



ESF - Short Visit Grant - Final Report

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APPLICATION DATA

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SHORT VISIT GRANT

Reference Number : 1563
Report submitted : 23/03/2007 16:51:40

ESF ACTIVITY

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

PROJECT

Title of the proposed research project : Landscape genetics of five mammal species of the Eastern Italian Alps
Date of visit (starting date) : 05/03/2007
Duration : 10 day(s)
Travel Granted : 350 €
Applicant's Name : Dr. Cristiano Vernesi, Trento, Italy

MAXIMUM AMOUNT GRANTED

TOTAL ESF Grant FUNDING : 1200 €

HOST INSTITUTE(s)

Professor Oscar Gaggiotti, Grenoble Cedex 9, France

ACTUAL EXPENDITURE

Travel Cost : 246 €

Cristiano Vernesi
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**SCIENTIFIC REPORT OF THE ESF SHORT VISIT GRANT (REFERENCE # 1563): MONDAY MARCH 5TH
/ THURSDAY MARCH 15TH, 2007**

The main purpose of the visit to prof. Gaggiotti's lab was to analyse my data set (mtDNA and autosomal microsatellites from five mammal species, chamois, red deer, roe deer, mountain hare and brown hare) within the framework of a new method developed by prof. Gaggiotti's team. That method implements a hierarchical Bayesian approach that makes full use of the data in terms of allele frequencies. This procedure is particularly tailored for identifying the environmental factors that underlie the spatial patterns of observed genetic diversity. My data set is, in fact constituted by genetic and environmental georeferenced variables.

The method is actually implemented in a dedicated software, GESTE, so that my work has been mainly devoted to set up the input files and to carefully check and interpret the results. Of course, before each run, I discussed with prof. Gaggiotti which factors were to be included in the analysis. The method, in fact, allows performing the correlation between the genetic data and two environmental variables at time. The discussion was, therefore, aimed at better understanding which factors could be considered more relevant to be compared against genetic data. Along with a set of factors common to all the species (namely temperature, mean annual precipitation, altitude, Euclidean and least-cost path distance among populations), other species-specific factors were taken into account, according to the specific life history traits of each species.

The parameters are estimated by the method through the use of Markov chains so that we were particularly careful about reaching the adequate level of convergence of the runs. It is well known, in fact, that Markov chains can be prone to be stuck in some local optima: in order to avoid it, the comparison of the output of different runs was performed.

The results of the analyses showed that none of the environmental factors considered can effectively explain the current pattern of genetic structure recovered for the different species. It has to be reminded that for four out of the five species (i.e. mountain hare, red deer, roe deer and chamois) the genetic data highlighted a clear picture of genetic structure: there is a strong and statistically significant differentiation between populations living in the areas East of the Adige river valley and those living in areas West of this valley. The fact that we didn't recover any signature due to the effect of some environmental variable is, therefore, reinforcing the view that the main cause of the recovered genetic structure is actually linked to the presence of this strong barrier.

Together with prof. Gaggiotti we, thus, decided to devise a strategy for better understanding whether the genetic structure pattern recorded is due to the effect of the barrier or to some colonisation process.

To come out with statistical testing of this hypothesis it will be necessary to extend our collaboration that, therefore, has to be considered continued for all the time necessary to reach the expected results. It is foreseen that specific coalescent simulations will be run.

My short visit grant has created the basis for a more stable collaboration with the host institution, the main purpose being not only the publication of the results in a peer reviewed journal such as *Molecular Ecology*, *Evolution* or *Conservation Genetics* but also some future studies in the field of landscape genetics.

The paper resulting from this short visit will certainly represent a significant improvement in the conservation genetics literature: in fact, very few are the studies in which different species from the

same restricted area are analysed with several unlinked markers. Even fewer are the studies that take into account not only genetic data but also all the main environmental features of that area. Our study has the potential for really understanding which are the most important causes in shaping the current pattern of genetic diversity and structure. In other terms, the opportunity is offered for considering at the same time evolutionary, abiotic and biotic factors and understanding the interplay among them. The results of this study will hopefully constitute an extraordinary support to local policy makers for improving the design of conservation/management plans in the Alpine ecosystem.