UK Biodiversity Research Advisory Group

GENETIC CONSERVATION RESEARCH NEEDS

FINAL REPORT

Edited by
Michael F. Fay and Richard Ferris

On behalf of the UK BRAG Genetic Conservation Subgroup

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UK BRAG

biodiversity research in action

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1. Introduction

In recent years, the role of genetics in plant and animal conservation has increased both in prominence and in the scope of the questions to which genetic data are being applied. Examination of the UKBAP and other European and global frameworks reveals that many Action Plans (e.g. SAPs in particular) and similar documents contain explicit suggestions for research relying on the collection of genetic data, indicating the importance of genetics in conservation. In addition, many other plans contain recommendations implicitly involving a need for genetic research. Genetic data have been used to inform both *in situ* activities (e.g. translocations, site management) and *ex situ* activities (e.g. which populations/individuals should be sampled for *ex situ* conservation).

To date, the emphasis of UK conservation policy has been on maintaining the genetic distinctiveness of different species, sub-species or populations due to concerns that we need to maintain existing phenotypes, genetic integrity and local adaptations. There are numerous knowledge gaps requiring research.

Some questions are of a relatively straightforward nature, whereas others are more complex, and in some cases it is not clear what type/s of genetic data should be collected or how these should be analysed to answer the questions. Explicit types of questions relying on genetic data in the UKBAP include:

- Are populations distinct, and how can this inform conservation practice? Examples include greater horseshoe bat (*Rhinolophus ferrumequinum*) and sand lizard (*Lacerta agilis*).

- Is this taxon/population/individual native to Britain? Examples include pool frog (*Rana lessonae*) and lady's slipper orchid (*Cypripedium calceolus*).

- Which individuals/populations should be used as source material for translocations? Examples include wild asparagus (*Asparagus officinalis* subsp. *prostratus*) and woolly willow (*Salix lanata*).

- Can genetic data be used to clarify taxonomic problems? Examples include an endemic lady's mantle (*Alchemilla minima*), wild asparagus (*Asparagus officinalis* subsp. *prostratus*), rock sea lavender (*Limonium* endemic taxa) and Scottish crossbill (*Loxia scotica*).

However, faced with environmental change, the conservation of species adaptability and the processes sustaining and providing diversity might be of greater general importance than conserving specific local adaptations. This gives rise to other, less straightforward questions, relating to the role of genetic data in adaptation, response to climate change and in the functional significance of genetic variation.

There is commonly perceived to be a gap in knowledge transfer/understanding between the scientist and the conservation practitioner. Gregory et al. (2006) comment that:

"UK conservation actions which make use of genetic information and which have sought to act explicitly in the best interests of species' genetic sustainability are growing in number. Nonetheless, the expansion of this management approach has been hampered by the technical nature and relative inaccessibility of conservation genetics academic research to conservation practitioners and by gaps in scientific knowledge on questions of direct relevance to applying wildlife management strategies. Conservation actions incorporating genetic information have also tended to be implemented in isolation from each other and, so far, no clear or general policy guidance exists to direct best practice. Thus, there is a need for extended coordination between conservation genetics scientists, organisations involved in wildlife conservation and policy makers so that the best available knowledge and evidence can be used to formulate policy guidance for conservation practitioners."

Although members of this subgroup do not perceive this to be as great a problem as has been suggested, there is still scope for an increase in dialogue between the two groups. It is also clear that different questions can be applied to plants and animals. However, there are many gaps in knowledge relating to the application of genetics to the conservation of individuals, populations and species that apply to both animals and plants. These gaps are the focus of this report.

Increasingly, this raises questions about how we manage not only populations of species, but also habitats and ecosystems at a range of spatial scales. Consideration of the entire "genetic footprint" of species will include the need to understand the role of gene flow across species boundaries and the significance of protected areas and the wider landscape, how their resilience can be enhanced, and new strategies to allow greater adaptation to change. At landscape scales, an understanding of the permeability of habitats to migration between populations, and the appropriate time and source populations from which to supplement such gene flow, will be of importance in the effective management of genetic resources.

In a world in which dramatic changes are happening (and likely to become more extreme), questions of local adaptation are likely to become superseded by questions relating to adaptability in the face of climate change. As such, we should recognise that priorities identified in this report may have to evolve to reflect these changes.

2. Terms of Reference of the Genetic Conservation Subgroup

The terms of reference for the subgroup were as follows:

- Identify the knowledge gaps relating to genetic conservation restricting the delivery of the UKBAP and other European and global frameworks, and the research needed to address these.

- Formulate an outline strategy for research, including prioritisation of key issues and a delivery plan; and recommend a cost-effective process for delivering the research agenda.

- Identify links and potential synergies between UK BRAG genetic research and other biodiversity research programmes, both within UK BRAG and more widely, including EU initiatives (note: restricted to programmes explicitly addressing biodiversity), the Ecological Genetics Group of the British Ecological Society (BES) and the Plant Conservation Working Group.

- Raise the profile of issues surrounding the conservation of genetic diversity

- Encourage effective knowledge transfer among scientists, policymakers, conservation practitioners and the general public

- Facilitate networking in both the national and international research community, including research activities, research needs and dissemination of results

3. Background

This Research Strategy has been developed on behalf of the UK Biodiversity Research Advisory Group (UK BRAG) by a specialist subgroup, members of which exchanged ideas by email (the subgroup did not meet due to time constraints). Members of the subgroup were drawn from a variety of organisations, representing policy makers, researchers and practitioners. The subgroup was chaired by Dr Mike Fay of the Royal Botanic Gardens, Kew. A full list of the people who participated in the discussion can be found in Appendix 1 at the end of this Strategy.

There have been various workshops aimed at bringing together the research and conservation communities and elucidating the remaining research needs. A one-day workshop was held at the Royal Botanic Gardens, Kew in 2001 (Fay *et al*., 2003) to discuss these issues in relation to plants, and a more wide-ranging workshop covering animals and plants was organised UKPopNet in 2005 (Gregory et al., 2006). The conclusions from these meetings formed the basis of the discussions of this subgroup, and the conclusions presented in this report follow on from those formulated at those meetings.

