

The ConGRESS project and workplan was divided into six work packages (WP) focusing on design and implementation of the web portal and project management (WP 1), design, implementation and population of databases of relevant scientific publications, experts and end-users and genetic data (WP 2), design and implementation of a Sample Planning Tool (WP 3), design and implementation of a Decision Making Tool (WP 4), design and production of educational materials for dissemination of basic information on conservation genetics (WP 5) and organisation and management of project meetings and workshops (WP 6). These work packages and their results will be described in order.

## **WORK PACKAGE 1**

The major non-management objective of WP 1 was the design, construction and implementation of the web portal – a task overseen by the coordinator (Prof Michael Bruford, Cardiff University), who was the WP leader, with input from six partners. This WP also included project management. The major deliverables included producing a trial version of the web portal (Month 18), the full version of the portal (Month 34) and the post-project web portal updating plan (Month 36).

Design and production of the web portal was subcontracted to the web design company Idox ([www.idox.co.uk](http://www.idox.co.uk)) after a tendering and interviewing process carried out in August 2010. The portal design needed to include the following features:

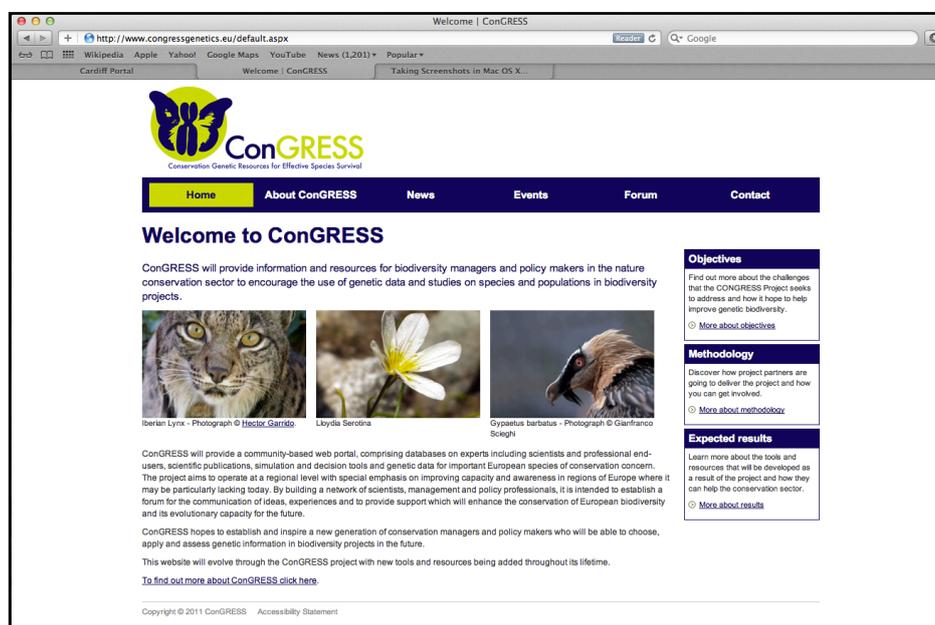
1. Attractive, user-friendly interface;
2. Generic features including registration, forum, Twitter Feed, RSS News feed, site guide, description of project and partners and link to Cordis web site;
3. Database of relevant scientific publications on the genetics of European threatened wild species with links to abstract pages in the appropriate journals, genetics specialists and end-users and of relevant genetic data for use in other modules in the portal;
4. Sample Planning Tool, a statistical module enabling interested end-users and researchers to assess the power of their experimental design to answer the management question they were asking;
5. Decision Making Tool, a means to enable end-users to query a decision tree using both management and genetic entry points to identify which genetic approaches are relevant to their management problem, how they may be tackled and what are the practical implications (e.g. cost, time);
6. Educational materials download section, including a 'Knowledge Pack' (Presentation, basic leaflet) and a series of 'How To' leaflets describing ways to answer the most pressing management problem facing the end-user community.

The concept included the idea that the portal modules would be linked together and could therefore cross-refer to enable an easy-to-use and joined up experience for the user.

An initial evaluation of tenders was carried out by all partners involved in WP1, using the specification established in our original proposal. Interviews involving three tenderers were carried out with the coordinator, a representative of Cardiff University's Information Services Division and P04 (Prof Rus Hoelzel, UDUR).

Unanimous agreement was reached that Idox Group produced the best tender and interview and provided the best experience and range of skill-sets for the sub-contract. Idox group was formally appointed in October 2010 (Month 6). Construction of the web pages proceeded during the following seven months, with four meetings carried out between November 2010 and July 2011 between the coordinator and Idox group. The first task was to produce an attractive web site for the project ([www.congressgenetics.eu](http://www.congressgenetics.eu)), the format of which was simply designed to advertise the existence of the project, including a link to the project's CORDIS page. Also at this stage the project logo was designed by one of project's post-doctoral researchers, Dr Katie Frith (P04) following a competition amongst the partners and end-user representatives initiated at the Kick-off meeting. The colour scheme of the logo set the colour tone for the web page and we were extremely happy with the logo and the way it utilised the project's powerful acronym (Figure 1).

FIGURE 1 HERE – FIRST FRONT PAGE



After further consultation with the coordinator and WP1 partners on the web site's functionality, design and an enhanced colour scheme, Idox Group had produced a working site (beta) with some of the functionality in place by the time of the Mid-term meeting (Month 16) for feedback from the partners and end-user representatives (Figure 2). Idox Group attended the Mid-term meeting and presented the different web pages including their ideas and current functionality to the partners and end-user representatives.

FIGURE 2 – SECOND FRONT PAGE

After the Mid-term meeting further modification took place before, during and after the workshops and proceeded smoothly to the extent that the portal was able to go 'live' three months ahead of schedule on December 1<sup>st</sup> 2012. To enable the required modifications, Idox staff held face-to-face meetings with the leaders of WP's 1, 2 and 4 on six occasions and also attended both the Mid-term and final workshops to present the main features of the portal for feedback and at the final meeting to discuss handover/legacy issues. Although not all pages were finalised at this point, the basic functionality of the portal was in place and had been extensively tested, enabling us to feel confident that it was fit for purpose and at this point we reverted from the beta site to the congressgenetics.eu domain and announced the portal as being available on our Facebook page and via press releases (Figure 3). As of 20<sup>th</sup> May 2013, the website had received over 375,000 hits and 6,200 website visits. There have been 675 community searches, 156 profile views and 740 publication searches. The forum Homepage has received 1,238 visits, the Sample Planning Tool has received 2,514 visits and the Decision Making tool has received 1,976 visits.

The legacy plan for the portal was developed at the final workshop and has been aided by our ability to dedicate resources towards the hosting and infrastructure for the next six years at QMUL, and a small contract with Idox group to provide software support for up to person six days as needed. Furthermore, in terms of the portal content, partners will continue to compile the publications on conservation genetics of European threatened taxa, will maintain the social media component of the website. A scientific publication has been written to describe the web portal and is currently in

revision for the *Journal of Nature Conservation* (see Figure 4 for schematic diagram included).

FIGURE 3 HERE – PRESS RELEASES

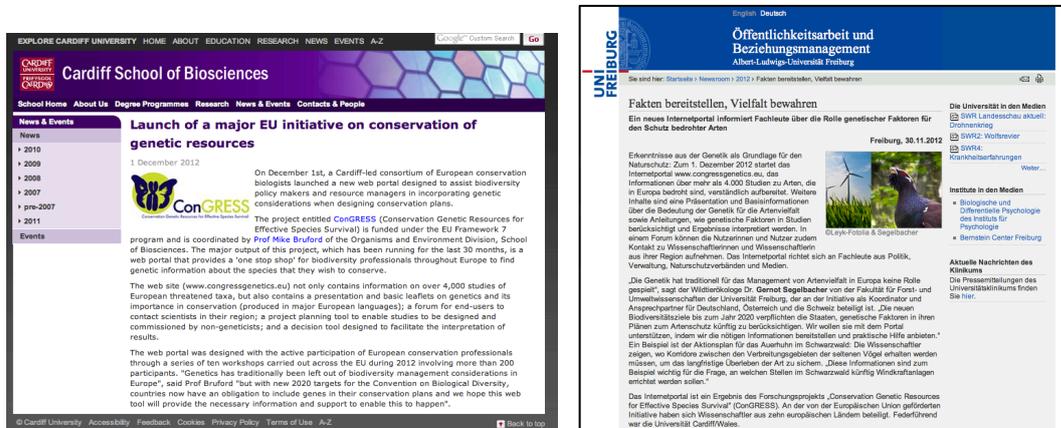
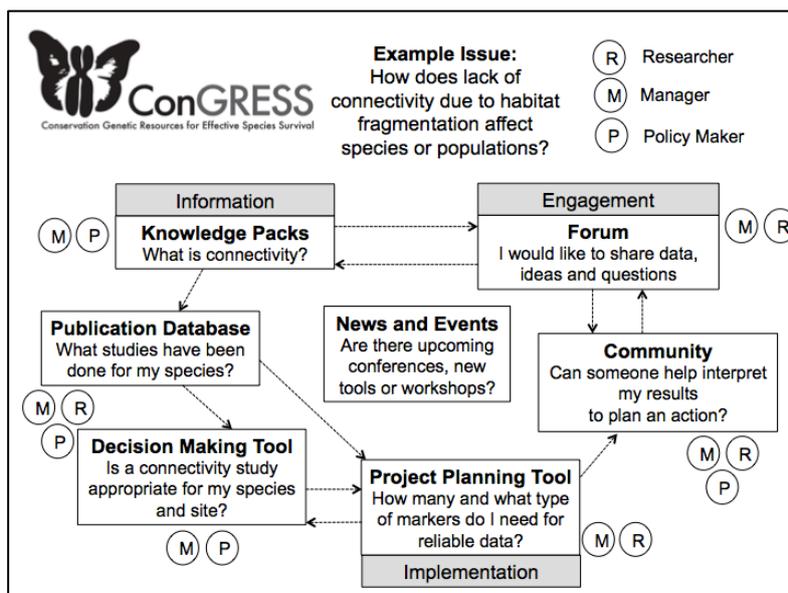


FIGURE 4 HERE JOURNAL OF NATURE CONSERVATION FIGURE



Work Package 1 has also included coordination activities, including management of reporting (financial and progress), co-organisation of kick-off and Mid-term meetings (in Belgium and Italy), organisation of the final meeting in the UK, coordination of liaison with and analysis of end-users and the first end-user questionnaire, in collaboration with WP 3 and some additional work that was not originally foreseen. Additional activities have included presenting the project at a FP7 call launch event at the Wales European Office, Cardiff in July 2012, co-organising a symposium on genetics and its application in conservation biology at the European Society for Conservation Biology congress in Glasgow in August 2012 and attending three ConGRESS regional workshops (Debrecen, Copenhagen and Trento) between March and September 2012 to monitor progress and helping to present the project. The coordinator also presented the project at the 6<sup>th</sup> World Congress on South American

Camelids in Arica, Chile in November 2012. Finally, and perhaps most importantly, the coordinator established collaboration between ConGRESS and the Biodiversity Indicator Partnership (BIP - <http://www.bipindicators.net/>) to become a project partner and help to refine the population genetic indicators for Target 13 of the Convention on Biological Diversity. Activities in this domain included attending a BIP meeting in Cambridge, December 2012 to present the ConGRESS concept, coordinating a partner-wide project (additional effort) to survey the literature for genetic indicators between September and December 2012, initiating a theoretical re-evaluation of genetic indicators (January - May 2013) and inviting Dr Damon Stanwell-Smith of the BIP secretariat to the final meeting to present the BIP concept in April 2013. We are currently working towards a synthesis paper on genetic indicators for submission before the end of the calendar year. Data from the first questionnaire was used in an article entitled “*Bringing genetic diversity to the forefront of conservation policy and management*”, authored by all partners and published in the journal *Conservation Genetics Resources* in 2013.

