetics in a multidisciplinary way. The advantage of integrating these disciplines were discussed. The integration of experimental, theoretical and applied conservation genetics will certainly have synergistic effects and contribute to improve our understanding of methodological and applied aspects of conservation genetics.

2) Description of the scientific content of and discussion at the event

First, Richard Frankham described in his talk "*Conservation Genetics: Where are we now and where do we need to go?*" the state-of-the-art. Genetics contribute to conservation biology as genetic factors contribute to extinction risk, genetic information helps resolve taxonomic uncertainties, and molecular genetic methods contribute to forensics and to providing information on aspects of species biology important to conservation of threatened species.

While many areas require research or management actions, highest priority should be given to (i) seriously address genetic management of wild populations of threatened species, especially fragmented ones, (ii) agree upon a definition of species for conservation purposes, (iii) collect extensive data on the occurrence and severity of outbreeding depression across a broad range of taxa, and evaluate means for predicting its occurrence, (iv) agree upon a definition for conservation units within species, and (v) evaluate the contribution of genetic factors to extinction risk in asexual, selfing, haplo-diploid and polyploid species.

The second talk by Phil Hedrick was on "*Measuring Population Structure and Effective Population Size with Examples from Endangered Topminnows, Salmon, and Florida Panthers*". Understanding both population structure and effective population size are fundamental to conservation genetics. These concepts were illustrated by discussing four topics: (1) Measuring population structure using highly variable markers, such as microsatellites, may give values that are smaller than for markers with less variation. (2) Estimating and understanding effective population size (N_e) and the ratio of effective population size to census number (N_e/N) are important in successful conservation. (3) In endangered species, small effective population size due to management action is often of great concern. (4) Often the past population size of endangered species is not known or difficult to estimate. All four topics were illustrated with examples from threatened species.

The third contribution by Isabelle Olivieri presented "*A research agenda in single-species conservation evolutionary biology: case-studies in endemic mediterranean plant species*".

She argued that, provided we agree that conservation at the single species level is worthwhile doing (if only as examples), one should as often as possible combine demographic, ecological and genetic studies into an evolutionary framework (Conservation Evolutionary Biology).

That is, we should not aim solely at documenting demographic trends and estimating (past or present) population effective size and gene flow using neutral molecular markers (as often the case in conservation ecology and conservation genetics), but also try to predict (and modify) the course of evolution under the combined action of drift and natural selection, taking into consideration inbreeding depression and heterosis, but also genotypes or phenotypes

themselves. As illustrations, she described her work on *Brassica insularis* and *Centaurea corymbosa*, two endemic plant species of the Mediterranean basin. She took the evolution of self-incompatibility and the evolution of dispersal as examples where "evolutionary thinking" could be useful in conservation biology.

The final talk of the first session was given by Markus Fischer on "*Thoughts about conservation genetics, case studies from plants, and conclusions about future directions*".

In his opinion, conservation genetics is fascinating, highly necessary, and nevertheless highly improvable. He argued that genetics matters for conservation for three reasons: as a tool, as far as genetic variation itself is a conservation target, and (most fundamentally) as far as genetic variation matters for plant fitness and population persistence. Today, conservation genetics is biased with regard to questions (mostly addressing non-adaptive evolution; hardly ever addressing biological interactions; hardly ever addressing plasticity), methods (single species, mostly observational, and if experimental, hardly in the field; frequently high-tech), taxa, and ecosystems. In case studies focusing on plant fitness in fragmented landscapes he illustrated that both non-adaptive evolution involving drift and inbreeding and adaptive evolution involving selection matter for conservation, that population size plays an important role not only for drift, and that observational studies can be fruitfully combined with experiments. He concluded that conservation genetics needs to overcome the biases mentioned above, and that it is strongest, when it combines molecular and quantitative observational and experimental data in question- (rather than method-) driven and fitness-minded study designs.