Barbara Jones in her summary for the Kew workshop (pages 35-36) identified several areas where improvement was desirable. These included:

- Education of conservationists in the importance of genetics
- Education of researchers in the needs of conservationists
- Integration of genetics with ecological and biological surveys/research
- Development of a European scale programme covering climate change, evolutionary history, and how British species fit in a wider perspective
- Large scale studies of British species, including common species
- Monitoring genetic effects of management intervention (restoration, importation etc.)

In the UKPopNet report (Gregory *et al.,* 2006), the conclusions (pages 62-71) were grouped under the headings:

- Defining populations
- Defining units of conservation
- Conserving evolutionary processes
- Hybridisation
- Understanding and managing gene flow in the context of adaptation and adaptability
- Understanding adaptation
- Management of species, populations, habitats and landscapes
- Conservation of habitats and landscapes

Under each of these topics, knowledge gaps were identified and research questions and recommendations were suggested (see Appendix 3). There was also a section on policy limitations and responses and a list of actions which should be progressed as a matter of priority.

4. Setting Priorities

It is important to recognise that research priorities will differ, according to whether they are determined by the conservation practitioner community or the research community. This is mainly because conservationists are faced with problems and issues which are often driven by practical and policy requirements which need rapid and focused investigation. However, this does not exclude “blue skies” research; this should continue as a vital underpinning for applied, conservation action.

From the discussions in the earlier UKPopNet workshop (Gregory *et al.,* 2006), the case was made for using genetic concepts and information in conservation. It was generally agreed that there are three main areas in which conservation has underlying genetic concerns:

- The maintenance of the adaptive potential of species in the face of environmental change;
- Avoiding the loss of genetic diversity;
- Avoiding inbreeding and outbreeding depression.

In practice conservationists are currently concerned with:

- Identifying situations where genetic constraints limit population viability;
- Learning whether species can be grouped meaningfully according to the level of genetic risk, in order to identify generic conservation policies;
- Conserving habitats and processes to facilitate evolutionary responses to changing environmental conditions;
- Potential conflicts between species and genetic conservation.

It is important to build a research needs agenda that satisfies these concerns and requirements.

The highest priorities identified by the group were as follows:

Managing genetic diversity *in situ* **HIGH PRIORITY 1**

Aim: *to provide assessments of when genetic problems are likely to occur, and to obtain the necessary information to guide management for mitigation*

The importance of research which considers genetic diversity and landscape management was identified by the UKPopNet workshop (Gregory *et al.,* 2006) and reinforced by an assessment by Hollingsworth *et al.* (in press) of genetic studies on the British flora, which showed this issue to be severely under-represented.

There is a need to provide conditions under which genes, populations and species are able to adapt and survive in a fragmented and changing environment. This is particularly important with respect to climate change, which has the potential to have enormous impacts on habitats and species in the UK. Knowing something about the response of different species to this, and the degree to which they may be able to adapt to such changes, will help some of the fundamental conservation management decisions we will have to make in the near future.

This issue relates to issues of fragmentation, connectivity and edge-of-range populations. Many of our species of conservation concern are at the edge of their range in the UK and may be genetically distinct. The effects of increasing connectivity/reducing fragmentation on adaptation of edge-of-range and small, isolated populations (inbreeding/outbreeding depression etc.) and whether we need to take account of the genetic distinctiveness of British populations are currently key conservation issues. The former is important because habitat connectivity is an important issue in policy circles, e.g. in relation to improving SSSI condition in order to meet the 2010 targets for biodiversity conservation; and the latter is important because of the need to prioritise our actions due to the resource limitations that exist for management activities.

Evolutionary processes are also important in that the targets for getting habitats into favourable condition and/or meeting UK BAP targets, together with increasing agri-environment schemes; will result in much more conservation management. We need to ensure that this management allows evolutionary processes to continue rather than trying to 'preserve' moments in evolutionary time. This also relates to climate change, where organisms need "room to evolve and adapt", and we need to know the best ways to allow them to do this.

The following research tasks have been identified:

- Provide a realistic appraisal of the specific landscape/management conditions over which populations of different species with different life history traits are likely to become genetically isolated, and also to establish their abilities to disperse to new sites.
- Provide combined genetic and field-based studies to evaluate the fitness consequences of genetic isolation versus population networks in the context of different population sizes, different environmental gradients and different species attributes.
- In the context of the above, assess the likely response of different species and populations to large scale environmental change.
- Trial and further develop explicit conservation frameworks aimed at linking the above types of genetic information with targeted management action.

Translocations **HIGH PRIORITY 2**

<u>Aim</u>: *to establish the best strategies for active movement of organisms.*

Managing gene flow through translocations is extremely complex, as many issues need to be addressed. In the face of climate change, these will inevitably become more complex. Frankham *et al.* (2002) list a number of key questions, namely: which individuals to translocate? How many? How often? From where to where? When should translocations begin? When should they be stopped? Although there is a general understanding, including some individual case studies, of how translocations can work and the potential genetic problems associated with poorly selected material

(Hollingsworth *et al.*, in press); robust guidelines need to be developed, based on a more extensive evidence base. Therefore, the following task is identified:

- Further experimentation, meta-analyses and experimental coordination and monitoring of re-introductions, to enable the development of robust conservation guidelines for translocations.

Units to conserve **HIGH PRIORITY 3**

Aim: *to establish the diversity of species/divergent lineages*

A clear link can be seen between this area of genetic knowledge and the conservation of biodiversity. Even where it does not directly inform management, it may create a situation where management must or can take place. For example, recent research on hares (*Lepus timidus hibernicus*) in Northern Ireland (Hughes *et al.,* 2004) has shown very pronounced genetic distinctiveness, i.e. it represents an endemic lineage. This knowledge has led directly to conservation action to afford a greater level of protection to hares in Northern Ireland (McDonald, pers. comm.). Much of the biodiversity found in the UK is known or expected to be a subset of that found elsewhere in Europe, and from a global biodiversity perspective, the lineages of species (or species) that are only found in the UK can be argued to be the most significant.

