

## STRATEGIES FOR INTEGRATING HUSBANDRY, GENETICS, GEOGRAPHIC AND SOCIO-ECONOMIC DATA FOR SUSTAINABLE CONSERVATION

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Michael W. Bruford, Cardiff University, Wales, UK, BrufordMW@Cardiff.ac.uk and the Econogene Consortium (P. Ajmone Marsan, R. Negrini, E. Milanese, M. Pellecchia, G. Canali, Università Cattolica del S. Cuore, Piacenza, Italy; M. Abo-Shehada, Jordan University of Science and Technology, Ibid, Jordan; P. Baret, A. Fadlaoui, Université Catholique, Louvain, Belgium; M. Bruford, G.Juma, T. Perez, Cardiff University, U.K.; R. Caloz, S. Joost, Swiss Federal Institute of Technology, Lausanne, Switzerland; A. Carta, T. Sechi, Istituto Zootecnico e Caseario per la Sardegna, Olmedo, Italy; M. Cicogna, P. Crepaldi, F. Fornarelli, S. Giovenzana, M. Marti, Università degli Studi di Milano, Italy; P. Dobi, A. Hoda, Faculty of Agriculture, Tirana, Albania; S. Dunner, J. Canon, P. García-Atance, Universidad Complutense de Madrid, Spain; G. D'Urso, S. Bordonaro, D. Marletta Università degli Studi di Catania, Italy; M.A.A. El-Barody, Minia University, Egypt; G. Erhardt, C. Peter, K. Gutscher, S. Lipsky, Justus-Liebig University of Giessen, Germany; O. Ertugrul, Ankara University, Turkey; L. Fesus, A. Istvan, Research Institute for Animal Breeding and Nutrition, Herceghalom, Hungary; A. Georgoudis, K. Karetsoy, G. Kliambas, O. Kutita, J. al Tarrayrah, Aristotle University, Thessaloniki, Greece; G. Hewitt, S. Dalamitra, M. Taylor, L. Wiskin, University of East Anglia, Norwich, U.K.; C.Ligda, National Agricultural Research Foundation, Thessaloniki, Greece; R. Niznikowski, Ewa Strzelec, D. Popielarczyk, Warsaw Agricultural University, Warsaw, Poland; J.A. Lenstra, I.J. Nijman, L.M. Van Cann, Utrecht University, The Netherlands; G. Obexer-Ruff, M.-L. Glowatzki, Universität Bern, Switzerland; F. Pilla, A. Angiolillo, E. Pietrolà, Università del Molise, Italy; P. Taberlet, G. Luikart A. Beja-Pereira, P. England, University Joseph Fourier, Centre National de la Recherche Scientifique, Grenoble, France; J. Roosen, M. Bertaglia, University of Kiel, Germany; R. Scarpa, University of York, U.K.; S. Jones, The Sheep Trust, UK; I. Togan, Middle East Technical University, Ankara, Turkey; M. Trommetter, Université Pierre Mendès, Grenoble, France, A. Valentini, L. Pariset, I. Cappuccio, Università della Tuscia, Viterbo, Italy; A. Vlaic, University of Cluj-Napoca, Romania).

### Summary

The ECONOGENE project is among the first to yield complementary data on population and evolutionary genetics, on animal husbandry practices, from GIS and including socio-economics over a large geographic scale. Integrating this information poses special challenges in livestock conservation because such data have rarely been combined previously and data are both quantitatively and qualitatively diverse. Here, we will discuss issues pertinent to the combination at various scales and to the use of such information to assist conservation management, policy and planning for marginal agriculture in the EU and surrounding countries, drawing parallels with natural genetic resource management but paying special attention to the unique attributes that characterise Farm Animal Genetic Resources on a local, regional and continental scale.

### Keywords

Genetics, adaptation, husbandry, geographical information, socio-economics

## **Introduction**

The aims of the ECONOGENE project focus on extending previous knowledge of sheep and goat biodiversity in western Eurasia including unstudied marginal breeds, by investigating the broad and fine-scale geographic patterns of variation in both species to identify and map populations of high conservation priority and investigating the socio-economic conditions where these breeds are raised. The outcome of this research aims to identify areas where sustainable conservation of the most valuable populations has a high chance of success, using estimates of the economic value of priority breeds and regions to justify specific management or conservation actions. We therefore aim to segue molecular, husbandry, geographic and economic data, retaining the maximum amount of information while needing to summarise the patterns observed from a highly data-rich source at the individual, farm, breed and species level. The specifics of each element of this database and how they have been analysed independently are dealt with in the contributions of Lenstra (1), Joost (2) and Fadlaoui *et al* (3). However, the biggest challenge facing the project from a development perspective is the approach taken to synthesise and combine these diverse elements.

