



ESF - Science Meeting - Final Report

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APPLICATION DATA

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SCIENCE MEETING

Reference Number : **1088**
Report submitted : **27/06/2007 09:15:50**

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 : **Adaptive vs neutral genetic variability in conservation genetics**
Location : **Tvärminne Zoological Station, Finland**
Date of Science Meeting : **09/02/2007 - 13/02/2007**
Convenor Name : **Dr. Bob O'Hara, Helsinki, Finland**

BUDGET

Total estimated Expenditure : **24750 €**
ESF Grant requested : **24750 €**
Co-sponsorship Income : **0 €**

BUDGET GRANTED

ESF Grant FUNDING : **20000 €**

ACTUAL EXPENDITURE

Travel : **0 €**
Accommodation : **0 €**
Meals (lunch and dinner) : **0 €**
Local administrative costs * : **0 €**
TOTAL EXPENDITURE : 0 €

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

Adaptive vs neutral genetic variability in conservation genetics

Summary

The meeting took place at Tvärminne Zoological Station near Hanko, on the south coast of Finland. The purpose in organising the meeting was to bring together researchers interested in investigating the importance of adaptive and neutral processes for phenotypic divergence in natural populations, and the conservation implications of this research. The formal part of the meeting consisted of 21 talks, along with 6 posters and two formal discussion sessions. The presentations varied from theoretical talks to presentations of empirical data, laying out approaches to investigating whether population divergence can be explained by neutrality, or whether selection needs to be invoked. In both the talks and the discussion sessions, it became clear that issues of divergence are being studied actively, and that there are developments from both the theoretical side (e.g. in understanding how Q_{ST} behaves under neutrality) and the empirical (e.g. from developments in genomics). The workshop helped in synthesising the knowledge we have at present, and in showing directions for future work, and for application of the work in the conservation context.

Scientific Content

The formal part of the meeting consisted of 21 talks, along with 6 posters and two formal discussion sessions. The presentations varied from theoretical talks to presentations of empirical data. These were interspersed between each other in the programme, so there was less incentive to skip a session.

Q_{ST} is a statistic used for quantitative traits, and can be compared to F_{ST} , a measure of genetic divergence. However, one point that emerged from the meeting was the utility of F_{ST} for analysis of adaptive divergence in its own right. David Balding presented methods for using F_{ST} estimated for individual loci to detect selection: in essence, a large value of F_{ST} (compared to a population average) suggests that a locus could be under selection. Pierre Taberlet proposed the “Population Adaptive Index”, which builds on the locus-specific F_{ST} approach to produce an index that has potential for use in conservation genetics to identify populations that are adapted to their specific locale.

Several talks discussed theoretical issues around Q_{ST} and its estimation. Jerome Goudet and Judith Miller both showed that the usual assumption that, under neutrality, $Q_{ST}=F_{ST}$ may not be true, as it can be affected by (respectively) dominance and stochastic fluctuations within an evolutionary history. Mike Whitlock also discussed how Q_{ST} should be compared to F_{ST} , and suggested some approaches to calculating population-specific Q_{ST} s.

Several speakers outlined their work using Q_{ST} in their studies. Armando Caballero showed how the sinking of the oil tanker Prestige off the north-west coast of Spain changed the genetic variation in shell morphology of marine snails (*Littorina saxatilis*), and Barbara Giles showed evidence for disruptive selection over short spatial scales in red campion (*Silene dioica*). At the opposite scale, Isabel Magalhaes used F_{ST} - Q_{ST} comparisons to show evidence for divergence between species of Lake Victoria cichlids. Divergence due to adaptation was also observed from molecular data. For example, Mikael Lönn showed that there was significant divergence in a third of AFLPs in *Cirsium arvense* (creeping thistle) between habitat types in Uppland, Sweden.

Several talks concentrated on clinal variation: Timo Knürr looked at differentiation for budset time along a latitudinal cline of Scots pine (*Pinus sylvestris*), and Pernille Sarup showed variation along an altitudinal gradient for starvation and knock-down resistance in *Drosophila buzzatii*. The analysis of genetic structure along a cline was discussed by Patrick Waldmann, who showed the effects that selection at loci has on the inference of isolation by distance.

The first discussion session was split into two sections, one focussing on empirical and the other on theoretical matters, and the outcomes of both were reported in the second discussion session. Both discussions covered a variety of subjects, but one of the main points that came out of the theoretical group was that the divergence of multiple traits was not well understood. Averaging Q_{ST} over traits is not a good solution, because there may be correlations between traits, and it may also cover up divergence in a few traits. The quantification of the effect of selection on Q_{ST} is also still an open question. The second (empirical) group discussed how Q_{ST} - F_{ST} comparisons can be used, within the grander scheme of understanding divergence: essentially, it seems to be a tool for early investigation of the problems, to see whether there is non-neutral divergence.

Overall, the meeting gave a survey of the state of the field at the moment. It is clear that molecular markers will be used increasingly: as the technology improves, it will be easier to genotype many individuals for many markers. The challenges are to develop the theory behind the behaviour of these markers under neutrality and selection, so that it is easier to detect loci under selection, and to characterise the type of selection. Added to this, techniques for relating these to phenotypic traits need to be developed: ideally we would like to measure the traits in the wild, to avoid problems with interpretation arising from using laboratory-based experiments.