The following tasks have been identified:

- Identification and conservation prioritisation of divergent intra-specific endemic lineages.
- Develop protocols and increase use of high throughput genetic tools for species identification and discovery, particularly to increase our understanding of the species-level biodiversity of lower plants/invertebrates.
- Coordinate development of dedicated action plans designed to cope with the challenges for actively diversifying and taxonomically complex groups.

Summary

An important priority underlying all this is our knowledge of how genetic markers inform species conservation. If conservation is to invest more effort and resources into genetic research, then we need to have useful answers from which management decisions can be made. All the above research should include elements of defining the best methodologies (not necessarily the latest), data analysis, and inclusion of ecological and demographic data, as well as relationships between genetic measures and fitness.

Issues such as inbreeding and outbreeding depression, taxonomic questions, hybridisation, and genetic factors influencing species invasiveness will continue to be important in general terms. Although targeted research will be needed to answer specific conservation questions, addressing the priorities outlined above will provide significant advances in our knowledge and management practices.

5. Delivery

In order to facilitate the delivery of research, there are a number of associated actions that are required. The UKPopNet workshop (Gregory *et al.,* 2006) considered these and identified four priority actions for immediate action:

- **Genetic Conservation Forum**
  Establish a genetic conservation forum or specialist group, to steer research, target statutory funding, improve science communication and aid implementation of research recommendations.

  This needs to recognise and build upon the excellent work undertaken in support of plant conservation by the Plant Conservation Working Group (Conservation Genetics technical working group). To be truly successful, this group needs to bridge the gap between the research and practitioner communities, helping to facilitate the involvement of conservation geneticists with the development and implementation of management plans (see below).

- **Genetic Conservation Handbook**
  Produce a Genetic Conservation Handbook. The handbook should, provide definitions of terms used in conservation genetics, in a form accessible to researchers, policymakers and practitioners. This should be written and reviewed by representatives of each stakeholder group. Its primary audience is envisaged as being managers without the technical knowledge of genetics, and it should include a glossary of key terms.

  Again, the Plant Conservation Working Group (Conservation Genetics technical working group) has made good progress towards this, with the production of two Natural England Reports, *Genetics and Conservation in the British Flora* (Hollingsworth *et al.,* in press) and the less technical *An Introduction to Plant Conservation Genetics* (Smith and Fay, in press). These should be evaluated and, if necessary, expanded to take account of information required beyond the field of plant conservation genetics. While there are many generalities, there are some specific issues related to animal conservation genetics which need to be highlighted.

  The animal genetics community should consider the possibility of building on these documents or, alternatively, producing the equivalent/s covering animal conservation genetics. There may be a role for UK BRAG in facilitating this action.

- **Integrated Conservation Planning**
  Produce and disseminate a flow chart or appropriate table with guidelines that allow managers, in the first instance, to formulate conservation management plans accounting for conservation genetic needs.

  Ultimately, it would be invaluable to have expert input from conservation geneticists in the management planning process. However, until the mechanism for this has been established (see below), guidelines to support managers are likely to be a useful addition to the decision-making process.

- **Peer Review Database**
  Establish a database of people with expert knowledge, who would be available for consultation and review of species management plans.

  An appropriate system for engaging the conservation genetics research community with conservation practitioners is needed, possibly incorporating a reward structure in order to encourage this activity. A valuable first step is the identification of expertise, and a trial of the added value that this brings to the management planning process should be undertaken.

6. Funding

- **Background**

Given the applied nature of much of the research highlighted, it is a matter of some concern among the sub-group that the major funders concerned with genetics research, namely NERC and BBSRC, have a strong focus on "Blue Skies" research and, where thematic programmes exist, these do not have a strong biodiversity element (for details of current priorities, see below).

Opportunities need to be taken to influence the thinking and prioritisation given to conservation genetics by the Research Councils; and, to this end, the current consultation over NERC's new strategy needs to be used effectively. However, equally important is the need to work in partnership with the two Research Councils, to encourage a jointly-funded programme in this area. With such a foundation in place, it may help to lever additional funding from the Country Agencies, Defra, the Scottish Executive, and others.

- **Funding bodies – an introduction**

BBSRC

Genes and Developmental Biology

BBSRC's *Genes and Developmental Biology Committee* supports research which seeks to establish fundamental principles of genetics and gene function in all organisms, or which seeks to understand developmental mechanisms in animals, plants and model microbes including fungi.

The remit includes: genetics of developmental processes including differentiation; morphogenesis and comparative developmental biology; stem cell biology; genetics of ageing; genomics including sequence analysis and genome organisation; quantitative genetics; behaviour of genes in populations; evolutionary genetics; molecular evolution including diversity and phylogeny; forced evolution; fundamental studies of gene regulation, expression and action; genetics of the cell cycle and recombination; and gene therapy.

The Committee's role is to support high quality basic and strategic research across the breadth of its remit. That remit is very broad and the Committee has developed a themed description of its main activities to help the scientific and user communities to understand the major areas in which it operates. The themes are intended to be illustrative rather than exclusive:

Genome Analysis	
Developmental Biology	BBSRC Priority
Gene Action and Regulation	
Cell Cycle and Recombination	
Evolution and Population Biology	BBSRC Priority

Clearly, the last of these is likely to be most closely aligned with the agenda identified by UK BRAG. This theme covers the related areas of evolution and population genetics. Evolutionary biology encompasses the study of organismal adaptation and origins. Areas of interest address a variety of levels of biological organisation, from molecular aspects of evolution, to organismal structure and performance. Topics that can be addressed include: molecular evolution, genome evolution, speciation, phylogenetics, and evolutionary developmental biology. Population genetics projects may employ molecular genetic, genomic, mathematical and bioinformatics approaches.

The interests of the Committee overlap to some extent with those of NERC. In recognition of this, the Committee particularly encourages applications that investigate the specific molecular and genetic mechanisms that underpin evolution of organisms. Whilst the Committee typically supports projects which study model organisms and populations, projects that study species within their natural environment are not excluded providing that they address a fundamental (and appropriate) biological question of generic relevance.