## WORK PACKAGE 2

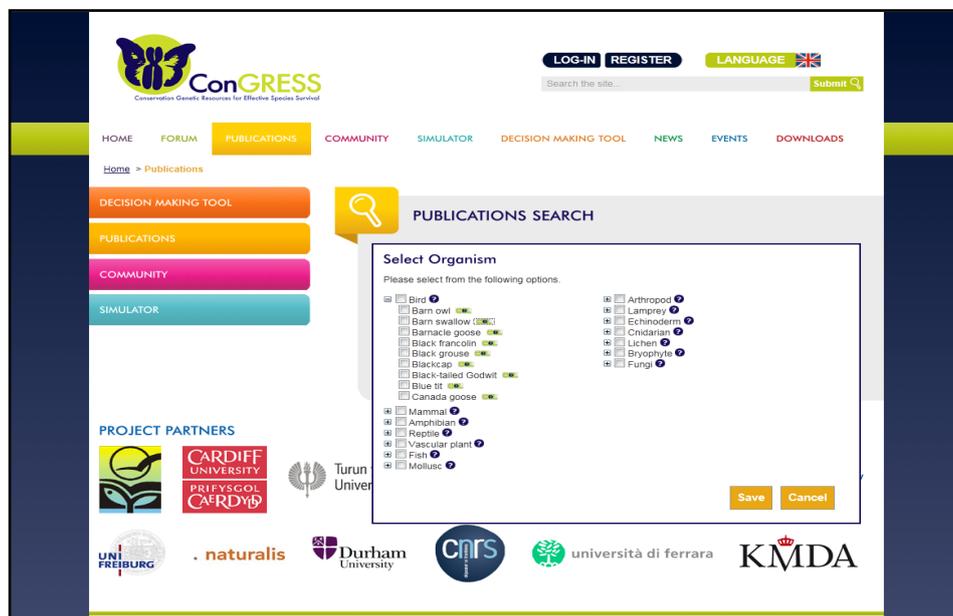
The major objective of WP 2 was the design, population and management of the databases within the web portal - a task overseen by the WP leader (Prof Richard Nichols, Queen Mary University of London), with input from six partners plus the coordinator. The major deliverables were: database description and specification (Month 2), a list of key taxa for the database (Month 2) and the key scientists and professionals list (Month 24) and final publications and genetics databases (Month 31).

A 30 month 50% FTE post-doctoral researcher was allocated to this WP, but the outstanding candidate, Dr Silvia Pérez-Espona, specifically requested for the employment to be full-time for a shorter period. After consultation with key project partners who coordinated with WP 2 and the coordinator, we rearranged the timetable accordingly. This decision required that the key objective, the *complete* population of the publications database, would need to be completed within the shorter period of employment. This target was duly met by month 18, four quarters ahead of the original schedule. This decision had major advantages, since the completion of the database allowed the choice of illustrations for the Decision Making tool and educational materials to be coordinated with the examples in the database.

A total of 346 species were selected as European ‘key’ species on the basis of the availability of *genetic information*, *iconicity*, *status of conservation*, their *importance as a resource* (game, fisheries, forestry, horticulture) and *representation* of as many *taxonomic groups* as possible. The groups comprise one alga, ten amphibians, 59 arthropods, 76 birds, four bryophytes, three cnidarians, two echinoderms, 34 fish, one fungus, three lampreys, two lichens, 56 mammals, 17 molluscs, 11 reptiles and 65 vascular plants. The uneven taxonomic representation reflects the paucity of genetic studies for certain poorly studied groups. This involved an extensive research in finding and assessing genetic studies of potential interest to end-users and a total of 6,300 studies were entered into the preliminary database for evaluation. Filtering and categorisation of studies was carried out using the criteria of: subject covered, genetic markers used (renamed ‘data type’ in the latest release), and taxonomy. The number

of studies passing all quality checks was 3,897. Figure 4 shows the searching criteria and entry point for the database.

FIGURE 4 – ENTRY POINT FOR THE PUBLICATIONS DATABASE



One consequence of the publications database has been that additional publications, produced after month 18, could be added. Dr Silvia Pérez-Espona, who left QMUL to take up a lectureship at Anglia Ruskin University, indicated that she would be willing to continue this task if the project could buy her out of her lectureship contract for a total of three person months until the end of the project, and this was enacted with Commission consent. This decision has meant that the rigorous standards established during the first round of the database population could be applied. This process remains ongoing and the database is in the process of being populated with a further 600 records covering the period from 2011-2013. A publication describing the contents of this unique database is in preparation for submission within the coming months.

An early decision taken regarding the key scientists and professionals database was to opt for **self-population** by interested scientists and end-users (renamed the 'Community' for the portal). This was decided after consultation with end-users at the regional workshops, which were used as an opportunity to encourage and subscribe users 'on the spot'. The decision was taken because partners and end-users believed that adding names to the database without consultation was unethical, the information might be outdated and we did not wish to make the names available of individuals who might not respond to requests for help. The database is continually being updated as users decide to become members of the Community, and currently stands at 168 (see previous sections). The registration entry point is shown in Figure 5. To preserve the anonymity of the registered users we have not provided an example registration, but below we show the geographical distribution of registrants (Figure 6). Currently there are 58 conservation practitioners and policy makers in the total of 168, which means that approximately 65% of registrants are practicing geneticists, although many of these also classified themselves as 'conservation professionals'. These results

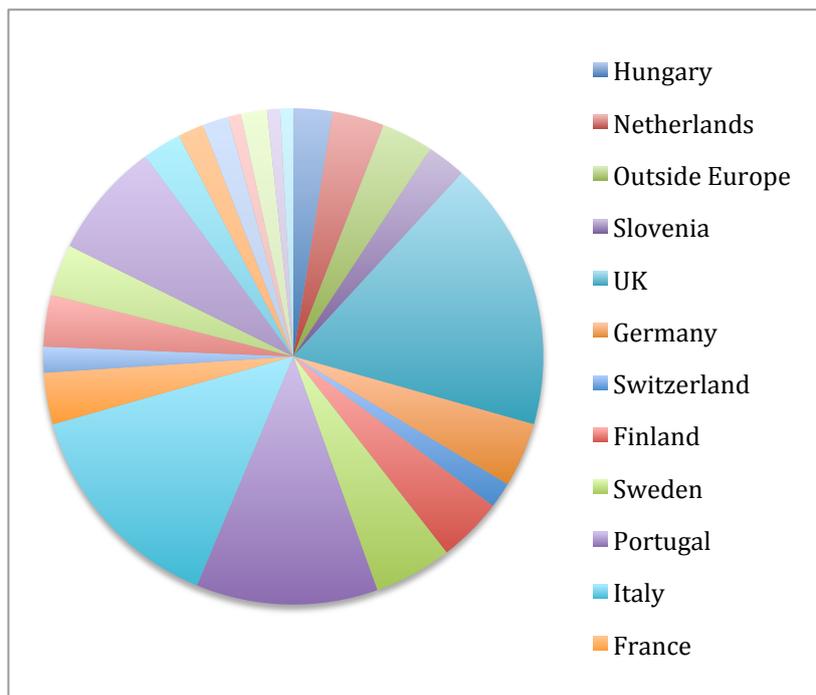
highlight the fact that we must continue our efforts to encourage end-users to register on the portal. At the final meeting, as a further incentive to use the portal, it was decided that registration would only be required for access to the Community data and the Sample Planning Tool (retained as 'private' to provide an incentive for registration).

FIGURE 5 – ENTRY POINT FOR THE PUBLICATIONS DATABASE

The screenshot shows the ConGRESS website interface. At the top, there is a user greeting: "Welcome back, Mike\_Bruford. (Click here if you are not Mike\_Bruford)". To the right, there are links for "PROFILE" and "LOG OFF", and a language selector set to "English (UK)". A search bar is located below the navigation menu. The navigation menu includes: HOME, FORUM, PUBLICATIONS, COMMUNITY (highlighted), SAMPLE PLANNING TOOL, DECISION MAKING TOOL, NEWS, EVENTS, and DOWNLOADS. On the left side, there are four vertical buttons: DECISION MAKING TOOL, PUBLICATIONS, SAMPLE PLANNING TOOL, and FORUM. The main content area is titled "COMMUNITY SEARCH" and contains a search form. The form includes a "Search term" field with the example "e.g. fungi, chloroplast", "Match options" (Any word selected, All words, Exact phrase), "Country" (Please choose...), "Role" (Conservation professional, Other, Policymaker, Scientist/researcher), "Organism" (Please select organisms), "Data type" (Please select data types), "Subject" (Please select subjects), and "Publishing status" (Live). A "SEARCH" button and a "CLEAR" button are at the bottom right of the form. The footer contains links for "Contact Us", "About Us", "Site map", "Project partners and affiliates", and "Copyright © 2012 ConGRESS".

Another important decision that was taken soon after the Kick-off meeting was not to create another repository of genetic data, as originally specified. This was decided since well-developed and publicly available databases of population genetic studies - DRYAD ([www.datadryad.org](http://www.datadryad.org)) and GenBank ([www.ncbi.nlm.nih.gov/genbank/](http://www.ncbi.nlm.nih.gov/genbank/)) already exist for precisely these kinds of data and it was therefore deemed unnecessary to replicate this. However, data from example studies have been used for comparison in the Sample Planning Tool simulations (see below).

FIGURE 6 – COUNTRY AFFINITIES OF REGISTRANTS



### WORK PACKAGE 3

The major objective of WP 3 was the design and implementation of a genetic variation simulation module for the web portal - a task overseen by the WP leader (Dr Giorgio Bertorelle, Università degli Studi di Ferrara), carried out in collaboration with Dr Oscar Gaggiotti (Centre National de la Recherche Scientifique, Laboratoire d'Ecologie Alpine, Université Joseph Fourier, Grenoble). The major deliverables were the analysis of a report and questionnaire to the end-user community (Month 3) and the design and construction of a prototype and final version simulator (Months 18, 27 and 34).

