



ESF - Science Meeting - Final Report

In Confidence

This form must be signed and return to the ESF Finance Department.

APPLICATION DATA

Page 1/2

SCIENCE MEETING

Reference Number : **635**
Insertion date : **15/03/2005 12:52:38**

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 : **Refining the conservation genetics paradigm: genetic sources of extinction, environmental stress, and the maintenance of adaptive diversity**
Location : **Santiago de Compostela, Galicia, Spain**
Date of Science Meeting : **15/11/2005 - 18/11/2005**
Convenor Name : **Dr. Carlos Garcia, Corunha, Spain**

BUDGET

Total estimated Expenditure : **21600 €**
ESF Grant requested : **20000 €**
Co-sponsorship Income : **1600 €**

BUDGET GRANTED

ESF Grant FUNDING : **23500 €**

ACTUAL EXPENDITURE

Travel : **6286,43 €**
Accommodation : **8542,88 €**
Meals (lunch and dinner) : **5123,16 €**
Local administrative costs * : **462,27 €**
TOTAL EXPENDITURE : 20414,74 €

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

Refining the conservation genetics paradigm: genetic sources of extinction, environmental stress, and the maintenance of adaptive diversity

*ESF Workshop Santiago de Compostela Galicia Spain, November 17-19 2005.
Organizers: Ilik Saccheri and Carlos Garcia*

1) SUMMARY

Forty two invited and thirteen self-funding researches attended the workshop, making 27 oral and 29 poster presentations in three days.

One of the focuses of the workshop was the importance of adaptive variation in Conservation problems, and its interplay with inbreeding depression, which is the other main source of genetic threats for population survival. While recent results suggested that inbreeding depression would be a more serious and consistent concern, several presentations showed that adaptive diversity may still be critical for traits involved in disease resistance and other coevolutionary interactions, or in situations of clear, physiological relevant environmental heterogeneity. Several presentations dealt with the optimization of breeding schemes to conserve genetic variation in small populations

The value of genetic markers in characterising adaptive diversity was addressed by several participants. These markers have been the basic tool in most published work on conservation genetics in recent years. They are valuable because they may provide much information about the demography of populations, but present limitations at measuring the variability of the genes most relevant for conservation problems, i.e., those related with the fitness of individuals and the viability of populations

The second aim of the workshop was to determine the possible value of selection to reduce genetic load in small populations. Optimum schemes were proposed for the application of this selection, but it was concluded at the same time that unless most deleterious mutations have relatively large effects on fitness and the species has reproductive ability high enough to cope with the depressed fitness and thus increased risk of extinction with inbreeding, it is not justified to apply a breeding program aimed to eliminate deleterious recessive genes by enforcing inbreeding and selection to a population of conservation concern. Thus, this approach does not seem to be very promising in general.

Overall, the programme of the workshop presented a rather well balanced array of conservation genetics problems, provided a reasonably good view of the role of adaptive variation and also of the dynamics and population effects of deleterious genes causing inbreeding depression. However, a deeper knowledge of the genetic architecture of inbreeding depression is needed to optimize in practice the genetic management of threatened species.

2) DESCRIPTION OF THE SPECIFIC CONTENT OF AND DISCUSSION AT THE EVENT

Forty two invited and thirteen self-funding researches attended the workshop, making 27 oral and 29 poster presentations in three days. As explained in our original proposal, the two main aims of the workshop were:

- 1) deconfounding the effects of inbreeding depression and reduced adaptive variation on mean fitness and extinction risk, particularly in relation to environmental stress; and
- 2) outcomes of selection on genetic load in small populations and metapopulations for effective population size and mean fitness.