NERC

Important to note here is that your section on NERC fails to highlight the potential importance of their Blue Skies programme, in which pure and applied conservation genetics can be funded. Quoting from their web site "The world is losing huge numbers of plant and animal species and this loss is accelerating. People are overwhelmingly responsible for this loss. Many NERC-funded scientists in many research centres and universities are investigating: biodiversity loss, the implications of this loss, and how best to target conservation efforts." Furthmore, I was a member of the NERC Biodiversity Research Strategy Working Group, and Blues Skies funding will definitely be made available in large quantities potentially to fund this kind for work, between 2008 and 2012.

Environmental Genomics

The *Environmental Genomics* programme, which has run between 2000-2006, has been acquiring and exploiting sequence data for whole and partial genomes, helping us to understand environmental biology. One important aim has been to demonstrate to the environmental community, in particular regulators and industry, how post-genomic technologies can be applied to tackle environmental issues. The programme has aimed to advance the understanding of how organisms perceive change at the molecular and genetic level, and make functional responses within their local environment, and to what extent variation in these responses is adaptive.

The programme has established a nation-wide community of researchers, both empiricists and theoreticians, with the skills to develop and apply post-genome technologies to the study of how organisms and ecosystems function. Training in genomic techniques, particularly for ecologists who are new to the field, continues to be an important part of the programme.

Post-Genomics and Proteomics

The *Post-Genomics and Proteomics* programme is a five-year themed programme, started in 2004, and explores environmental influences on the genome and proteome, in plants, animals, and micro-organisms. NERC invited the UK science community to put forward ideas for research, and scientifically rigorous topics best fitting NERC's strategic priorities were selected by an advisory group. For example, work is underway to investigate the molecular mechanisms that either stop or let plants expand their ranges into different environments. This may enable us to predict how species' distributions will alter in response to climate or land-use change.

The programme's four themes consider:

(1) integrating post-genomics and proteomics to study host-parasite interactions in aquatic and terrestrial vertebrate hosts in ecology and evolution;
(2) what makes species, populations and taxa resistant or vulnerable to environmental change and environmental impact?
(3) the application of a meta-genomic approach, coupled with measurements of biodiversity and nutrient flux, to study all the genes and proteins in an aquatic or terrestrial microbial assemblage; to improve knowledge of the biogeochemical cycles that underpin sustainable ecosystems; and
(4) environmental regulation of the proteome.

UKPopNet

Another potential route for funding research in this area is through the *UKPopNet* programme. This is a network of institutions, funded by NERC with support from Natural England. The network was founded by researchers from the universities of Aberdeen, East Anglia, Leeds, Sheffield, and York; plus the Centre for Ecology and Hydrology. It addresses two main themes:

(1) Dynamics of biodiversity, and
(2) Sustainable landscapes.

The *Dynamics of Biodiversity* theme develops a strategic approach to the management of the substantial changes in pattern and scale of biodiversity that will inevitably occur in the UK landscape in response to environmental change. There are three studentships funded through this theme which are relevant here:

(1) linking population and genetic changes during range shifts induced by climate change;
(2) consequences of changes in genetic diversity during climate-driven range shifts; and
(3) genetic variation in the landscape.

Centre for Ecology and Hydrology

CEH undertakes a wide range of research focused on conservation genetics or with genetic components, within a number or research themes. The following is not an exhaustive list, but is included here to illustrate this range:

- Estimation of eukaryotic picoplankton biodiversity in lakes

- Analysis of genetic diversity in the freshwater diatom *Asterionella Formosa*
- Development of molecular probes for the identification of phytoplankton
- Developing models of species invasions that incorporate increased biological and environmental detail, such as genetics and habitat variability
- Understanding how elevated mutation rates may lead to antibiotic or pesticide resistance
- Atlantic salmon population structure
- Gene flow between genetically modified crops and conventional crops
- Genetically modified crops and wild plants
- Development and application of molecular genetics to study microbial community dynamics, habitat regulated gene expression, and the functional activity of individual cells

EPSRC

Life Sciences Interface

The *Life Sciences Interface* programme aims to support research at the boundary between the Engineering/Physical Sciences and the Lifesciences, to maximise opportunities for discovery in the lifesciences. The programme funds work in partnership with other Research Councils and/or other EPSRC programmes. Funding is available through responsive mode and specific calls for proposals. The former can include feasibility studies, instrumentation development, long-term studies or equipment to support research. Special measures apply for funding biomolecular science.

Basic Technology Research

The *Basic Technology Research* programme is managed by EPSRC on behalf of the Research Councils. It is intended to create fundamental capabilities for pursuing front-line research to provide the approaches for underpinning future technological development. Proposals need to contribute to a generic technology base, adapted to a diverse range of research problems across the range of interests of the Research Councils.

Defra

Defra's support for genetic research spans a number of Directorates and policy areas. For example, within the *Wildife and Countryside Research* programme, Global Wildlife Division has supported a project on the conservation genetics of basking sharks, using molecular genetic techniques to analyse the population structure and dynamics of basking sharks (*Cetorhinus maximus*) in NE Atlantic waters and those further afield. DNA profiling of birds of prey is another project supported within this programme, building on earlier work on micro-satellite DNA markers for CITES enforcement.

The marine environment policy area currently supports work by CEFAS on the development of population genetics markers in dab (*Limanda limanda*) and European flounder (*Platichthys flesus*), in order to assess population structure in impacted and unimpacted areas. The use of genetic biomarkers will help ascertain the existence of genetically separate stocks around the UK, since they may exhibit markedly different responses to contaminants, disease and other biotic and abiotic variables.

Some research expenditure addresses non-food crops, such as a current project by IGER and PRI to look at genetic improvement of miscanthus for biomass. This aims to assess the genetic resources available in the UK and elsewhere for yield, canopy development, flowering time, over-wintering, and combustion quality; undertake hybridisation and selection; and make improvements to breeding efficiency. There is also research underway to improve short-rotation coppice through breeding and genomics, this work being undertaken by Rothamsted Research (BBSRC) and Southampton University. This aims to deliver a breeding programme and plant materials that will allow further improvement of the willow crop, focusing on the generation of high-yielding, pest and disease-resistant elite genotypes that are optimal for UK environmental conditions.