The first four talks were followed by a lively discussion, centering mainly around the question, whether current efforts in conservation genetics pay too little attention to fitness-related quantitative traits.

The Saturday session contained several talks on theoretical concepts and started with the presentation by Oscar E. Gaggiotti on "*Understanding and predicting the effects of global change: Identifying the factors that influence species distributions*". Changing climate forces populations of organisms to adapt to novel conditions and/or change their range with suitable environment. Thus, understanding and predicting the effect of current global change requires the identification of the factors that control dispersal processes and set the limits of species ranges. Current genetic patterns, when combined with environmental data, can help us identify these factors. For many years, this integration of genetic and non-genetic data has been done in a qualitative and ad-hoc fashion; people first estimated the parameters of population genetic models (e.g. N_e , migration rates, composition of colonising groups, etc.)

and then attempted to explain the results using our knowledge about the biology of the species. In this talk it was shown that hierarchical Bayesian approaches combined with Reversible Jump Markov Chain Monte Carlo (RJMCMC) methods allow us to go beyond the simple estimation of parameters and formally test for the factors that control dispersal processes and the degree of genetic structuring of natural populations. The information provided by these methods (i.e. knowledge about the environmental factors that influence the dispersal abilities of a species) can help us predict the effect of global climate change on species ranges.

Next, Mark Beaumont spoke about "*The separation-of-timescales result for the structured coalescent and its implications for conservation genetics*". He reviewed the application of separation-of-timescales approximations to the analysis of population structure. This work, largely driven by John Wakeley and colleagues, implies that many models of demographic history converge on the same basic approximation. This makes it difficult to use genetic data to distinguish between such models. Conversely, if this is a good approximation, it implies that the methods suggested by Cavalli-Sforza and Lewontin and Krakauer for using FST to identify loci subject to local selection are going to be relatively robust to demographic history. These twin aspects were discussed in relation to conservation genetics.

A seminal talk by Jinliang Wang covered "*Population genetics in conservation biology: modelling and data analyses*". In the past few decades, population genetics theory and methods have been applied successfully to the conservation biology and management of endangered species in the wild and in captivity. These applications are largely in two directions. One is to understand the genetic factors affecting extinction risks, and to design and optimize breeding schemes aimed at minimizing extinction risks from these genetic factors. The other one is to infer the population parameters and evolutionary mechanisms that are responsible for the observed amount and pattern of genetic variation in the current populations. As examples, he presented some recent developments in four research areas of conservation genetics: optimizing selection schemes to maximize effective size, evaluating the genetic effects of supporting breeding, estimating the effective size and migration rate from marker data, and inferring genetic relationships among individuals from multilocus genotype data.

The final talk by Ettore Randi viewed "*Conservation genetics in the "Real World"*".

The aims of applied conservation genetics are (1) to preserve genetic diversity (allelic variation, heterozygosity) in natural populations, (2) to preserve the legacy of natural evolution (taxonomic diversity) and (3) to preserve endangered taxa (against extinction).

Preserving genetic variation is essential for the future of the evolutionary process and for a non-destructive use of genetic resources. The conservation of species and ESUs is the main mandate of international conventions on biodiversity. The survival of endangered taxa is a main concern for both international and national action plans. Therefore: "the ultimate test of conservation biology is the application of its theories in actual management situations" (Soulé 1986). In his presentation, Ettore Randi suggested how theoretical and experimental population genetics can support practical conservation genetics efforts.

The final discussion identified several important future directions for conservation genetics, namely (1) the need of standardization in Conservation Genetics, (2) integration of demographic and genetic data, (3) effects of biodiversity on population stability, (4) the use of non-neutral markers and microarrays techniques in Conservation Genetics, and (5) the role of phenotypic plasticity. Multidisciplinary approaches are still scarce, but have the potential to greatly advance the field of conservation genetics.

3) Assessment of the results and impact of the event on the future direction of the field

The main disciplines which try to resolve the above mentioned problems in the conservation genetics field would vastly improve their effectiveness, should their potentials be combined.