Results and Impact

Our intention in organising the meeting was to clarify where we are in the analysis of adaptive and neutral diversity, and see what are the open questions for future research. In this regard, the meeting was very successful. Some of the questions that were raised included the following:

1. How should multiple traits be combined for Q_{ST} analyses?
2. How do multiple traits diverge under neutrality?
3. How will the genomic revolution affect our approaches: should we be preparing to move to the DNA level (e.g. using genome scans or microarrays)?
4. How should the importance for conservation of populations be assessed?

By raising these questions, the workshop should focus future work in these directions.

As with any workshop, there are indirect benefits. In one late talk, the speaker (Chris Wheat) presented some analyses of locus-specific F_{ST} s that he had only thought to do during the workshop: he is now following up these result, by looking at two loci he had identified as being under selection. At least two additional manuscripts have come about as a direct result of the workshop (indeed one, albeit a short note, has already been submitted to *Evolution*).

Final Programme

Saturday

9.00-9.15: Introduction

9.15-10.00: Jerome Goudet, *Empirical and theoretical issues in the estimation of Q_{ST}*

10.00-10.30: Isabel S. Magalhaes, *Identifying traits under disruptive selection in speciation of Lake Victoria cichlids*

10.30-11.00: Coffee

11.00-11.30: Timo Knürr, *Analysing Differentiation and Selection in Timing of Bud Set Along a Latitudinal Cline of Scots Pine*

11.30-12.00: Pierre Taberlet, *The Population Adaptive Index: A New Index to Help Measure Intraspecific Genetic Diversity and Prioritize Populations for Conservation*

12.00-13.00: Lunch

13.00-13.45: Emmauelle Porcher, *Adaptive vs neutral genetic structure in predominantly inbreeding species*

13.45-14.15: Mikael Lönn, *Few neutral AFLP-markers in *Cirsium arvense* – landscape scale local adaptation.*

14.14-14.45: Pernille Sarup, *Acclimation change clinal variation in knock-down time and starvation in *Drosophila buzzatii*.*

14.45-15.15: Coffee

15.15-15.45: Barbara Giles, *High gene flow, strong drift AND diversifying selection in populations on the move!*

15.45-16.15: Jack Windig, *Genetic diversity within and across populations: Q_{ST} , F_{ST} , Marker estimated kinships and genetic variance covariance matrices in cattle populations.*

16.15-16.45: Poster Presentations

16.45-18.00: Poster Session

18.00: Dinner + Sauna

Sunday

9.00-9.45: Armando Caballero, *Quantitative versus neutral genetic variation: applications in evolutionary and environmental impact studies using the marine snail *Littorina saxatilis**

9.45-10.30: Bob O'Hara, *F_{ST} and Q_{ST} : Where are we, and where could we go?*

10.30-11.00: Coffee

11.00-12.00: *Discussion Session*

12.00-13.00: Lunch

13.00-13.45: Judith Miller, *Q_{ST} and F_{ST} under neutrality*

13.45-14.15: J.P. Vähä, *Inferring spatial structuring and ecological correlates of Atlantic salmon within a river system.*

14.15-14.45: Björn Rogell, *Quantitative and neutral genetic variation in northern fringe populations of the natterjack toad*

14.45-15.15: Coffee

15.15-16.00: David Balding, *Some Methods for Detecting the Signature of Adaptive Selection*

16.00-16.30: German Orizaola, *Adaptability in natural amphibian populations: a comparison between pool frog (*R. lessonae*) and moor frog (*R. arvalis*), two species with contrasting conservation status in Sweden*

16.45-17.15: Daniela Salvini, *Gene flow in a Mediterranean oak complex: the effects space and time*

17.15-18.00: Discussions

Monday

9.00-9.45: Mike Whitlock, *Demographic and genetic factors affecting the distribution of F_{ST} values for neutral loci*

9.45-10.30: Patrik Waldmann, *The effect of selection on inference of isolation by distance based on a Bayesian spatial method*

10.30-11.00: Coffee

11.00-11.30: Chris Wheat, *Studying balancing selection in a metapopulation.*

11.30-12.00: Justin Travis, *Mutation surfing and the dynamics of neutral versus adaptive mutations at expanding range margins.*

12.00-12.45: Lunch

12.45: Bus to Helsinki

Posters

Olivia Burton, *Ecology and divergence of the wagtail *Motacilla alba* in Great Britain*

Joao Sollari Lopes, *Approximate Bayesian Computation vs MCMC*

Cino Pertoldi, *The consequences of the variance-mean rescaling effect on effective population size*

Bénédicte Poncet, *Potential of AFLP technique and regression models to identify genes under selection in response to environmental variation: hundreds of AFLP markers in 198 populations of the alpine plant *Arabis alpina*.*

Simona Sušnik, *Conservation Prospects for Admixed Populations: a case of Adriatic Grayling (*Thymallus thymallus*) in Slovenia*

Maciek Konopinski, *Influence of glacial refugia and postglacial expansion on genetic variation in Clouded Apollo butterfly (*Parnassius mnemosyne*) in Central Europe.*