



ESF - Short Visit Grant - Final Report

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SHORT VISIT GRANT

Reference Number : 518
Submission date : 14/03/2005 16:49:36

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 : The use of molecular markers to assist conservation programmes
Date of visit (starting date) : 15/07/2005
Duration : 15 day(s)
Travel Granted : 450 €
Applicant's Name : Miguel Toro, Madrid, Spain

MAXIMUM AMOUNT GRANTED

TOTAL ESF Grant FUNDING : 1725 €

HOST INSTITUTE(s)

Dr. Asko Maki-Tanila, Jokioinen, Finland

ACTUAL EXPENDITURE

Travel Cost : 284 €

Scientific report of the *Short visit to the MTT Agrifood Research Finland* in Jokioinen

The aim of the visit was to discuss on THE USE OF MOLECULAR MARKERS TO ASSIST CONSERVATION PROGRAMMES. The motivation was that the recent development of molecular makers has rise a great interest on its possible use as a tool to improve the management of conservation programs. There are several topics where molecular makers could have an impact. The first is to estimate relatedness between individuals from information of molecular markers. The second is the implementation of optimal methods of management of captive and semicaptive populations or to study mating systems, parental care and dispersal. The third topic is the use of markers as a complementary tool to establish conservation priorities. I have developed new methods on this topics (together with other Spanish colleagues mainly A. Caballero and J. Fernandez, see References) that I thought will be interesting to discuss during my visit

MTT Agrifood Research Finland is coordinating the national programme for the conservation activities in cattle, sheep, horse and chicken in Finland. MTT is representing Finland in the Nordic Genebank for Farm Animals and in the FAO global programme for animal genetic resources.

The visit starts on 26 of July and finish the 13 of August. I developed the activities in the Department of Animal Breeding of the MTT with the chief of the Department Asko Maki-Tanila as counterpart. I can classify the activities according to three aspects:

Seminars: Because I have been working in the topic of the visit both from a theoretical perspective and from a practical one I gave a seminar the 22 of August on Characterisation and conservation of genetic diversity between populations explaining the methodology we have proposed to analyze genetic diversity in a subdivided metapopulation and I gave another seminar the 29 of August on Thoughts on marker-assisted selection where I developed some ideas on the use of markers in a more applied settings.

Work carried out during the visit and preliminary results obtained. I start to analyse 1194 individuals genotyped for 19 microsatellites. They belong to 36 sheep breeds from several countries (23 from Russia, 3 from Finland, 3 from Poland, 2 from Ukraine and 5 from Azerbaijan). The overall genetic diversity was 0.81, part attributed to within breed diversity (0.76) and part to genetic distance between breeds (0.05). The preliminary results indicate that breeds Karakul (Russia) and Capathian Mountain (Ukraine) are the ones that contributed more to the global genetic diversity whereas Olkuska (Poland) and Alands (Finland) the ones that contributed less.

Future collaboration and projected publications. In two or three months I will calculate the loss or gain of diversity if one or several groups are removed, recalculating the global average genetic diversity. We also will consider the following question: if we had to pool the different populations to produce a single one (a synthetic population or a germplasm bank), what would be the contribution of each population to the pool that would maximise its genetic diversity?. Besides, in the MTT other type of analysis (genetic clusters) will be carried out. The joint results will be used in prioritising populations for conservation and in understanding the domestication and cultural history of these populations. The final results will be sent for publication to a relevant international journal.

Other comments. We also discussed and interchange information on other topics: a) The estimation of relatedness from molecular markers and its application to Yukatian horses; b) The optimization of the genetic management of conservation and selection programmes with the use of the software EVA of Peer Berg that I did not know.

Overall impression. I think that the visit has been quite interesting. The Animal Breeding department of MTT is a very active and highly qualified scientifically and it is doing an important work in Biodiversity specially related to the poorly known domestic breeds of some countries as Russia, Ukraine, etc. Finally I was provided with all facilities for making my stay pleasant and scientifically interesting.

References

- Caballero, A. & Toro, M. A. 2000 Interrelations between effective population size and other pedigree tools for the management of conserved populations. *Genet. Res.* **75**, 331-343.
- Caballero, A. & Toro, M. A. 2002 Analysis of genetic diversity for the management of conserved subdivided populations. *Conserv. Genet.* **3**, 289-299.
- Fabuel, E., Barragán, C., Silió, L., Rodríguez, M. C. & Toro, M. A. 2004 Analysis of genetic diversity and conservation priorities in Iberian pigs based on microsatellite markers. *Heredity* **93**, 104-113.
- Toro M, Barragán C, Óvilo C, Rodrigáñez J, Rodríguez C, Silió L (2002) Estimation of coancestry in Iberian pigs using molecular markers. *Conservation Genetics*, **3**, 309–320.
- Fernández J, Toro MA (1999) The use of mathematical programming to control inbreeding in selection schemes. *Journal of Animal Breeding and Genetics* **116**: 447-466.

Madrid 29 August 2005

Miguel A. Toro