The first aim was addressed by Garcia and Vilas, who found that inbreeding depression was, at least in the short term, a much more serious concern than loss of adaptive diversity for the viability of reintroduced populations of an annual plant. Their results could not dismiss the existence of significant or even important adaptive variation in this plant species, but showed at least that samples of individuals taken in a single, genetically varied population could be sufficient to recolonize typical habitats within the original area of distribution of this species. Other participants found important roles for adaptive variation, however. Interestingly, these findings tended to be related with Major Histocompatibility Complex (MHC) (studied in marine mammals by Hoelzel and Vasselakos, and reviewed by Sommer), which is involved in immune recognition, susceptibility to infectious diseases and mating preferences. Variation in these genes is likely to be maintained by heterozygous advantage or frequency-dependent selection, so that their effect on population viability could be more in relation with the maintenance of genetic variation itself rather than with the evolution of an optimum genotype. The data presented by Puurtinen et al. could reflect a similar situation. They found that, while inbreeding depression was limited in the populations of freshwater snails they studied, parasite resistance increased with the level of genetic diversity of these populations. All these results indicated that maintaining population variability in itself, at least for genes involved in disease resistance and other coevolutionary interactions, could be critical for the conservation of many species.

Adaptive diversity may also be important in situations of clear environmental heterogeneity. Tejedo et al. found clear evidence of local adaptation of toad subpopulations to breeding ponds differing in saline concentration. This suggested that any identified habitat differences having clear functional consequences on fitness should be taken into account when discussing conservation issues. On a related note, Savolainen described a research project to study the conservation implications of life history differences between plant species; Zayed showed how the reproductive biology of haplodiploid insects may influence strongly their response to a loss of genetic variation; and Matyas discussed the possible effects of climate change-induced shifts in the distribution area of Central European forest trees. The field is now open to look for the genes involved in these functional differences that are important for adaptation. Lurgiader et al. explained their work using cDNA microarrays to identify genes causing the resident and migratory phenotypes within populations of salmonid fishes.

The value of genetic markers in characterising adaptive diversity was addressed by several participants. These markers have been the basic tool in most published work on conservation genetics in recent years. They are valuable because they may provide much information about the demography of populations, but present limitations at measuring the variability of the genes most relevant for conservation problems, i.e.,

those related with the fitness of individuals and the viability of populations. Cano Arias presented fish and amphibian examples showing how population differentiation in neutral markers is constrained by large population sizes even when populations are completely isolated, but uncoupled with differentiation in genes coding for quantitative traits and levels of additive genetic variance. Frankham et al. showed how measures of genetic variability based on neutral microsatellites in a laboratory population of fruit flies failed to track the changes in variability for allozymes and quantitative traits potentially more related with flies' fitness. They showed also how balancing selection might slow the rate of loss of genetic variation for functionally relevant traits in contrast with neutral markers. Presentations dealing with wild, small populations also found some mechanisms slowing the loss of genetic variance. Haag and Ebert found that clonal competition favoured heterozygosity in four allozyme loci in *Daphnia*, and Consuegra showed that long distance gene flow may maintain considerable amounts of genetic variation even in very small salmon populations. In fact, small population size could even favour gene flow in some cases. Petit found that pollen limitation and the extremely small size of a very isolated population of Mediterranean oaks could have favoured the arrival of pollen from very distant populations with enough frequency to maintain unexpected levels of genetic variation.

Several presentations dealt with the optimization of breeding schemes to conserve genetic variation in small populations. Caballero made a review of recent work in this field. Van Rijswijk compared the conservation of evolutionary potential in subdivided and undivided laboratory populations of fruit flies in a homogeneous environment and found an advantage for undivided populations. Toro and Fernandez reviewed and presented new methods for using genetic markers to estimate coancestry between individuals. Such methods will be critical for the genetic management of populations conserved in the wild. Perrin described an index to measure the ability of a metapopulation to resist both genetic drift and demographic extinction.

The environmental dependence of inbreeding depression could be a very important issue in the Conservation practice. If this dependence were important, the environmental change associated for example with the reintroduction of a species to the wild, or the recolonization of very heterogeneous habitat could result in marked changes in inbreeding effects. Therefore, the outcome of a given intervention would be difficult to predict. Bijlsma found synergistic relationships between inbreeding depression and environmental stress in fruit flies, but Keller failed to detect a clear relationship in a review of animal, mostly birds, experiments.

The second aim of the workshop, to determine the possible value of selection to reduce genetic load in small populations, was directly addressed by Wang through stochastic simulations. He found that a breeding scheme with equal within- and between-line selection and crossing alternatively with full-sib mating was the most desirable scheme for purging deleterious mutations. However, he concluded that unless most deleterious mutations have relatively large effects on fitness and the species has reproductive ability high enough to cope with the depressed fitness and thus increased risk of extinction with inbreeding, it is not justified to apply a breeding program aimed to eliminate deleterious recessive genes by enforcing inbreeding and selection to a population of conservation concern.