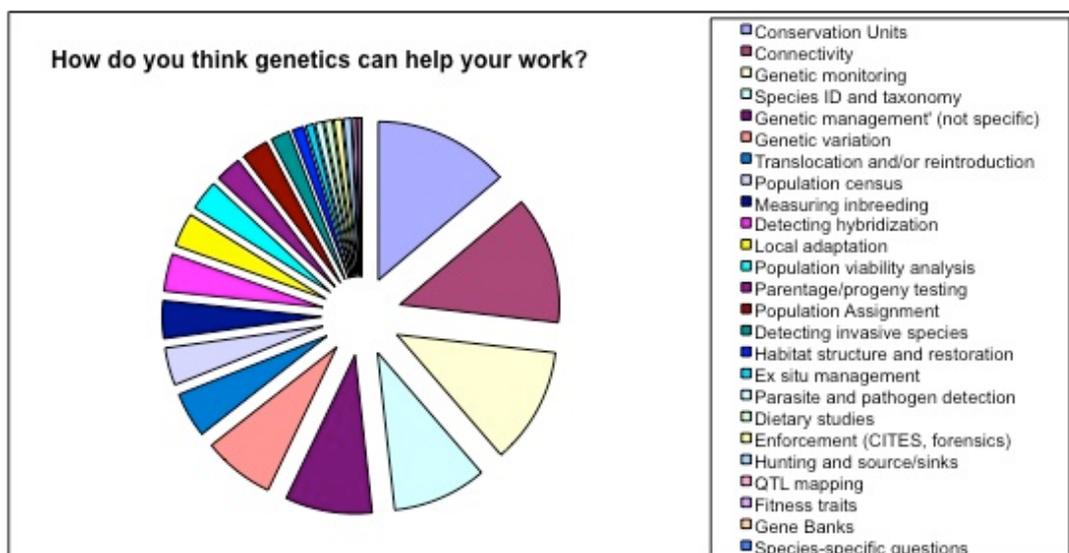
A post-doctoral researcher, Dr Sean Hoban, was hired and commenced at the beginning of month 3 with additional funds being secured from the University of Ferrara to employ him almost until the end of the project. Due to a delay in Dr Hoban commencing the position, the questionnaire work was carried out largely by the coordinator after the Kick-off meeting and was sent to relevant end-users by project partners. The questionnaire was designed to be very simple and quick to complete following strong advice of our end-user representatives at the Kick-off meeting. This advice was well made because we were able to obtain 131 responses. The questionnaire is detailed in Figure 7.

FIGURE 7 – END USER QUESTIONNAIRE

1. Which species/region/taxonomic group do you work with, and what are your responsibilities and role?
2. What are your background, qualifications and expertise?
3. What type of conservation/management/policy activities do you carry out?
4. Have you used genetics in your work and if so, how?
5. How do you think genetics could help your work in the future?

The respondents originated from 19 European countries plus Turkey and represented a wide spread of governmental and non-governmental organisations, ranging from scientific specialists to heads of organisations. We found that 42% of respondents had not commissioned, participated in or utilised existing genetic data in their work. We also found, however, that only 6% of respondents did not envisage a use for genetic data in policy and management of biodiversity in their region. We categorised responses for Questions 4 and 5. **Figure 8** shows a pie chart of the responses to Question 5 and their distribution. ‘*Genetic Management*’ was taken to imply a non-specific reference to the applied use of genetic data in population interventions; ‘*Monitoring*’ included any project that monitors the presence of movement (including spread) of individuals, hybrids, invasive species or indigenous taxa; ‘*Units for Conservation*’ was represented at approximately 95% by Management Units (i.e. demographically isolated populations with distinct frequencies). ‘*Understanding Genetic Diversity*’ comprised within-population diversity studies including detecting changes in size, evolutionary lineages and historical admixture and ‘*Connectivity*’ included the inverse (evidence for recent demographic disconnection or fragmentation). There was considerable overlap between the top ten applications currently being applied and those desired for the future (seven of ten), but the order varied with, for example, *Detecting Connectivity* coming much higher up the list of future applications than current practice. It was clear that in addition, ‘*Species ID*’ (DNA Barcoding), ‘*Units for Conservation*’, ‘*Monitoring*’, ‘*Translocation/Reintroduction*’ and ‘*Population Census*’, ‘*Population Assignment*’ and ‘*Hybridisation*’ were deemed extremely relevant by the end-users. The results of this questionnaire were incorporated into a paper published in *Conservation Genetics Resources* in 2013. Our interpretation of these concordant results gave us a strong steer for our work and to some extent reflect the few policy drivers in place where genetics has relevance in the EU, for instance in the need to demonstrate that ‘*Connectivity*’ reflects the mention of genetics in this context within the Habitats Directive.

FIGURE 9 – RESPONSES TO THE QUESTION “HOW DO YOU THINK GENETICS CAN HELP YOU IN THE FUTURE?” (CATEGORIES WITH MORE THAN TEN RESPONSES WERE FROM *IDENTIFYING UNITS FOR CONSERVATION TO DETECTING HYBRIDISATION*)



A second questionnaire was designed and used at the regional workshops to further explore attitudes and experiences of the end-user community, although the goal of this more detailed survey was not to inform the development of the portal but to provide feedback on the workshops and to provide data for a second, more detailed analysis intended for a further, more detailed study.

The general objective for the Sample Planning Tool was to create a series of web-based utilities enabling managers, policy makers and scientists to: a) compare (by simulation) the efficiency and effectiveness of different hypothetical sampling strategies and b) predict (by simulation) the genetic outcomes of different hypothetical action plans. We called the first set of tools **PPM**, Power and Precision Modules, and the second set of tools **MPM**, Management Predictions Modules.

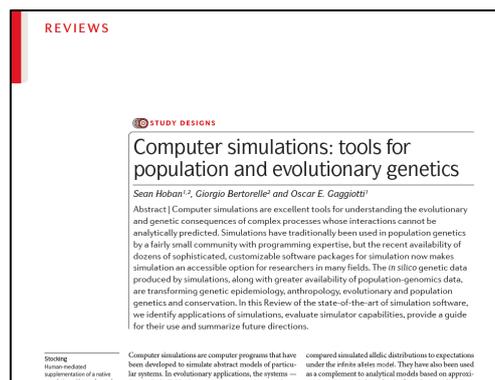
Sampling strategies are defined essentially by the number of individuals and populations to be sampled in the field, together with their spatial distribution, and by the number and category of genetic markers to type in the molecular laboratory. Using **PPM** before real sampling and typing can therefore be very useful to make informed decisions about what resources to commit to a study. It can also be used after a study to determine the power that a given set of samples/markers had, to help interpret results. On the other hand, using **MPM** to predict the genetic effects of different action plans, before implementation, can be useful to select the plan with the highest chances to reach a specific objective. It can also be used to reveal sensitivity to particular parameters (e.g. migration and fecundity), which may be more important to focus management on than other parameters. After a detailed analysis of the available software packages that could be adapted to produce the web-based tools, and a careful consideration of the questionnaires, we made several early decisions. First, we chose to use the simulator engine called *Simcoal2*, an established and flexible software, and second we chose to use the Java programming language, an environment allowing to link simulations with data analyses. We decided to have the

computing resources to run the simulations available to user via the web (i.e., no need for local computing resources). Our initial analysis also indicated that **PPM** are more urgent than **MPM**, the latter case already having the widely-used software, VORTEX that is a well-established functional tool in conservation biology with an efficient genetic simulator. We thus **focused on PPM**, and in particular on six modules for genetics project planning targeted at six specific conservation situations (see below).

The modules were designed with three aims: to allow easy entry into the software for the end-user (a task-oriented approach), to facilitate a connection to the decision tree module (**WP 4**), and to make simulation easier as by pre-specification of the evolutionary scenario (the user only needs to enter in parameters specific to their species). *The last aspect is a major difference from simulation programs that have been developed previously*, which are often too broad and offer too many options and considerations for a non-geneticist to operate. The comparison between simulation packages allowed us to write a review paper: “Computer simulations: tools for population and evolutionary genetics” published in *Nature Reviews Genetics* in 2012 (Figure 10).

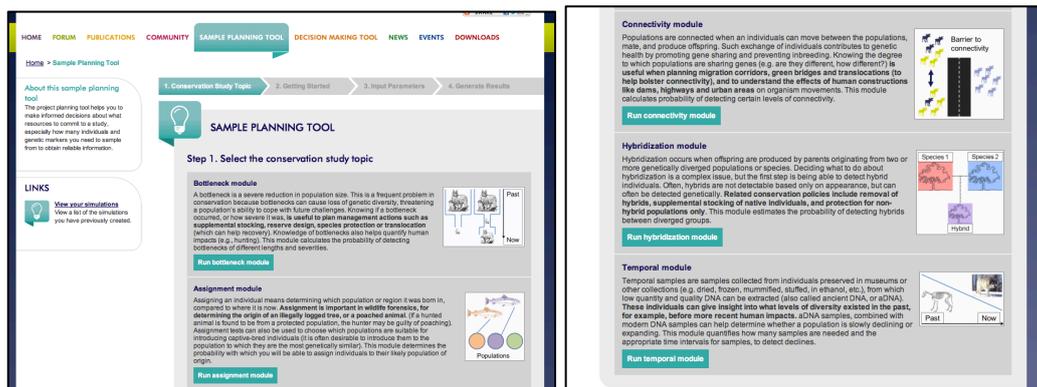
Following discussion and analysis of the first set of questionnaires, the six Power and Precision Modules (**PPM**) were finalised (see Mid-term report) but were ultimately refined into five mutually exclusive modules with the *CensusEst* module being discarded after further consultation with end-users. The newly named ‘Sample Planning Tool’ is now highly developed and is already being used by practitioners. It is featured in a *Molecular Ecology* publication by the WP 3 team (utilising the *Bottleneck* module) and the module is the focus in a paper recently published by the team in *Methods in Ecology and Evolution* and has recently been highlighted in a special online issue of this journal.