## **Issues when combining data**

What are the specific challenges of analyzing such a dataset? Analysis is ongoing, but several issues are immediately apparent. Firstly, the data from each approach deal with parameters that are measured (and must be summarized) at different scales: molecular data pertain to individuals, populations/breeds and species, geographic data starts at the farm level, progresses through breeds and then can be analysed at any meaningful level beyond this (here, for the European Union, we have taken the standard regional boundaries described by the 'NUTs-3' system), socio-economic data are collected at the farm, breed and NUTs level and husbandry data are collected at the farm and breed level. The disparity among these data sets poses problems and has necessitated, for example, the characterization of summary genetic data at the farm-level (three individuals per breed) to coincide with the geographic, socio-economic and husbandry data and the characterization of breed geographic coordinates (characterized by centroids) to coincide with genetic and socio-economic requirements.

Secondly, the scale issue is also important when asking which comparisons are relevant. For example, husbandry practices may vary at the farm, region or breed level according to, for example, geographical parameters (e.g. altitude), country of origin, levels of regional assistance and all of these may impact on the amount or distribution of genetic diversity at different scales. Further, while the farm and NUTs levels may be the most appropriate for summarizing socio-economic data, they may be less important than the breed or geographic position for summarizing genetic data. The complexity of carrying out many comparisons, and especially inferring process from pattern thus requires extreme care.

Thirdly, there needs to be a 'common currency' among fields if prioritization and policy are to emerge from such comparisons. For example, geographically and socio-economically, it may make sense to focus on specific regions where several breeds and both species play an important role, however these breeds may be neither especially distinctive or diverse at the genetic or husbandry level.

Regarding the latter question, approaches such as those described by Weitzman (4) and Simianer (6) have been developed to derive prioritization methods and these may need to be extended to encompass the complexity of the present dataset. However, additional models for the application of molecular data in conservation also exist in the wildlife literature (e.g. 7, 8), which encompass the still widely debated issue of how to conserve diversity as well as distinctiveness (e.g. 8). Molecular data have been used directly or indirectly to make management decisions in endangered wild populations but using these data remains a

challenge facing biodiversity managers today. Much of the debate focuses on which ‘units’ of diversity that should form the basis of conservation planning. The rise of phylogenetics in conservation raises serious questions about the universality of even the idea of a species, subspecies and breed and their meaning. Moritz (6) defined two levels of conservation unit which could be recognised using molecular markers: the Evolutionary Significant Unit (ESU) and the Management Unit (MU), whose definition involve explicit analysis of the patterns of diversity using commonly applied molecular markers and will not be further discussed here. However, once a conservation unit has been diagnosed, the question of prioritisation arises, and specifically, the importance of preserving distinctiveness (8) as opposed to groups which demonstrate evidence of ongoing diversification (9) – a particularly problematic issue for livestock conservation and the Weitzman Approach. Should we protect those populations with unique adaptations, regardless of their within breed diversity and long-term viability (livestock populations may survive with low genetic diversity if their genetic load has already been purged by selection (10) or should we instead target those breeds which possess large amounts of diversity (either partitioned within or between populations and/or subtypes) since these have the greatest possibility for adaptation to future environmental and market conditions? As already pointed out by Fadlaoui *et al* (this volume), within breed diversity often accounts for the large majority of genetic variation in livestock populations.

#### **Issues within data-types: an example**

Within data-types, complex issues of prioritization and relative importance may arise in different relational contexts. For example, the ECONOGENE project, by analysing genetic variation at functional (genic) loci, which are implicated in phenotypic variation potentially of economic use, as well as those markers which reflect demographic history, provides levels of genetic information which can potentially be used differently within the context of the husbandry, environmental and socio-economic parameters with which it can be linked. For example, currently for sheep, genetic variation at neutral markers *per se*, may not have as strong an implication for the future viability of a livestock breed as the frequency of the ‘ARR’ and ‘ARQ’ alleles in the single gene (PrP) which confers resistance to scrapie, in the present economic and management policy environment. Furthermore, these two measures of variation are not necessarily expected to be related if selection has acted strongly on breeds very recently impacted by scrapie. Clearly, a strongly resistant breed may prove extremely important economically, once the various national scrapie plans are enacted, but this could potentially be the case for a breed despite it lacking any phylogenetic distinctiveness or substantial within-breed diversity as measured by neutral markers. The question arises, which is more important, and should we be taking a short-term or longer-term view?

The complex relationships within and among data types can at least be explored, however, once large datasets such as the ECONOGENE have been assembled. It is not only the means by which data are summarized and combined that requires careful attention, but also the identification of common, or equivalent, aims and goals within and among fields that challenges projects such as ECONOGENE and projects which attempt to take a broad and holistic view of diversity in the modern world.

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