However, when trying to resolve some of these problems, the real situation is much more complex and attacking one problem evokes many new ones. Conservation biologists have increasingly turned to molecular genetics to study threatened populations. One goal of these studies is to use current patterns of genetic structure to elucidate underlying population processes, in particular, those dealing with migration dynamics. However, this approach has some serious limitations. Importantly, because many different population processes, such as population bottlenecks or local extinction lead to similar patterns of genetic structure, particular processes are difficult to infer from such patterns. In addition, the population genetic models most commonly applied to these systems are based on equilibrium conditions typically not found in nature, surely not in disturbed ecosystems. Influences of current and historical conditions are not easily separated. Furthermore, neutral molecular marker loci will provide little insight into adaptive variation, unless a large fraction of the former are tightly linked to the relevant quantitative-trait loci. Therefore, a lack of molecular divergence among populations at neutral loci is potentially uninformative, as it cannot exclude local adaptations. The complexity and the problems associated with the use of genetic investigations for conservation purposes may partly explain why this kind of investigation has largely been confined to controlled laboratory conditions. There is however a rising discontent with the lack of ecological relevance of many laboratory experiments and an awareness of that extrapolation from laboratory findings to real-world situations is often impractical. An additional taxonomical bias exists in the literature, as still today the large majority of studies in conservation is focused on endangered species of birds, mammals and reptiles. The long-

term preservation of biodiversity requires understanding not only of the demography and genetics of small populations, but also of the ecology and evolution of abundant species.

In the light of the tremendous advances of the different sub-disciplines of conservation genetics, despite the evident limitations that are afflicting such advances, an apparent optimistic mood seems to impregnate the scientific community. However, as it often happens in disciplines where the advances have happened too quickly, some shortcomings regarding the robustness of the fundamentals on which this discipline has been build, are getting more and more evident. In fact, most of the fundamentals of conservation genetics are more or less postulates, which have rarely been demonstrated empirically and from which several corollaries have followed which also need validation. As a result, all these sub-disciplines can still substantially benefit from a further development of their theoretical foundations.

4) Final Program of the meeting

Schedule

Friday, April 22: Chair Volker Loeschcke

- 13:30 **Kuke Bijlsma** (University of Groningen) *Opening and introduction*
- 14:00 **Richard Frankham** (Macquarie University) *Conservation Genetics: Where are we now and where do we need to go?*
- 14:45 **Philip W. Hedrick** (Arizona State University) *Measuring Population Structure and Effective Population Size with Examples from Endangered Topminnows, Salmon, and Florida Panthers*
- 15:30 Coffee break
- 16:00 **Isabelle Olivieri** (University of Montpellier) *A research agenda in single-species conservation evolutionary biology : case-studies in endemic mediterranean plant species*
- 16: 45 **Markus Fischer** (University of Potsdam) *Thoughts about conservation genetics, case studies from plants, and conclusions about future directions*
- 17:30 Topic discussion
- 19:00 Dinner at the “Krongut Bornstedt”

Saturday, April 23: Chair Ralph Tiedemann

- 9:00 **Oscar E. Gaggiotti** (University Joseph Fourier) *Understanding and predicting the effects of global change: Identifying the factors that influence species distributions*
- 9:45 **Mark Beaumont** (University of Reading) *The separation-of-timescales result for the structured coalescent and its implications for conservation genetics*
- 10:30 Coffee break
- 11:00 **Jinliang Wang** (Institute of Zoology) *Population genetics theory and methods in the modelling and data analyses in conservation biology and management*
- 11:45 **Ettore Randi** (Istituto Nazionale per la Fauna Selvatica) *Conservation genetics in the "Real World"*
- 12:30 Lunch at the ” Drachenhaus”
- 13:30 **Discussion session and closing remarks**
- 15:30 Coffee break

16:00 **Steering Committee meeting**

19:00 Dinner at the “Historische Mühle - Mövenpick”

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