## FIGURE 10 – NATURE REVIEWS GENETICS ARTICLE COMPARING GENETICS SIMULATORS



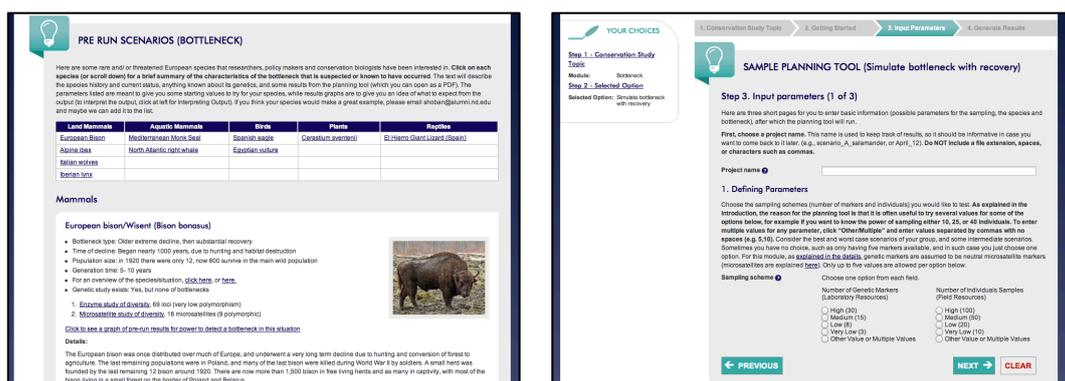
The five **PPMs** (*Bottleneck*, *Assignment*, *Connectivity*, *Hybridisation* and *Temporal*, Figure 11) each feature pre-run scenarios using real molecular data (e.g. for the *Bottleneck* module see Figure 12), downloadable PDF tutorials, a PDF entitled “*Understanding the Results*”, and a technical document for those wishing fuller details.

FIGURE 11 – START POINT FOR THE SAMPLE PLANNING TOOL, FEATURING THE FIVE PPMS.



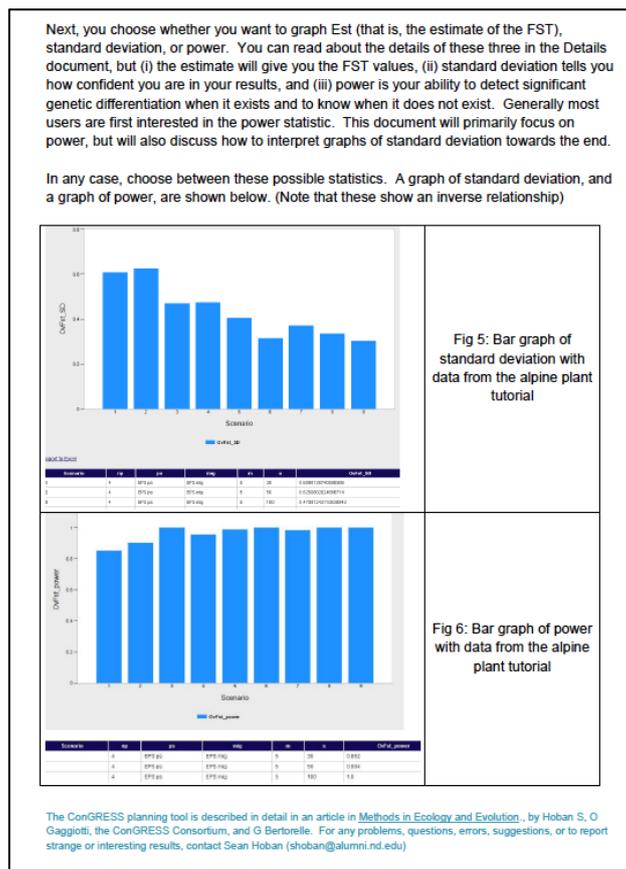
The user is guided through a series of explanatory pages where a project name can be defined and either categorical or user-specified continuous variables can be applied, allowing a whole range of users with different levels of expertise to be accommodated (Figure 13). The user is able to go backwards and forwards in the screens at will to change scenarios, before setting the simulation to run. Once the simulation is started, the computation is carried out on our server at QMUL using the back-end simulation program. The user can subsequently visit a ‘view your simulations’ page to see the result of their analysis. An important feature is that the simulations can only be carried out by registered members of the portal. It was decided to maintain this exclusivity because this module is seen as the most unique selling point of the portal and because an email is supposed to be sent to the user once the simulation is completed.

FIGURE 12 – SCREENSHOT OF THE BOTTLENECK PRE-RUN SCENARIO SCREEN SHOWING THE EXAMPLES AVAILABLE AND EXAMPLE INPUT PAGE.



Tutorials are in the ‘Understanding the Results’ files and are comprehensive and example-led. Figure 13 shows an example of how one of these files looks (for the *Connectivity* module).

## FIGURE 13 - CONNECTIVITY RESULTS GUIDE LINKED TO SET EXAMPLE (ALPINE PLANT)



The title of the Sample Planning tool was changed as a result of feedback during the regional workshops since it was felt that the word ‘simulation’ was somewhat intimidating for the uninitiated. However, it was stressed from the outset at the regional workshops, that running these simulations was something best attempted by collaboration between end-users and local conservation genetic scientists. What was clear from all the presentations made and interaction with the end-users was that there is a big need for a tool such as this, not only so that new projects could be properly designed but also to retrospectively evaluate previous projects to assess whether there was sufficient power in the original experimental design to expect a conclusive outcome of the research. Evidence of uptake of this tool has been seen both in terms of web portal activity statistics (over 2,500 visits with 910 scenarios submitted). The *Bottleneck*, *Assignment* and *Connectivity* modules are proving most popular at this early stage.

### WORK PACKAGE 4

The major objective of WP 4 was the design, development and construction of a decision matrix web module – a task overseen by P04 (Prof Rus Hoelzel, Durham University), who is the WP leader, with input from six partners. The major deliverables were the decision matrix research (Month 18), the decision matrix text pages (Month 30), the decision matrix structure (Month 30) and the operational decision matrix (Month 36). The postdoctoral researcher contracted for this Work WP, Dr Katie Frith was engaged on a part-time (50%) basis for the duration of the

project. This WP also crucially depended upon the outcome of the questionnaire linked to WP 3 and direct linkage between WP 3 and WP 4 was an integral functional feature of the portal.

Our objective for this WP was to develop a Decision Matrix Tool that would help managers to quickly access information on genetic applications for specific management issues. At the same time, we wanted to make the tool effective for a wide range of end-users with varying needs. To that end a parallel pathway was built into the tool, so that the wider conservation genetics community can find clear, up-to-date information on analytical approaches, and follow the threads back to the relevant management needs.

We began by designing the basic architecture of the tool. This involved the development of two pathways, one for *managers* and one for *geneticists*. A manager can choose among topic categories that reflect important problems they need to address. These are represented as ‘threads’ providing options from broad down to narrower sub-categories (e.g. population monitoring – population viability – genetic diversity). Choosing a thread leads to a short more detailed description (e.g. “*Population monitoring involves the on-going assessment of population parameters relevant to its conservation and management. The question of population viability in the context of conservation genetics considers the risks associated with the loss of genetic diversity and the likelihood of population extinction. The genetic diversity of a population is increased by mutation and immigration, and lost through inbreeding and genetic drift. It can be quantitatively assessed at specific loci using molecular genetic methods*”). The next step allows for modification based on species or habitat types of relevance to the user’s problem in particular (or they can choose the general case). The user then sees a recommendation page which describes the relevant genetics methods and applications, with links to detailed descriptions of the methods, together with links to other resources within the ConGRESS website and elsewhere. Choosing the other pathway brings the user to lists of genetic application options (e.g. ‘population structure’, ‘estimating effective population size’ or ‘individual identification’), and then straight to the detailed methods pages. These pages have links back to management issue threads, and to other relevant pages within the website or elsewhere.

Ultimately, the final format included 18 key management questions defining 127 different threads. Each thread involves original text, and as such represents a monumental effort for a single, part-time postdoctoral researcher (Dr Katie Frith) and an enormous amount of editorial effort by the WP leader. The Operational Decision Matrix was nonetheless delivered on time. The final Decision Matrix Tool links to other elements of the portal, as originally conceived. This WP proved to be the most conceptually challenging of all in the ConGRESS project and the one that received the greatest feedback and modifications during the regional workshops. Indeed an *ad hoc* additional workshop was convened in Durham involving targeted UK end-users in July 2012 to iron out some areas that end-users were finding complex.

An important factor in the way this WP developed was the existence of a related project in the UK, funded by the Natural Environment Research Council’s Knowledge Exchange Program. The project is led by Prof Terry Burke (University of Sheffield), Prof Andrew Pullin (Bangor University) and Dr Peter Hollingsworth (the

Royal Botanic Gardens, Edinburgh). We worked closely with this group and the responsible postdoctoral researcher, Dr Linda Neaves, who are also developing a 'Decision Tool' as part of their project. Drs Hollingsworth and Neave attended the ConGRESS Kick-off meeting and met with the Coordinator and WP leader subsequently (April 2011). The two projects have therefore developed in a complementary manner, with the NERC approach adopting a 'Decision Tree' structure, analogous to a taxonomic key, exploring different management issues and species-specific issue in much more detail than in the ConGRESS portal (the NERC project is aimed at more specialised scientists). There will be direct links between the pages of the two projects and we will ensure, as far as possible, that the outcomes are mutually reinforcing and complementary. As of the time of writing, the NERC website and 'Decision Tree' have not been finalised and their project has been extended until November 2013. The ConGRESS Decision Making Tool is therefore the first available to the conservation community. The amount of information contained within the Decision Making Tool is prodigious, so much so that we decided in the final workshop to compile an e-book from the materials produced. An example of the extensive detail contained in the end-sheets is shown below (Figure 14a - d).

No stand-alone scientific publication is envisaged to describe this tool, however its functionality is described in the following manner in a publication currently under review for *Journal of Nature Conservation* – “*Decision-support tools are important for guiding decision-makers to specific actions, and can also be used to spark discussions and highlight knowledge gaps (Howes et al. 2009). The “Decision-Making Tool” provides a formal path for practitioners to identify how conservation genetics can help them address familiar management issues and questions. Users choose among a series of topic options to refine their question, leading to an Outline*”.

**FIGURE 14** - AN EXAMPLE OF AN OUTPUT SHEET FROM THE MANAGEMENT THREAD (MEASURING CONNECTIVITY: IDENTIFYING ISOLATED POPULATIONS).

## 14A – HEADLINE SCREEN WITH BASIC INFORMATION

Home > Decision Making Tool > Results

**YOUR CHOICES**

**Step 1 - Search Type**  
Search type: Management Issues

**Step 2 - Management Issues**  
Management Issues: Measuring connectivity  
Sub-filter: Identifying isolated populations

**Step 3 - Habitat/Species**  
Habitat: All  
Species: All

**FURTHER INFORMATION**

Search for papers and publications.  
[Click to search PUBLICATIONS](#)

Find other members who have expertise in this area.  
[Click to search COMMUNITY](#)

Discuss your results with other members in the forum.  
[Click to access the FORUM](#)

Run your results through the study planning tool.  
[Click to access the SIMULATOR](#)

**Content Management**

- [Method Summaries](#)
- [Methodologies](#)
- [Habitats](#)
- [Species & Considerations](#)
- [Glossary](#)

Step 1. User Type   Step 2. Management Issues   Step 3. Habitat/Species   **Step 4. Outline recommendations**

**DECISION MAKING TOOL**

SAVE DETAILS   PRINT PAGE   CREATE PDF   EDIT DEFINITION

**Step 4 - Outline recommendations for Measuring connectivity -> Identifying isolated populations**

**Overview**

**Why?**

When populations become isolated they receive little new genetic material from migrants and this has a number of important conservation genetic implications:

- genetic diversity is lost through stochastic processes and elevated **inbreeding**, with a severity that is inversely proportional to population size.
- Populations become more genetically different from one another.
- In the long term low diversity reduces the ability of a population to adapt to environmental change.
- In the short term inbreeding limits individual health/reproductive potential and increases the chance that heritable diseases will be passed on to offspring.