However, much of Defra's funding for genetics research is directed towards support for policy on Genetic Resources for Food and Agriculture. A keyword search of Defra's research database using the term "genetics" reveals in excess of fifty funded projects since 1998. Naturally, many of these will develop techniques that are transferable to biodiversity conservation, and have considerable thematic overlap, e.g. the agriculture and climate change policy area.

There is considerable potential for overlap and collaboration between the domestic animal and plant genetic resources research funded by Defra and non-domestic biodiversity, e.g. the use of native breeds for conservation grazing for management of native plants and invertebrates.

Wales

<u>The Welsh Assembly Government</u>
Environmental research relevant to Wales is funded mainly by Government Departments and Agencies e.g. Department of Environment, Farming and Rural Affairs (Defra), Natural Environment Research Council (NERC), Environment Agency (EA) and the Countryside Council for Wales (CCW). The Assembly programme aims to complement this research, ensuring that through collaborative funding and steering of projects, specific Welsh issues are researched adequately.

<u>The Countryside Council for Wales</u>
CCW have supported research on forest habitat networks in Wales (in conjunction with Forest Research; Watts *et al.*, 2005), which has relevance to metapopulation dynamics and conservation genetics. Through CCW's new habitat connectivity programme, there is scope for further funding of conservation genetics research.

CCW have supported species reintroduction programmes, such as that concerned with sand lizard (*Lacerta agilis*) populations on sand dune systems in Denbighshire, following earlier work in Flintshire and Meirionydd. This work aimed to establish populations from captive-bred individuals, in order to ensure a good age range and genetic variation.

Northern Ireland

The Environment and Heritage Service (Northern Ireland)
EHS supports research on conservation genetics, e.g. a current study by Quercus on the conservation biology and genetics of the marsh fritillary butterfly (*Euphydryas aurinia*) in Northern Ireland.

European Funding
Through the European Union's Objective 1 funding, the Northern Ireland Community Support Framework (CSF) has provided research funding associated with biodiversity, through the *Building Sustainable Prosperity Programme*. For example, Quercus have undertaken research on: (1) establishing a molecular basis for a Species Action Plan for the red alga *Ahnfeltiopsis* spp.; (2) conservation genetics of Northern Ireland seagrass beds; (3) conservation genetics of Northern Ireland peat bogs.

Scotland - The Scottish Executive

The Scottish Executive Environment Rural Affairs Department (SEERAD) funds a wide range of agricultural, biological and environmental research. The main programme of research amounts to approximately £45m each year and is managed on behalf of SEERAD by the Science and Analysis Group (SAG). The research funded is mainly strategic and applied work; basic research, which forms a maximum of 10% of the portfolio, is supported only where relevant to policy needs. SAG-funded research is conducted primarily through its Main Research Providers (MRPs), which include MLURI, the RBGE, SAC, and SCRI.

MLURI
A variety of projects have genetic research components. PROBECO – processes and biodiversity in native woodland ecosystems – includes work on phytochemical diversity in Scots pines (*Pinus sylvestris*), to understand its genetic basis. Variation in monoterpene concentrations in Scots pines is an important issue in research concerned with how trees might affect the feeding preferences of capercaillie (*Tetrao urogallus*); this research project is funded by the British Ecological Society.

Research on the management of red deer (*Cervus elaphus*) at an appropriate scale, looks at the degree of genetic variability between local subpopulations of deer, allowing researchers to determine the degree to which genes are exchanged between them, and how the genetic flow differs between the sexes. With this information, the research team are studying how other factors limit deer distribution and gene flow in and between populations, such as landscape topography, vegetation cover, distance, and the structure and density of local deer populations.

RBGE
The RBGE is very research active in this area, through the Genetics and conservation section. The remit of the section is: (1) to evaluate patterns of intra-specific variation, (2) elucidate evolutionary population genetic processes, and (3) support and establish scientifically-based conservation programmes. The Population Genetics group works on three themes: (1) evolution, (2) molecular tool kits, and (3) conservation. Specific programmes include the International Conifer Conservation

Programme (ICCP); the Conservation Genetics Programme; and the Molecular Tools for Biodiversity Research Programme.

The Conservation Genetics Programme aims to underpin the formulation of appropriate conservation management strategies (focusing on the conservation of genetic biodiversity). The overall aim of the Molecular Tools for Biodiversity Research Programme is to provide empirical and theoretical assessments of the molecular tools used in biodiversity research (to establish situations under which different techniques and methods of analysis can be informative or misleading).

RBGE leads research on the taxonomy, genetics and ecology of sub-arctic willow scrub, in a partnership with both SAC and SCRI; as well as the Scottish Plants project.

SAC

Within the Land Economy research group at SAC, genetics research is focused on socio-economic issues associated with the SCRI-led research on barley, potato and soft fruit genetics (see below). Within the Crop and Soil Systems research group, genetics research is part of a number of projects, among them sustainable crop systems – biodiversity and function in plants, which aims to identify the extent of genetic variation in key below-ground traits, especially under low nutrient supply (in order to identify characters for selection and breeding of plants for sustaining essential ecosystem processes).

SCRI

The Genetics Research Programme undertaken by SCRI focuses on: (1) genome biology, (2) genetics and breeding, (3) genes and development, (4) biodiversity, and (5) bioinformatics, biomathematics and statistics. The biodiversity theme is concerned with clarifying the relationships between existing groups of species, investigating the link between sequence variation, recombination and linkage disequilibrium; and quantifying biological diversity of native and endangered species for conservation purposes. SCRI also has current research on barley, potato and soft fruit genetics, as part of SEERAD's *Profitable and Sustainable Agriculture – Plants* programme.

The Forestry Commission

The Forestry Commission supports research through Forest Research as well as commissioning research from other providers. Support is provided for research on: (1) the breeding and production of conifers, and (2) selection and testing of conifers. The former aims to provide a bank of material of known genetic quality for advanced tree breeding and production of seed orchards. In addition, this work develops micropropagation techniques for use in the vegetative propagation of improved clonal material. The selection and testing of conifers focuses on breeding programmes for five coniferous species: sitka spruce (*Picea sitchensis*), hybrid larches (*Larix eurolepsis*), Scots pine, Douglas fir (*Psuedotsuga menziesii*) and Corsican pine (*Pinus nigra*).