Direct evidence obtained by Pedersen et al in a cDNA microarray experiment with fruit flies indicated that many genes change their expression level in response to inbreeding, and thus that many genes might generate inbreeding depression. If this was the case, deliberate purging could be of limited use in conservation. In fact, no

experiment has shown unambiguous evidence that purging can be efficient against inbreeding depression in the short term in a small population. García-Dorado showed in her presentation however, that purging could be more effective in the middle term for populations of not too small size. López-Fanjul showed that changes in genetic variance after population bottlenecks would hardly increase the evolutionary potential of endangered species.

Finally, some presentations dealt with conceptual matters. Frankham's opening presentation provided an overall and updated introduction to Conservation Genetics, O'Hara discussed objective procedures to define and delimit populations, and Ouburg discussed areas of research that could result in the expansion and refining of the conservation genetics paradigm: distinguishing between individual and population average inbreeding when discussing extinction risk; having a deeper understanding of the many possible relationships between small population size and extinction risk; considering population size and degree of isolation as separate variables affecting simultaneously to extinction risk; comparing the effects of these two variables in endangered and non-endangered populations, to understand better the nature of genetic threats of extinction; and to use modern genomics to study the population genetics of functional genes, to get a deeper understanding of the process of adaptation and to separate the role of natural selection from the effects of genetic drift.

Most of the poster presentations were of a more applied tone. In this sense, they were a good complement to the more theoretical content of oral presentations. They showed conservation problems and ongoing conservation schemes in domestic sheep (Brdic et al.; Koban), brown bear (García-Garitaigotia), Iberian lynx (Godoy), red deer (Gomendio et al.), spotted suslik (Gondek and Konopinski), grouse (Segelbacher), Imperial eagles (Martínez-Cruz and Godoy), Galapagos iguanas, Iberolacerta lizards (Naveira et al.), Bombina (Hauswaldt et al.) and Bufo toads (Rogell), Rana frogs (Matsuba; Teplitsky and Laurila), brown trouts (Martínez et al.), Amphipods (Källström), Melitaea butterflies (Sarhan), and forest trees such as pines (Robledo-Arnuncio), spruce (Heuertz et al.), chestnuts (Fernández-López) and poplars (Vanden Broek et al.).

Some other posters discussed more theoretical problems such as the genetic architecture of inbreeding depression (Reszka et al.; Saccheri), the use of genetic markers to measure genetic diversity (Gunn et al.; Windig), the significance of core and range-marginal populations for species conservation (Hampe; Whitlock), the role of mutational input of genetic diversity on adaptation (Teotonio et al.), inbreeding depression for canalisation (Sorensen et al.), and a discussion of indices to measure genetic diversity (Sherwin et al.).

3) ASSESMENT OF THE RESULTS AND IMPACT OF THE EVENT ON THE FUTURE DIRECTION OF THE FIELD

This workshop was a great opportunity for the meeting of Conservation Genetics researchers working in conceptual and theoretical issues, through laboratory experiments or computer simulations, with researches that are more involved in actual conservation plans for real endangered populations. Perhaps not very surprisingly, most of the information went from theoreticians and laboratory researchers to those occupied with the management of real populations, as the opportunities to do formal research are reduced for the latter. However, these managers offered a wide and varied view of the nature of Conservation Genetics problems, and in some cases provided useful information about population genetic mechanisms important in Conservation. For example, several different presentations revealed an important role for mechanisms maintaining and restoring to some extent genetic variation in real endangered populations. This was interesting because many theoretical analyses tend to overlook these mechanisms.

Overall, the programme of the workshop presented a rather well balanced array of Conservation Genetics problems, provided a reasonably good view of the role of adaptive variation and also of the dynamics and population effects of deleterious genes causing inbreeding depression.

This workshop could have a considerable impact on the future of the field, as it assembled many influential and active research groups working in Conservation Genetics in Europe. A list of the main lines of research emphasized by this workshop it would include:

- 1) Obtaining a better understanding of the role and the nature of adaptive variation in population survival.