These processes act together to increase extinction risk in isolated populations.

**When?**

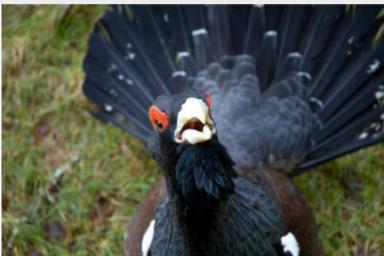
As habitats become increasingly anthropogenically modified many populations may become isolated from one another, as individuals are no longer able to cross barriers imposed by habitat change. Although tracking and observational methods allow us to follow movement among populations there are some limitations. Firstly, such methods can detect dispersal but they do not provide us with information about gene exchange (**gene flow**) as a consequence of these dispersal events. Secondly, it can be challenging to follow migration in organisms that are small, highly mobile, cryptic or those that are found in large numbers. In such cases genetics can provide an invaluable tool to identify whether populations are isolated from one another. Genetics can also complement observational studies by determining if current trends are likely to have been true over a longer time-frame.

[Case Studies](#)

## 14B – CASE STUDY EXAMPLE (CAPERCAILLIE) WITH LINK TO ORIGINAL STUDY (PUBLICATIONS DATABASE)

**Case study 1:**

**The species:** The Capercaillie (*Tetrao urogallus*)



*Tetrao urogallus.*

**The problem:** Habitat fragmentation in the Black Forest confined capercaillie populations to isolated patches. The impact on gene exchange among the patches and on genetic diversity within patches has important implications for the persistence of these populations.

**How genetics helped:** Genetic data revealed that populations in the north of the Black Forest were significantly isolated from other populations. Although there was no indication of reduced genetic diversity, there is a significant risk of future diversity loss if populations remain isolated.

To link to the original study click [here](#).

**Case study 2:**

**The species:** The dog whelk

**The problem:** Designing marine reserves to ensure that natural connectivity among populations is maintained.

**How genetics helped:** Genetic assignment methods determined that dog whelks found in an isolated marine reserve were exchanging few or no migrants with other coastal populations in the region. The implication is that the reserve network did not adequately facilitate connectivity among populations, thus informing future reserve design to extend the network of protected areas.

To link to the original study click [here](#).

To find further examples of where genetics has been used to detect isolated populations search the [Publications Database](#).

## 14C – METHODOLOGY SECTION INCLUDING SECTIONS ON PRACTICAL CONSIDERATIONS, WITH LINK TO SAMPLE PLANNING TOOL

**Methodological Approaches**

A given population will have a characteristic distribution of genetic variation. When different populations exchange migrants they become more genetically similar, and when they stop exchanging migrants they diverge and become more genetically different. This information can be used to determine the extent to which populations are isolated from one another. We can also use more sophisticated modeling approaches to estimate the rate and direction of migration among populations, again allowing us to identify isolated populations.

**Relevant methods:** [Assignment to population](#) , Geographically explicit population structure, [Population structure](#) , Directional gene flow ( [coalescent](#) methods), [Ongoing gene flow \(non-equilibrium models\)](#) .

**Practical Considerations**

Note that these details will depend on the particulars of the study, and as technology develops, costs and the time investment required may change. Please contact individual labs for specific time and cost estimates.

|  |   |
|--|---|
| Cost and time                              | Using standard methods the costs and time required should be low to moderate. See <a href="#">Budget Examples</a> file for more detail and use the <a href="#">Community Database</a> for further advice.   |
| Number of samples                          | Population samples will require a statistically robust sample size (30+ samples per population). See the connectivity module of the <a href="#">Sample Planning Tool</a> to estimate power using different sample sizes.  |
| Implications of using non-invasive samples | Working with degraded DNA will require sample replication and can be facilitated with more expensive reagents.  |
| Other considerations                       | It can be difficult to detect migrants using <a href="#">assignment tests</a> if migration rates among populations are high. Increasing sample sizes and marker number increases the power to detect structure among putative populations, and the <a href="#">Sample Planning Tool</a> can help determine the requirements for a specific study. |

## 14D – SECTION ALLOWING FURTHER DETAILED INFORMATION TO BE ACCESSED (METHODS SUMMARIES) WITH LINKS TO GENETIC MARKER GUIDE, PLANNING TOOL AND COMMUNITY.

To find information on the different genetic markers that can be used to measure connectivity see the [Genetic Marker Guide](#).

To determine the optimal number of markers and individuals to sample for assessing connectivity and assignment tests please refer to the [Planning Tool](#).

To search for people/labs who may provide you with further information about using genetics to identify isolated populations search the [Community Database](#).

Community database keywords: [Dispersal](#), [Landscape/environmental effects](#), [Population subdivision](#).

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**METHODS SUMMARIES**

|  |   |
|--|---|
| <p><b>Assignment to population</b> +</p> <p>Assignment tests use genetic markers to determine the population membership of individuals or groups of individuals.</p>   | <p><b>Species and habitat considerations</b></p> <p>You have chosen All. General considerations about habitat relevant to conservation genetics include area size, since small areas may restrict population size. Reduced population size increases the rate at which diversity is lost (and genetic diversity is positively correlated with individual fitness, while also providing the raw material by which populations respond to environmental change). Habitat patchiness or fragmentation is also important since fragmentation that inhibits gene flow will mean smaller populations and less diversity, and generate differentiation among fragments. Certain types of habitat may be more or less likely to provide barriers to gene flow, with the marine environment providing generally greater connectivity. For a given species there may also be habitat characteristics that create barriers within or among habitats. For example, a habitat with defined structure and boundaries (like a forest) may show differences with respect to population size and/or selection at the edges (edge effects) compared to the centre. Various kinds of human disturbance or influence can also impact populations in ways that can be assessed using genetics, such as the impact of GM crops, or the selective removal of a component of the ecosystem (e.g. through hunting). The impact of habitat characteristics will also depend on characteristics of the species, especially dispersal mode, dispersal range and population density.</p> <p><b>All</b> +</p> |
| <p><b>Directional gene flow (coalescent methods)</b> +</p> <p>Directional gene flow measures asymmetrical migration rates between sub-populations and can be estimated using a theory called 'The Coalescent'.</p>   |   |
| <p><b>Geographically explicit population structure</b> +</p> <p>The genetic structure of a population is strongly influenced by geographic and environmental variables that differentially affect migration and mating (gene-flow) across a landscape.</p>                                 |   |
| <p><b>Ongoing gene flow (non-equilibrium models)</b> +</p> <p>Gene-flow between contemporary populations is dynamic and ongoing and we can use genetic methods based on a model called isolation with migration (IM) to quantify rates and direction of gene-flow between populations.</p> |   |
| <p><b>Population structure</b> +</p> <p>Population structure is the quantitative measure of genetic differentiation among populations.</p>   |   |

**Considerations**

*“Recommendations page explaining the issue, why and when it is of concern, and which genetic approaches and data are applicable. Applications on the chosen topic*

are illustrated with case studies illustrating best practice, and advice is given about practical aspects of establishing a study.”

## WORK PACKAGE 5

The major objective of WP 5 was the design, development and production of information and educational materials for end-users – a task overseen by P12 (Prof Craig Primmer, University of Turku), who is the WP leader, with input from five partners (although in practice all partners are involved). The major deliverables for this WP included the English version of the Knowledge Pack (basic leaflet on conservation genetics and PowerPoint presentation, Month 18), the translated version of the Knowledge Pack (Month 24), the English language versions of ‘How to’ information sheets (Month 32), production of the other language versions of the ‘How to’ sheets (Month 34), and the legacy plan for updating the sheets (Month 36).

Completion of the first information sheet and an associated PowerPoint presentation involved first developing the text in collaboration with the WP 5 partners, followed by a round of feedback from end-users from several countries, and a final round of discussion and feedback with end-users and partners at the Mid-term meeting. Once the text was finalised, it was felt extremely important that a graphic design company should be used for preparing the pamphlet format and PowerPoint slide base as it was agreed that a high quality design would be imperative for the impact of the documents. As this represented a change in the work plan, permission for this re-allocation of funds was requested from the Commission. The leaflet is in the form of a foldable A5 pamphlet and is shown in Figure 15a & b. Also see an example of some of the PowerPoint sides (Figure 16).

FIGURE 15A - FORWARD SIDE OF CONGRESS PAMPHLET

**Fast facts**

- DNA for genetic analyses can be obtained from a single hair, scale, feather or leaf.
- 80% of endangered species suffer from low genetic diversity.
- Genetic diversity is one of the three dimensions of biodiversity.

Conservation genetics analyses are no longer prohibitively expensive and can be out sourced to reduce costs.

Ecosystem resilience and future evolution of populations depends on genetic diversity. Therefore, genetics is a key factor when assessing the Favourable Conservation Status of species.

ConGRESS (Conservation Genetic Resources for Effective Species Survival) is an EU consortium dedicated to transferring current knowledge in conservation genetics and in the analysis of genetic variation data to management professionals and policy makers.

**Conservation genetics can help to**

- Check whether a population is suffering from low genetic variation or genetic erosion
- Predict the effects of management actions, such as harvesting or translocation
- Identify distinct populations that are valuable for conservation
- Detect whether species or populations are exchanging genes in the wild
- Determine where individuals come from and what species they belong to
- Choose which populations or individuals to use for breeding or populating new areas
- Reveal isolation or prove connectivity between populations
- Understand the significance of genetic diversity for ecosystem resilience

**ConGRESS**  
Conservation Genetic Resources for Effective Species Survival

**Have you got your hands on biodiversity?**

SEVENTH FRAMEWORK PROGRAMME

www.congressgenetics.eu

www.congressgenetics.eu

FIGURE 15B – REVERSE SIDE OF CONGRESS PAMPHLET

CongRESS is a unique community of wildlife and plant geneticists. From the black rhinos of Namibia to the salmon of northern Lapland – CongRESS scientists have unveiled the genetics of the most endangered species as well as those of economic importance.

DNA sequencing, barcoding or genetic profiling – conservation genetics is a new discipline, but has already made remarkable advances in applying new technologies to wildlife research. Now, CongRESS geneticists are combining cutting-edge science with practical conservation. Free online tools for wildlife management professionals are evolving in the web. We invite you to make the best use of them.

**Protecting species and habitats – is it enough?**

Since the Convention on Biological Diversity, the international community has made great efforts to safeguard endangered species and their habitats. However, managing habitat fragmentation, climate change and the loss of biodiversity preoccupy professionals working with wildlife conservation. These overlapping threats pose an enormous challenge. Can our best effort ever be enough?