The *Genetic Conservation* programme aims to improve understanding of the genetic resources present in British tree populations, by: (1) utilising modern molecular methods to assess the genetic structure and diversity of British populations of native tree species such as oak (*Quercus* spp.), black poplar (*Populus nigra*), wild cherry (*Prunus avium*), and aspen (*Populus tremula*); and (2) setting up provenance trials of native tree species in order to assess the level of adaptive variation present within and between British populations.

The Genetics Society

The Genetics Society provides field-based research grants of up to £1K, to cover travel and accommodation associated with a field-based genetic research project. The scheme is only open to members of the Genetics Society, and there is a single closing date for applications each year.

7. **Glossary**

BBSRC	Biotechnology and Biological Sciences Research Council
CCW	Countryside Council for Wales
CEFAS	Centre for Environment, Fisheries and
CITES	Convention on Trade in Endangered Species
EHS	Environment and Heritage Service (Northern Ireland)
EPSRC	Engineering and Physical Sciences Research Council
EU	European Union
IGER	Institute of Grassland and Environment Research
MLURI	Macaulay Land Use Research Institute
NERC	Natural Environment Research Council
PCWG	Plant Conservation Working Group
PRI	Plant Research International
RBGE	Royal Botanic Garden Edinburgh
SAC	Scottish Agricultural College
SAPs	Species Action Plans
SCRI	Scottish Crops Research Institute
UKBAP	United Kingdom Biodiversity Action Plan
UK BRAG	The UK Biodiversity Research Advisory Group
UKPopNet	UK Population Biology Network

8. References

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9. Appendices

Appendix 1
Membership of the UK BRAG Genetic Conservation Sub-group

Mike Bruford	Cardiff University
Joanna Drewitt	Scottish Executive
Michael Fay	Royal Botanic Gardens, Kew
Richard Ferris	UK BRAG Secretariat, JNCC
Peter Hollingsworth	Royal Botanic Garden, Edinburgh
Barbara Jones	Countryside Council for Wales
Robbie McDonald	Queen’s University, Belfast
Nigel Maxted	University of Birmingham
Richard Smithers	Woodland Trust
Ian Taylor	English Nature

Appendix 2
Links to relevant organisations

Defra Science and Research Projects, Genetics
http://www2.defra.gov.uk/research/project_data/projects.asp?M=KWS&V=Genetics

The Biotechnology and Biological Sciences Research Council, Genes and Developmental Biology
http://www.bbsrc.ac.uk/science/areas/gdb.html

The British Ecological Society, Ecological Genetics Group
http://www.britishecologicalsociety.org/articles/groups/genetics/

The Genetics Society
http://www.genetics.org.uk/

The Natural Environment Research Council, Environmental Genomics
http://www.nerc.ac.uk/research/programmes/genomics/

The Natural Environment Research Council, Post-Genomics and Proteomics
http://www.nerc.ac.uk/research/programmes/proteomics/background.asp

The Plant Conservation working Group, Genetics sub-group
http://rbg-web2.rbge.org.uk/pcwg/index.htm

The Royal Botanic Garden Edinburgh, Genetics and Conservation Section
http://www.rbge.org.uk/rbge/web/science/research/conservation/index.jsp

The Royal Botanic Gardens Kew, Molecular Systematics
http://www.kew.org/scihort/molec.html

Appendix 3

A summary of the knowledge gaps and research needs identified by the UKPopNet workshop, *The conservation of genetic diversity: science and policy needs in a changing world* , 19-21 October 2005.

General conclusions and knowledge gaps

The recommendations in the table are by no means exhaustive and provide a basis for future discussions. They reflect opinions expressed at the workshop and are not prioritised in any way.

• Defining populations

Knowledge gaps	**Research Questions**	**Recommendations**
Definition of a population	How can populations and their boundaries best be defined? What is the relative importance of geographic and genetic criteria in defining populations? Which attributes of the population concept do we need to consider most, to facilitate effective conservation and the assessment of conservation priorities? How does the scale of populations vary for different taxa (UK/regional/European e.g. consideration of 2010 targets)? How does our definition of a population allow us to define more accurately units such as ESUs or MUs, and are these useful concepts?	Apply genetic approaches that define populations or identify migrant individuals, in order to address these questions, e.g. assignment tests or measurements of contemporary gene flow based on genetic markers. Improve our understanding of the scale of populations, to determine at what scale species should be managed.
There is limited understanding of what constitutes an 'effective population size' and its relevance to conservation?	Is the concept of effective population size useful to the management of all UK taxa? What is the best way to measure effective size if it is to be a meaningful concept? Are current effective population sizes in the British	Synthesise existing evidence and initiate further research to support the development of new recommendations.

	Isles adequate to sustain genetic diversity?	
• **Defining units of conservation**		
Knowledge gaps	**Research Questions**	**Recommendations**
There is a limited understanding of how we can define units of conservation to ensure effective site protection, and what the costs and benefits to such definitions are.	Are protected areas more effective in ensuring genetic conservation than non-site based approaches? How can critical units of conservation such as ESUs and MUs be defined? What are the ESUs, MUs, dispersal distances, colonisation distances, boundaries and permeability of unsuitable habitats?	Undertake comparative studies of the genetic composition of populations in protected areas versus the wider landscape. Investigate the potential application of selectivity measures and conservation of 'designated population segments'.
An understanding is required as to whether life-history and demographic information could be used as a surrogate for measuring genetic diversity to inform conservation (as 'conservation short-cuts')	Does knowledge of species breeding system, functional group, or life history allow inferences about expected levels of population neutral and adaptive diversity, or susceptibility to genetic risks such as inbreeding depression? Can we use such short cuts to make generic conservation protocols? What are the costs and benefits of this approach?	Undertake the meta-analysis of existing research to establish relationships. Develop and test models, and in partnership with practitioners and policy makers, apply this knowledge to issues of practical conservation.
Conserving evolutionary processes that generate and sustain genetic and taxonomic diversity		
Here we consider the evolutionary processes of population size and inter-specific hybridisation. The process of gene flow among populations, which can also sustain genetic diversity, is dealt with in a separate section. There is a need to consider the conservation of evolutionary processes rather than just of *status quo* taxonomic units; this has genetic implications. Networks and connectivity of populations, related species and habitats are likely to be particularly important in the context of conserving the ecological processes that support biodiversity.		
Knowledge gaps	**Research Questions**	**Recommendations**
Limited understanding of the key	Which evolutionary processes sustain and generate	Conservation actions should take into