- 2) Obtaining a deeper knowledge of the genetic architecture of inbreeding depression, to optimize in practice the genetic management of threatened species.

- 3) Obtaining a more rigorous distinction between the effects of true inbreeding depression and those of genetic drift.

WORKSHOP PROGRAMME

ARRIVAL Wednesday 16 November 2005

19:00 **Registration at Hotel Rosarosae**
21:00 **DINNER**

DAY 1 Thursday 17 November 2005

9:20 **INTRO**

- 9:30 Richard Frankham
 'Genetics and extinction'

- 10:30 Joop Oubourg
 'The rough edges of the conservation genetics paradigm'

- 11:05 Lukas Keller
 'Inbreeding depression and conservation biology: the right answer to the wrong question?'

- 11:40 **BREAK** (30min)

- 12:10 Carlos López-Fanjul
 'Changes in the genetic variance-covariance matrix after bottlenecks'

- 12:45 Carlos García
 'Genetic sources of extinction: a field experiment'

- 13:20 Nicolas Perrin
 'On metapopulation resistance to drift and extinction'

- 13:55 **LUNCH** (90min)

- 15:30 Christoph Haag
 'Selection for heterozygosity among equally inbred *Daphnia* clones'

- 16:05 Mikael Puurtinen
 'The effects of genetic variability and mating system on reproductive output and parasite resistance in populations of an aquatic snail'

- 16:40 Amro Zayed
 'Death by diploidy: sex determination and elevated extinction risk in haplodiploids'

- 17:15 **BREAK** (30min)

- 17:45 **Poster session**

- 19:00 **BREAK**

- 21:00 **DINNER**

DAY 2 Friday 18 November 2005

- **9:30** Kuke Bijlsma
‘Environmental and genetic stress in relation to population extinction: insights from *Drosophila*’

- **10:30** Marielle van Rijswijk
‘Consequences of fragmentation on stress resistance and evolutionary potential in experimental metapopulations of *Drosophila melanogaster*’

- **11:05** Kamilla Pedersen
‘Effects of inbreeding and temperature stress on genome-wide gene expression patterns’

- 11:40 **BREAK** (30 min)

- **12:10** Miguel Tejedo
‘Genetic basis of local adaptation in *Bufo calamita* to hyperosmotic aquatic environments’

- **12:45** Outi Savolainen
‘Genetics of local adaptation and response to environmental change’

- **13:20** Csaba Mátyás
‘Genetic limits of tolerance and stability of zonal forest cover in a changing climate’

- 13:55 **LUNCH** (90 min)

- **15:30** Carlo Largiader
‘Gene expression diversity involved in life history differences in salmonid fish’

- **16:05** Simone Sommer
‘The importance of immune gene variability (MHC) in evolutionary ecology and conservation’

- **16:40** Rus Hoelzel
‘Evolution of the MHC DQB locus in marine mammals: evidence for differential selection pressure in regional populations’

- 17:15 **BREAK** (30 min)

- 17:45 **Discussion**

- 19:00 **BREAK**

- 21:00 **DINNER**

DAY 3 Saturday 19 November 2005

- **9:30** Armando Caballero
‘Genetic management strategies’

- **10:30** Aurora García-Dorado
‘The genetic consequences of moderate size population’

- **11:05** Jinliang Wang
‘Effects of population structures and selection strategies on the purging of inbreeding depression due to deleterious mutations’

- 11:40** **BREAK** (30 min)

- **12:10** Richard Frankham
‘Loss of genetic diversity in finite populations’

- **12:45** Miguel Toro
‘Estimating coancestry using molecular markers’

- **13:20** José Cano
‘Caution about the use of microsatellite markers as single predictor of conservation value’

- 13:55** **LUNCH** (90 min)

- **15:30** Sofía Consuegra
‘Asymmetric gene flow and the evolutionary maintenance of genetic diversity in small, peripheral Atlantic salmon populations’

- **16:05** Rémy Petit
‘Recovering from extreme founder events during invasion’

- **16:40** Bob O’Hara
‘What is a population?’

- 17:15** **BREAK** (25 min)
- 17:40** **Discussion**
- 19:15** **BREAK**
- 21:00** **DINNER**