Gradually, the importance of genetic variation, the third dimension of biodiversity, has been recognised and incorporated into legislation. In the USA and Canada, endangered species legislation protects both species and their populations – therefore recognising the importance of genetic variation within species. In Europe, genetic diversity is mentioned in the Habitats and Marine Directives as well as in the Green Paper on Preparing Forests for Climate Change. In 2010 at Nagoya, genetic diversity was included in the revised 2020 Biodiversity Targets (Target 13). A commitment is sought to halt the 'genetic erosion' of species as far as possible. Will this add to workload of the professionals in the field – or could it offer new solutions to unsolved problems?

**Unveiling the 'hidden level' of biodiversity**

DNA analysis has unparalleled power to reveal the history of species, populations and individuals. The genetic differences that exist between virtually all organisms are the raw material that enables species to adapt to environmental change. In other words, the conservation of genetic diversity means safeguarding biodiversity.

Genetic diversity is therefore crucial for the future survival of species. Genetic erosion caused by habitat fragmentation, isolation or invasive species can now be measured in great detail. Genetic studies offer highly useable approaches when planning sustainable environmental management, action plans for endangered species, hunting or stocking.

**New tools for effective species survival – online, now**

The CongRESS website offers free tools and information to all professionals of conservation biology from policy makers to scientists. Discover how to use these tools for effective species survival – test, use, comment and participate in our workshops. We want you to be able to make the best use of conservation genetics!

[www.congressgenetics.eu](http://www.congressgenetics.eu)



FIGURE 16 – EXAMPLE SLIDES FROM THE KNOWLEDGE PACK PRESENTATION (46 SLIDES IN TOTAL)



It should be noted that the PowerPoint slides are designed to be modular – i.e. a subset can potentially be used for different audiences, but they all have the same basic design so different combinations of modules can be used for different circumstances.

Completion of the Knowledge Pack involved developing the text, crowdsourcing photographs and planning the illustration in collaboration with the WP 5 partners. The Mid-term meeting included a discussion on the subjects identified in the first set of end-user questionnaires and which of these subjects should form the basis of more specialised topic pamphlets. It was decided that the subjects covered should be

*Species Identification* (including DNA Barcoding), *Genetic Management of Populations*, *Measuring and Protecting Gene-flow* and *How Much Genetic Variation is Enough?* Close cooperation was also established with WP 2 to make good use of the developing database in the production of the Knowledge Pack. The topics that were agreed in the Mid-term meeting were introduced in four leaflets. The final number of leaflets produced in WP 5 is, together with the introduction leaflet, five. Together with the '*Why Conservation Genetics*' presentation the material comprises a mini size conservation genetics textbook, which has been written in popular style, introduces the field, recent studies and available tools and is usable for various end-user groups.

When the English versions were approved by WP 5 partners and project leader, they were published in the project website following the project timetable. At the Mid-term meeting, project partners agreed that the Knowledge Pack would be translated into major European languages: French, German, Italian and Spanish, approved by the Commission. The aim was, furthermore, to translate the material into as many other languages as possible, following the official EU language policy. The '*Why Conservation Genetics*' PowerPoint presentation was translated into French, German, Italian, Spanish and Finnish. The leaflets were translated, in addition to the above five languages, into Czech and Dutch. The material contains scientific terminology, which is relatively new and therefore, the project partners agreed to do the translation as their own work. The production of the multilingual material was coordinated by P12, which also carried out the final layouts of the leaflets in all languages. Due to a sick leave of the French partner, the French translation of the introduction leaflet was, however, made with the help of the School of Languages and Translation Studies of the University of Turku. When the language versions were finally approved by native speakers, the leaflets were published on the project website. It was decided at the final meeting that some hard copies should be produced for these leaflets and mailed out to governmental conservation agencies to increase the visibility of the project. In addition to the Knowledge Pack, a web site guide to the project web portal was produced in WP 5. Some example sheets of different language sheets are highlighted below in Figure 17 & 18.

FIGURE 17 – EXAMPLE SHEET SHOWING ITALIAN VERSION OF SPECIES IDENTIFICATION LEAFLET.

**Identificare le specie usando il DNA - perchè e come?**

**Kit molecolari pronti all'uso**

Il DNA barcoding è la tecnologia che sta crescendo più velocemente nella moderna identificazione delle specie. La ricerca che sviluppa gli standard per i DNA-barcode (ovvero codici a barra basati sulla lettura di specifici frammenti di DNA) ha compiuto progressi considerevoli negli ultimi 10 anni. L'identificazione delle specie con il DNA barcoding è basata su marcatori molecolari che sono molto corti rispetto all'intero genoma.

La procedura di laboratorio e l'analisi dei database, che possono essere fatte eseguire all'esterno, possono essere completate in un paio di giorni o persino entro qualche ora. Il costo di un'analisi di DNA barcode può essere inferiore ai 20 €.

**CAMPIONI DI DNA POSSONO ESSERE OTTENUTI IN TEMPI RAGIONEVOLMENTE VELOCI E RIGENERICAMENTE CON METODI NON INVASIVI** molto vicini e che si sono evolute recentemente restano una sfida per la tecnologia. Tuttavia, soprattutto se integrata con altri metodi, la genetica offre strumenti potenti per risolvere i problemi dell'identificazione delle specie e della gestione.

**Azioni di conservazione con applicazioni del DNA - TOP 5**

Quando lo stato tassonomico di una specie è conosciuto adeguatamente, le risorse di conservazione possono essere indirizzate correttamente ed efficacemente. I metodi basati sul DNA possono essere utilizzati per:

- Migliorare l'identificazione delle specie e popolazioni che necessitano protezione e, quindi, prevenire l'estinzione di specie in pericolo non ancora riconosciute.
- Identificare con il profilo del DNA campioni di specie sottoposte a bracconaggio e contrabbando
- Evitare di sprecare risorse su specie abbondanti o popolazioni ibride.
- Evitare di mescolare specie identificate non correttamente con altre specie, fenomeno che può portare ad una riduzione della fitness.
- Riconoscere le popolazioni che possono essere usate per aumentare la fitness delle popolazioni con alto tasso di inbreeding.

**Per saperne di più:**

- Frankham R. & al. 2002. Introduction to Conservation Genetics. Cambridge University Press.
- von Crottel M. & al. 2011. DNA barcoding: a tool for improved taxon identification and detection of species diversity. *Biodivers. Conserv.* 20: 373-389.
- Griffiths A. M. & al. 2010. Molecular markers reveal spatially segregated cryptic species in a critically endangered fish, the common skate (*Dipturus batis*). *Proc. R. Soc. B*, 277, 1497-1503.
- Iglesias J. P. et al. 2009. Taxonomic confusion and market mislabeling of threatened skates: important consequences for their conservation status. *Aquatic Conserv. Mar. Freshw. Ecosyst.* 20: 119-133.

ConGRESS (Conservation Genetic Resources for Effective Species Survival) è un consorzio europeo dedicato a fornire le migliori conoscenze e gli strumenti di conservazione e di gestione e di adattare le strategie di conservazione ai professionisti della gestione e ai politici-amministratori.

[www.congressgenetics.eu](http://www.congressgenetics.eu)

FIGURE 18 - EXAMPLE SHEET SHOWING FINNISH VERSION OF CONNECTIVITY SHEET.

**Riittävän voimakas geenivirta ja miten se tunnustetaan**

Tutkimusten mukaan jo yksi ulkopuolelta tuleva yksilö voi pelastaa populaation sisäisiltä aiheutamilta haitoilta. Selkeä yksilöistä, joka määrätellään riittävän geenivirran erilaisissa tilanteissa, ei kuitenkaan ole. Monimuotoisuutta ylläpitävän geenivirran määrä riippuu lajin erityispiirteistä, alapopulaation koosta sekä ikä- ja sukupoljakaumasta.

Luonnon populaatioissa riittävän geenivirran ylläpitämiseen tarvitaan yleensä enemmän kuin yksi muuttava yksilö. Geenivirran tehokkuutta voidaan arvioida populaation välisten geneettisten erojen perusteella.

Genetiikan älykkäällä työkalulla kuten alkuperän määrittämistestillä tai sukulaisuuden ja risteymät tunnustavilla DNA-testeillä voidaan varmistaa yksilöiden alkuperä ja selvittää, kuinka hyvin populaation ulkopuolelta tulevat yksilöt omistuvat lisääntymään.

**Geenivirtaa mittaamassa**

Yksilöiden liikkumista ja lisääntymistä voidaan mitata tarkasti DNA:n avulla ja tutkia, miten geneettinen monimuotoisuus muuttuu elinympäristöjen muutoksen ja ajan myötä. Genetiikan menetelmillä voidaan:

- Tutkia populaatioiden erilaistumista ja arvioida tulosten perusteella geenivirran voimakkuutta
- Seurata eri yksilöiden leviytymistä määrätellillä niiden geneettinen alkuperä
- Todentaa, että geenivirta alkaa toimia uudelleen kahden eristäytyneen populaation välillä ja tunnistaa risteymät
- Tunnistaa elinympäristöissä olevia geenivirran esteitä ympäristö- ja populaatio-genetiikan menetelmillä

**Geenivirta - mitä se on? Miten sitä suojellaan?**

**Ympäristökeskus**

ConGRESS (Conservation Genetic Resources for Effective Species Survival) on EU-konsortio, joka toimii yhteisellä luonnonsuojelugenetiikasta. Lisätietoja: Alanjohtaja/professori Craig Primmer: [craig.primmer@utu.fi](mailto:craig.primmer@utu.fi)

[www.congressgenetics.eu](http://www.congressgenetics.eu)

The project partners agreed to print 11,340 copies of the leaflets and each partner was committed to distribute them. P12 organised the printing of the material, which is available in eight European languages. As an example, in Finland, 300 end-users who were listed in the mailing list of the project received printed leaflets and a letter from the project leader encouraging them to take further steps in the use of conservation genetics and reaching the 2020 biodiversity targets.

## WORK PACKAGE 6

Work Package 6 concerned the organisation and implementations of project meetings and workshops and was not conceived to produce science and technological

foreground. However, two specific outcomes from the workshop are expected to result in publications for the project, or at least to contribute to a publication. The first is the questionnaire that was produced for the regional workshops. Of particular interest to us was the interaction between participant age, region of origin, educational background, employer category (governmental, non-governmental, educational) and employer scale of operation (local/regional, national, international) with the types of genetic projects already commissioned and with those planned (if any). We received a total of 112 completed questionnaires (from 230 participants) comprising 12 from Fennoscandia, 24 from North-east Europe (BENELUX, France, Germany), 25 from Poland and Slovakia, 26 from the Carpathian region and 25 from Iberia and Italy. The data have already been coded according to all genetic study categories, and an example of the output is below (Figure 19). Analysis is ongoing with this dataset and the results will be published in a detailed analysis. This is scheduled for the end of 2013.