evolutionary processes *in situ*	biodiversity, and what is their relative importance? Should the focus of conserving processes generating biodiversity be upon identifying and conserving the processes themselves, or upon conserving the habitats and landscapes that allow those processes to occur? What conservation value should we place on processes and the novel taxa that they generate or sustain? To what extent does the current conservation approach (including guidelines for designating protected areas, such as SACs, and rare species) foster or restrict the processes that are currently generating novel taxa and/or genetic diversity?	account the processes generating and sustaining diversity as well as named taxa and units of biodiversity themselves. Research projects should aim to analyse processes as well as simply describing the extent and distribution of neutral genetic diversity.
• **Hybridisation**		
Knowledge gaps	**Research Questions**	**Recommendations**
Understanding hybridisation	How many species have been generated by hybridisation? How often does hybridisation result in genetic introgression, reduction in genetic diversity within parental types, sterile offspring, the generation of new taxa or the exclusion of one of the two parental types?	Undertake the meta-analysis of existing data to establish past hybridisation rates. Assess the frequencies of negative outcomes of hybridisation including laboratory and field based approaches.
Managing the products and outcomes of hybridisation	How should we value the results of hybridisation that occur through human-mediated environmental change - should these be the object of conservation actions (e.g. what is the value of SAPs for *in situ* conservations?) How much of a risk are the negative outcomes of hybridisation?	Recommendations must await cost-benefit analyses of the possible outcomes of hybridisation and their value to biodiversity and conservation. Hybridisation can have little discernable effect on fitness or viability, yet still be judged as ‘negative’ (e.g. the Scottish wildcat).

Understanding and managing gene flow in the context of adaptation and species’ adaptability		
Understanding and managing gene flow is central to the application of genetics in conservation. There is an inherent tension between • an emphasis on conserving potentially well-adapted local ecotypes, and • general maximisation of genetic diversity in every location to promote future adaptability.		
Knowledge gaps	**Research Questions**	**Recommendations**
There is a lack of methods to adequately and accurately measure gene flow.	What are the best ways to assess gene flow? When and where is it beneficial to manage gene flow? How do measures of gene flow compare? When and at what scales should we seek to increase landscape permeability to gene flow?	The effects of different levels of gene flow should be investigated in species with a range of effective population sizes and varying longevity and with different dispersal rates/mechanisms.
There is an incomplete knowledge of species dispersal ability, colonisation ability and the permeability of habitats	What are the best methods for assessing habitat permeability? What is the relative permeability of different habitats to different taxa? Over what distances can different species disperse and colonise? How frequent are long-distance dispersal events and what is their genetic significance? Does knowledge of species’ life history or breeding system help us to predict dispersal and colonisation ability?	Undertake a review of existing landscape metrics to assess reliability and possible needs for new measures. Undertake studies of dispersal in key species/taxa in a range of landscape types. Synthesise existing research.
There is a poor understanding whether there is any relationship between historical events and genetic composition of current populations?	How have the genetic constituents of populations changed or persisted over historical time scales? To what extent are functionally adaptive genes represented in some populations?	Undertake the meta-analysis of historical data.
Gene flow and outbreeding depression	How, and at what scales does outbreeding depression affect the genetic composition and fitness of populations?	Study inbreeding and outbreeding in a range of taxa and populations, including those undergoing environmental fluctuation and/or

		change
Adaptation and invasive species	Do invasive species have genetic characteristics that may allow problems to be predicted? Does the extent of adaptation in non-native species predict their invasiveness within UK habitats?	Initiate comparative studies on invasive species to establish whether genetic factors play a role in their invasiveness
• **Understanding adaptation**		
Clear and meaningful definitions of local adaptation are needed that are accessible to practitioners and policy makers alike		
Knowledge gaps	**Research Questions**	**Recommendations**
Mechanisms of adaptation	To what extent can genetic variation facilitate adaptation, and through which mechanisms? How rapidly does local adaptation occur? Are local adaptations constant over time, or does fluctuating environments cause them to shift and change in nature?	Review current data to establish current knowledge and initiate research where necessary: to assess local adaptation in terms of community interactions; Compare habitat type and distance in driving the differentiation of ecotypes.
Measuring adaptation	Are there useful surrogates for adaptation, such as common garden and reciprocal transplant experiments? Do comparisons of F_{ST} and Q_{ST} provide useful indications of the presence of adaptation? Is it possible or useful to measure adaptive diversity in small populations?	Investigate the use of reciprocal transplant experiments to identify adaptive diversity Undertake further studies on quantitative traits and local adaptation in wild populations, and compare results with those from common garden and reciprocal transplant experiments Undertake studies on quantitative traits and adaptation in small populations.
The extent and distribution of adaptive diversity	How much adaptive diversity can we expect to encounter within natural populations in the UK and	Review existing research and initiate further studies for key taxa.

	species' wider ranges? How do species breeding systems affect the extent and distribution of adaptive genetic diversity? How does outbreeding affect the genetic composition and fitness of populations?	Study inbreeding and outbreeding in a range of taxa and populations.
Adaptation and the response to environmental change	How do populations with different levels of neutral and adaptive genetic diversity respond to change? Can locally adapted populations cope with changing and variable environments? How do adaptable (genetically diverse or plastic) populations cope with changing and variable environments?	Review existing research and initiate studies of populations subject to environmental fluctuations and/or change.
Plasticity and adaptation to change	What are the relative contributions of phenotypic plasticity and microevolution on adaptation to changing environments? Does plasticity itself evolve with changing environments?	Review existing research that has partitioned out components of variability and, if necessary, instigate new research.
Management of species, populations, habitats and landscapes		
• **Conservation of species and populations**		
Knowledge gaps	**Research Questions**	**Recommendations**
A lack of generic strategies for conservation of species with certain breeding systems and historical demography	How do methods of setting conservation priorities compare across species with different breeding systems and populations characteristics? What are their costs and benefits? Should our approach to managing genetic diversity be different for endemic species?	Undertake a review and meta-analysis to compare prioritisation methods, including cost-benefit analysis.
Taxa that are poorly studied from a genetic viewpoint	What levels of neutral and adaptive genetic diversity are present in poorly studied taxa such as invertebrates and marine taxa?	Undertake studies to document genetic diversity in invertebrates including key functional or indicator groups.