FIGURE 19 – QUESTIONNAIRE RESULTS: GENETIC STUDY ALREADY CARRIED OUT AS A FUNCTION OF AGE CATEGORY OF PARTICIPANT

|   | Total        | AGE          |              |              |              |
|---|--------------|--------------|--------------|--------------|--------------|
|   |              | >35          | 35-45        | 46-55        | <55          |
| Sample Size   | 112          | 37           | 40           | 23           | 12           |
| <b>ALREADY DONE</b>   |              |              |              |              |              |
| Assignment of individuals to source population                      | 48.2%        | 64.9%        | 50.0%        | 34.8%        | 16.7%        |
| Detecting, measuring and managing inbreeding                        | 45.5%        | 51.4%        | 42.5%        | 43.5%        | 41.7%        |
| Detecting the presence of invasive species                          | 26.8%        | 29.7%        | 22.5%        | 30.4%        | 25.0%        |
| Detecting, measuring and managing hybridisation                     | 43.8%        | 56.8%        | 32.5%        | 39.1%        | 50.0%        |
| Detecting pathogens and parasites                                   | 30.4%        | 45.9%        | 20.0%        | 21.7%        | 33.3%        |
| Detecting locally adapted populations or genotypes                  | 36.6%        | 40.5%        | 32.5%        | 39.1%        | 33.3%        |
| Determining habitat structure and restoration                       | 17.9%        | 18.9%        | 20.0%        | 17.4%        | 8.3%         |
| Detecting the effects of hunting pressure                           | 17.9%        | 21.6%        | 22.5%        | 8.7%         | 8.3%         |
| DNA barcoding including taxonomy                                    | 26.8%        | 35.1%        | 25.0%        | 26.1%        | 8.3%         |
| Enforcement (including CITES, police work and forensics)            | 19.6%        | 13.5%        | 22.5%        | 26.1%        | 16.7%        |
| Establishing whether populations are connected or isolated          | 61.6%        | 70.3%        | 62.5%        | 52.2%        | 50.0%        |
| Establishing the role of landscape features on population structure | 29.5%        | 29.7%        | 35.0%        | 17.4%        | 33.3%        |
| Estimating population size  | 53.6%        | 59.5%        | 57.5%        | 52.2%        | 25.0%        |
| Genome mapping and diversity  | 14.3%        | 13.5%        | 17.5%        | 4.3%         | 25.0%        |
| Identifying units for conservation                                  | 38.4%        | 54.1%        | 20.0%        | 47.8%        | 33.3%        |
| Informing translocation or reintroduction programmes                | 38.4%        | 37.8%        | 40.0%        | 39.1%        | 33.3%        |
| Systematics and phylogenetics                                       | 40.2%        | 56.8%        | 45.0%        | 17.4%        | 16.7%        |
| Management of ex situ populations or resources                      | 22.3%        | 21.6%        | 22.5%        | 34.8%        | 0.0%         |
| Managing gene banks   | 16.1%        | 8.1%         | 15.0%        | 26.1%        | 25.0%        |
| Measuring fitness   | 14.3%        | 16.2%        | 12.5%        | 17.4%        | 8.3%         |
| Measuring genetic diversity of a measure of population fitness      | 42.9%        | 45.9%        | 42.5%        | 39.1%        | 41.7%        |
| Molecular studies of diet   | 6.3%         | 10.8%        | 5.0%         | 0.0%         | 8.3%         |
| Monitoring hybridisation  | 31.3%        | 37.8%        | 20.0%        | 39.1%        | 33.3%        |
| Monitoring individuals  | 37.5%        | 37.8%        | 37.5%        | 43.5%        | 25.0%        |
| Monitoring invasive species   | 21.4%        | 27.0%        | 17.5%        | 26.1%        | 8.3%         |
| Parentage or progeny testing  | 26.8%        | 32.4%        | 27.5%        | 26.1%        | 8.3%         |
| Population viability assessment                                     | 26.8%        | 29.7%        | 20.0%        | 30.4%        | 33.3%        |
| Species specific questions  | 27.7%        | 32.4%        | 25.0%        | 26.1%        | 25.0%        |
| <b>Average</b>  | <b>30.8%</b> | <b>35.7%</b> | <b>29.0%</b> | <b>29.5%</b> | <b>24.1%</b> |

The second outcome is a synthesis publication from the trans-border workshop held in Strembo, Trentino, Italy in September 2012. At this meeting researchers from eight European countries gathered for addressing conservation issues requiring trans-national collaboration and genetic tools needed to better tackle these problems. From the regional ConGRESS workshops, three major groups of organisms were previously identified, both from researchers and end-users, as particularly relevant for trans-border actions: large carnivores, birds and forest trees/vascular plants. Conservation actions inherently prioritise: we, therefore, identified the top five species within each group and summarise our findings for a few species among them below. This work is currently being written up for publication.

## Large carnivores

### *Brown bear*

The brown bear (*Ursus arctos*) is probably one of the most iconic European wildlife species. While endangered and strictly protected in some countries (e.g. Italy, France), brown bear is legally hunted in other (e.g. Croatia and Slovenia). Due to the trans-boundary nature of most populations this makes it difficult to set up common management guidelines. Although collaboration between scientists from different

countries, mostly within the Alps, is satisfactory, at the management level only small-scale collaborations are occurring. Though this scientific international cooperation has resulted in sharing protocols, thus favouring comparability of data-analysis methods and results, there are still some important aspects missing. Defining management units that make biological sense, focusing on the issues at the population level and, last but not least, pooling resources and saving time and money represent relevant targets to be pursued.

### *Wolf*

The situation of wolf (*Canis lupus*) is similar to that of brown bear, especially regarding the critical relationship with local residents. Due to its high dispersal capability, wolf management could significantly benefit from trans-border collaboration, both at scientific and end-users level. Some form of scientific trans-national cooperation for protocols and data sharing is already available but it is of a lesser extent than that established for brown bear. Priority actions include: sharing protocols, trans-boundary monitoring, definition of management/conservation units, understanding of the issues at the population level, comparability of data-analysis methods and results, pooling resources and saving money.

### *Monk seal*

The monk seal (*Monachus monachus*) is listed as Critically Endangered in the IUCN Red List. Within EU, major populations are only found in Greece. This is somehow limiting the international cooperation that, conversely, could be very important for monitoring population expansion and detecting migrants. Limited availability of genetic markers is hampering the use of genetics in this species. Several stakeholders are involved in monk seal conservation: governmental organisations, protected areas managers, NGO's (charismatic species), fishermen, commercial fish farms, tourism industry (local businesses).

Other important species include Eurasian lynx, wild cat and otter.

## **Birds**

### *Bearded vulture*

The bearded vulture (*Gypaetus barbatus*) inhabits the Alps (Italy, France, Austria, Switzerland, Germany, France (including Corsica), Spain (Pyrenees) and Crete. It is particularly valued from an ecosystem services and a cultural perspective, being exposed at the same time to several threats such as poisoning and habitat degradation. In the Alps it benefited from large reintroduction programs with founders coming mainly from Central Asia (fewer from the Pyrenees). Several EU LIFE projects have been devoted to bearded vulture. Genetics is seen as a real priority in the Alps and there is currently a Swiss company performing the genetic analyses of the Alpine populations. It is less clear who is studying the genetics in the Pyrenees, while no genetic analyses seem to have been done in Crete and Corsica. In the latter bearded vulture is phenotypically distinct. The main goal of future conservation actions is to bring the Alpine and Pyrenean groups together. To this end an international genetic collaboration would be crucial for documenting immigration and gene-flow between the two ranges. At the same time more information should be obtained for the truly indigenous populations from the Pyrenees, Corsica and Crete. The main stakeholders of bearded vulture conservation actions are: governments, NGOs (e.g. WWF), National Parks and researchers (Spain, Switzerland, France and Italy).

### *Capercaillie (and other tetraonids)*

The capercaillie (*Tetrao urogallus*) is a typical umbrella species for old growth forest and it has, mostly in Alpine region, a strong cultural significance and is strongly associated with protected areas. The species is facing several threats, from habitat fragmentation and climate change to human activities. It has been subjected to several reintroduction programmes. The management of the species heavily relies on genetic monitoring, mainly based on genotyping with species-specific microsatellites that are successfully used also on non-invasive samples (faeces, feathers). Among the main stakeholders are governments, hunters, forestry managers (local – European scale). The species has a particular relevance for local tourism but while it promotes ecotourism, other activities (e.g. alpine skiing and back-country skiing) pose some threats. Current international collaboration is on peer-to-peer basis, without any official acknowledgement. There is an Alpine expert group (foresters and researchers), coordination between ecology but genetics is missing. The species is studied by researchers in the Alpine region, Spain, UK, Scandinavia and Slovenia. There are a few groups in the Cantabrian region working independently. No common database exists although some samples are exchanged between some groups. Spanish and Slovenians are operating independently. Projects tend to be funded on a regional basis. A coordinated international activity would be extremely useful for: understanding population structure and genetic diversity, comparing data among different populations after developing a common marker panel. A good starting point might be to consolidate current overlap between datasets. Since translocation across several countries is a big issue, shared genetic resources could greatly help. There is a need to understand gene-flow and definition of source-sink populations in the Alps, while locating, at the same time, the major barriers. The same issues pertain in Dinarics and Cantabrians. Connectivity is a big issue in Spain that could greatly benefit from a more integrated international collaboration.

Other important species include the saker falcon, great bustard, white-headed duck and aquatic warbler.

### **Forest trees and vascular plants**

#### *European yew*

The yew is a widespread conifer throughout Europe. Though its IUCN conservation status is Least Concern there are several threats associated to land use change, fire, fragmentation, small effective population size, environmental variation and extraction of diterpenes, used as anticancer drug and anti-fungal compounds. The yew is, in fact, protected in most of Europe. The yew receives the attention of very different stakeholders: Nature Conservation authorities, Pharmaceutical and Agro-business companies and nurseries. A large collaborative research project based on genetic tools has been already focused on yew, European Forest Genetic Network (Euforgen), and other common research projects are running. Nonetheless there are important issues that could take advantage of a more integrated international collaboration: intensive sampling, sharing of results and reproductive material, designing of common projects. Other important species identified include various fir species, queen of the Alps, four leaf clover and waterwheel plant.

## **Potential impact in socio-economic and wider societal and main dissemination activities and exploitation (10 pages)**

As a **Coordination and Support Action** project, ConGRESS was designed from the very beginning to maximize its impact and indeed the project's philosophy has been that we can judge our success mainly in terms of our impact in the biodiversity management and policy community of the European Union and beyond. We consider our impact to have been unusually great and our project unusually visible during its existence. There are a number of indicators and metrics that can be used to measure our impact, which will be detailed below. These are:

1. The number of visits to our web portal and the different modules within them;
2. The number of registered members of our 'Community' and their geographic and professional diversity;
3. The number and regional spread of the workshops that we organised, the number of attendees at those workshops and their professional diversity;
4. The number and visibility of other meetings at which our dissemination tools have been demonstrated and at which our project has been described and advertised, and their regional spread;
5. The number of leaflets that have been distributed to end-users and their geographic and professional spread.