Genetic diversity, historical events and demography	How have patterns of genetic diversity changed or persisted over historical time? How well can we reconstruct species genetic and demographic history?	Synthesise the existing literature.
Incomplete knowledge of how genetic markers inform species conservation • The meaning of changes in genetic diversity • Baseline measures of genetic diversity and their relationship to population fitness • The integration of information from genetic studies into conservation actions	What are the key evolutionary and ecological processes driving change in the levels of genetic diversity contained within populations? Do meaningful baselines exist for genetic measures that may be useful conservation indicators, such as effective population size, heterozygosity, F_{ST}/Q_{ST}? Which baselines are 'desirable': those at present, or in the past; when in the past? Is there a relationship between genetic measures and population fitness? What are the costs and benefits of different genetic marker systems to conservation? How can different genetic indicators inform conservation actions? How should we incorporate and weight genetic information with other data such as ecological, habitat, life history, historical and past management information on a species of interest?	Undertake meta-analysis of research relating genetic data to conservation actions. Construct a conservation management decision assistance tool, to facilitate the use of genetic information on a species-specific basis. Pilot this tool using case studies whose management outcomes were known to see whether it can be used to recommend appropriate actions. Synthesise and disseminate costs and benefits of the existing molecular marker systems.
The significance of genetic diversity for community species diversity and ecosystem function • Little is known about the relationships between genetic diversity and species interactions within a community • Local adaptation and community interactions	How does genetic diversity within species influence species interactions within a community and ecosystem functioning? Are species replaceable? Does local adaptation facilitate species coexistence or alter community dynamics? To what extent are genes that affect the function of ecosystems represented in some populations?	Review existing genetic and ecosystem function research and facilitate closer working between these research communities.

• Conservation of habitats and landscapes

Knowledge gaps	Research Questions	Recommendations
The scale of gene flow	At what scales should we seek to increase landscape permeability to gene flow?	Undertake a review of the existing landscape matrix to assess permeability and the possible need for new agri-environment measures. Undertake studies of dispersal in key taxa in a range of landscape types.
Habitat fragmentation	How does habitat fragmentation affect gene flow? At what scales does fragmentation become problematic to the maintenance of gene flow?	Assess the impacts of fragmentation on different scales.
Population connectivity and range-edge populations	Does increasing population connectivity increase the risk of swamping adaptation at the edge of a species' range with non-adaptive genes? Will enhanced population connectivity help to alleviate inbreeding depression at the range edge?	Initiate landscape-scale field studies in near-natural systems and compare impacts across a range of taxa.
Management of connectivity at large spatial scales	What are the costs and benefits of encouraging landscape connectivity at a UK scale relative to a pan European scale? Do we need to worry about the genetic distinctiveness of UK populations?	Compare genetic parameters in UK and other populations and review the existing literature of the genetic distinctiveness of UK populations from the DNA literature.
The benefits of encouraging landscape connectivity at a UK scale relative to a pan European scale have not been fully explored. There is a limited understanding of the benefits of maintaining and conserving genetic diversity of species within the UK compared to wider geographic ranges.	Do UK populations represent sub-species or are they genetically indistinguishable from those in other geographical regions? What are the costs and benefits of adopting genetic conservation strategies at a range of geographical scales?	Comparison of genetic measures in UK and other populations.

There is little knowledge of how increasing connectivity may impact upon populations at the edge of their ranges.	Does increasing population connectivity increase the risk of swamping of populations at edge of a species' range with non-adaptive genes?	Initiate landscape-scale field studies in near-natural systems and compare impacts across a range of taxa.
The role of protected areas	What role should protected areas play in a wider landscape strategy to conserve genetic diversity and evolutionary processes? How can we manage the landscape between protected areas to make it more "wildlife friendly" in order to encourage natural gene flow among populations? Are protected areas more effective in ensuring genetic conservation than non-site based approaches?	The use of selectivity measures and 'designated population segments' should be considered. Recommendations in relation to the management of the landscape between, protected areas to encourage gene flow and protected areas themselves, must await discussion between policy makers, practitioners, and researchers in the light of the findings of future research.
The effectiveness of protected areas for the conservation of genetic diversity	To what extent do protected areas conserve genetic diversity? To what extent does the protected area network facilitate the operation of natural evolutionary processes such as gene flow, adaptation, etc?	Comparative studies of the genetic composition of populations in protected areas *vs*. those in the wider landscape are needed. Studies on the dynamics of gene flow between protected and unprotected areas are needed, as well as a better understanding of the process of colonisation.

Policy limitations and responses

The current legal framework and obligations emphasise the importance of conserving existing taxa and patterns of biodiversity. Policy needs reconsidering in context, taking into account the need for dynamic change in biodiversity and to include processes that generate and sustain diversity.

Limitations of Current Policy	Recommendations
The present need of policy makers to see a return on investments in conservation efforts presents a serious problem with the time-scale required to carry out and achieve some conservation objectives.	Given the current state of our knowledge regarding the role of genetic diversity in biodiversity, conservation policies need to be set within a longer timescale than at present.
Continued application of the precautionary principle (preserving distinctive units of biodiversity) in the conservation of species' genetic diversity may be practically difficult and biologically unsound if species' genetic diversity and adaptive potential is to be maintained	A flexible interpretation of the precautionary principle is needed, in which adaptability is accepted as an important conservation objective. The precautionary principle may be too conservative, and actually be detrimental to the long-term-sustainability of declining populations that have experienced some genetic depletion.
Future conservation strategies require a combined approach that can maintain existing species and populations but also allow for demographic dynamism and future environmental changes, e.g. those expected due to the climate.	There is a need to develop strategies that permit adaptation to environmental change.