### **The number of visits to the ConGRESS web portal, number of registrations and community members**

The following data were supplied by Idox and are correct as of 13<sup>th</sup> May 2013. The web page has received over 6,000 visits since it was first available and over 4,000 of these have occurred since our formal launch in December 2012. At the time of writing this report, registered community members had grown from 106 to 168 and our goal is to reach 300 by the end of 2013. By 20<sup>th</sup> May 2013, the portal had already facilitated more than 700 publications searches with more than 300 abstract views. Our Forum page had been visited more than one thousand times, indicating a promising start to building the discussion needed to make the Forum active. Perhaps most pleasing, however, has been the progress with the Sample Planning Tool. With 1,650 visits since launch and over 1,000 results viewed, it is clear that this tool is really making an impact. Almost as successful has been the Decision Making Tool, which is particularly pleasing given its complex nature and the time needed to complete the process: over 1,000 users have followed the Management route through the Tool and over 1,300 in total have reached the end of the process.

While it is clear that this remains early stages for the portal, we are very encouraged that it is already being used relatively extensively. ConGRESS clearly has gained substantial visibility. Our powerpoint file is now being widely used to promote the use of genetics in conservation (over 2,300 Slideshare uses since the file was first deposited) and articles posted on our Facebook site usually received between 60 and 100 views. Currently there are 58 conservation practitioners and policy makers in the total of 168, which means that approximately 65% of registrants are practicing geneticists, although many of these also classified themselves as 'conservation professionals'. These results highlight the fact that we must continue our efforts to

encourage end-users to register on the portal. At the final meeting, as a further incentive to use the portal, it was decided that registration would only be required for access to the Community data and the Sample Planning Tool (retained as 'private' to provide an incentive for registration).

**Table 1.** Web portal usage statistics

| <b>PORTAL TRAFFIC DATA</b>   |                                   |   |
|--|-----------------------------------|---|
| Time period  | Pre 1 <sup>st</sup> December 2012 | Post 1 <sup>st</sup> December 2012          |
| Number of Hits   | 105,631                           | 270,722                                     |
| Number of Visits   | 2,067                             | 4,106                                       |
| Number of new registrations  | 114                               | 205   |
| Total registrations  |                                   | 440   |
| New Community members  | 45                                | 123   |
| Community searches   | 304                               | 369   |
| Profile views  | 102                               | 54  |
| Publication searches   | 234                               | 506   |
| Publication views  | 72                                | 235   |
| Referrals to Google Scholar  | 22                                | 65  |
| Visits to Forum Page   | 381                               | 858   |
| Visits to Sample Planning Tool                                     | 864                               | 1,650                                       |
| Number of submitted input files                                    | 198                               | 712   |
| Number of results page views                                       | 320                               | 1,089                                       |
| Number of visits to Decision Making Tool                           | 696                               | 1,281                                       |
| Number of Users reaching the end of the Tool                       | 555                               | 1,322                                       |
| Number of Users taking genetics route                              | 157                               | 353   |
| Number of Users taking management route                            | 761                               | 1,019                                       |
| Number of Slideshare views of Power point file from Knowledge Pack |                                   | 2,374 (cannot be divided into time periods) |

### **The number and regional spread of the workshops that we organised, the attendees at those workshops and their professional diversity**

The ten workshops that we carried out and their geographic reach are detailed in Table 2 (taken from second periodic report). From the 230 attendees we received a total of 112 completed questionnaires (from 230 participants) comprising 12 from Fennoscandia, 24 from North-east Europe (BENELUX, France, Germany), 25 from Poland and Slovakia, 26 from the Carpathian region and 25 from Iberia and Italy. The information from these completed questionnaires has given us an insight into the demographic profile of the end-user community we have reached.

**Table 2:** Regional workshop details.

| <b>Region</b>   | <b>Location</b> | <b>Dates</b>                                     | <b>Organiser(s)</b>                           | <b>Attendees</b>                        | <b>Comments</b>  |
|---|-----------------|--|---|---|--|
| Czech Republic, Slovakia, Poland                      | Zvolen          | 25 <sup>th</sup> – 27 <sup>th</sup> January 2012 | Josef Bryja (IVB) with Ladislav Paule         | 62 including ConGRESS partners          | Large meeting – lots of networking                       |
| Belgium, Holland                                      | Antwerp         | 29 <sup>th</sup> February 2012                   | Peter Gabusera (KMDA), Pim Arntzen (NNM)      | 18 including ConGRESS partners          | Small meeting, focused only on ConGRESS tools            |
| Germany, Switzerland, Austria                         | Hegne           | 7 <sup>th</sup> March 2012                       | Gernot Segelbacher (ALU-FR)                   | 18 including ConGRESS partners          | Small meeting, focused only on ConGRESS tools            |
| Hungary, Croatia, Serbia, Slovenia, Romania, Bulgaria | Debrecen        | 15 <sup>th</sup> – 17 <sup>th</sup> March 2012   | Josef Bryja (IVB) with Katalin Pecsénye       | 45 including ConGRESS partners          | Large meeting – lots of networking                       |
| Italy   | Trento          | 14 <sup>th</sup> – 15 <sup>th</sup> March 2012   | Cristiano Vernesi, Heidi Hauffe (FEM)         | 22 including ConGRESS partners          | Medium sized meeting, mix of end-users                   |
| Spain, Portugal                                       | Madrid          | 20 <sup>th</sup> – 21 <sup>st</sup> March 2012   | Jose Godoy, Carles Vila (CSIC)                | 23 including ConGRESS partners          | Medium sized meeting, mix of end-users                   |
| Denmark, Sweden, Norway                               | Copenhagen      | 12 <sup>th</sup> – 13 <sup>th</sup> April 2012   | Hans Siegismund (UCPH) with Per Sjogren-Gulve | 21 including ConGRESS partners          | Medium sized meeting, mix of end-users                   |
| France  | Grenoble        | 31 <sup>st</sup> May – 1 <sup>st</sup> June 2012 | Oscar Gaggiotti (CNRS)                        | 17 including ConGRESS partners          | Small meeting, focused only on ConGRESS tools            |
| UK mini-workshop                                      | Durham          | 23 <sup>rd</sup> July 2012                       | Rus Hoelzel (UDUR)                            | 8 including ConGRESS hosts (6 external) | Very small meeting, focused only on Decision Making Tool |
| Finland   | Helsinki        | 23 <sup>rd</sup> – 24 <sup>th</sup> August 2012  | Craig Primmer (UTURKU)                        | 25 including ConGRESS partners          | Medium sized meeting, mix of end-users                   |

The age range of the workshop participants was skewed towards younger professionals with 37 and 40 individuals aged under 35 and between 35 and 45, respectively. The large majority of participants were educated to Master's level and above (60 to MSc and 43 to PhD level) and a majority (67 individuals) worked for governmental organisations. Nonetheless, 57 participants regarded the scale of operation of their institution as being 'international', with only 27 describing their work as 'local / regional'. The interaction between these data and the kinds of awareness that they had before the workshop on the use of genetics in conservation is still being analysed, but it nevertheless seems clear that we predominantly reached a young and highly educated demographic that was nevertheless working within a governmental context – and this is exactly the target demographic we were looking to influence at the outset of the project. It must be said that this conclusion is

preliminary and predicated on the assumption that those who did not complete the questionnaire were indistinguishable from those who did.

The ConGRESS regional workshop model has attracted some attention from other regions and in November 2013 the ConGRESS team will take the regional workshop outside of Europe – to Pretoria, where in collaboration with the National Zoological Gardens of South Africa we will demonstrate the web portal and tools to an end-user community invited from all over southern Africa.

**The number and visibility of non ConGRESS meetings at which our dissemination tools have been demonstrated and at which our project has been described and advertised, and their regional spread**

Table 3 (below) details the extensive dissemination activities using the tools we produced in WP5. This table does include Regional workshops for comparison (in italics), divided by language. ConGRESS was presented at a number of prestigious meetings, most notably the Kathryn Fuller 2011 Science for Conservation Symposium (Washington DC) and a workshop on “*Promoting the use of genetic and genomic data in conservation planning and legislation: forward from Nagoya*”, coorganised with the Royal Zoological Society of Scotland at the 3rd European Congress for Conservation Biology, in Glasgow UK (August 2012). Leaflets were taken and distributed as much as possible during these events and in as many languages as were available.

**Table 3.** ConGRESS dissemination events where education materials were used, including number of leaflets distributed.

| Language | Material/Theme   | Occasion   | Number of copies |
|----------|--|--|------------------|
| English  | Leaflet: Introduction to conservation genetics                   | ICCB conference in New Zealand, 2011   | 50               |
|          |  | Kathryn Fuller WWF Symposium for Conservation Science, Washington, November 2011   | 50               |
|          |  | European Society for Conservation Biology (ECCB), Glasgow, August 2012   | 30               |
|          |  | EAZA Conservation Forum, 2012  | 10               |
|          |  | <i>Slovakia and Hungary workshops</i>  | 60               |
|          | <i>Leaflet: DNA methods in species identification</i>            | <i>Slovakia and Hungary workshops</i>  | 40               |
|          | <i>Leaflet: Genetics in harvesting and management of species</i> | <i>Slovakia and Hungary workshops</i>  | 40               |
|          | <i>Leaflet: Gene-flow</i>  | <i>Slovakia and Hungary workshops</i>  | 40               |
|          | <i>Leaflet: Genetic diversity</i>                                | <i>Slovakia and Hungary workshops</i>  | 40               |
|          | All leaflets   | <ul style="list-style-type: none"> <li>• Conference: Criteria and Delineation of Significant Sites, Smithsonian-Mason School of Conservation, IUCN, Washington 2013</li> <li>• British Antarctic Survey cruise 2013 (Falkland Islands, Antarctica, South Georgia, Gough Island, Tristan da Cunha and Ascension Island) – visits with environmental groups and schools</li> <li>• The British Deer Society</li> <li>• IUCN</li> </ul> | 890              |

|         |   |  |      |
|---------|---|--|------|
|         |   | <ul style="list-style-type: none"> <li>• BirdLife International</li> <li>• The Tropical Biology Association</li> <li>• National Trust Conference of Ungulates and their Management Sicily</li> </ul>   |      |
|         | All leaflets  | For distribution after the project   | 3675 |
|         | PowerPoint presentation                                   | <ul style="list-style-type: none"> <li>• ECCB Glasgow</li> <li>• Hungary and Slovakia workshops</li> </ul>   |      |
| Italian | Leaflet: Introduction to conservation genetics            | <i>ConGRESS Regional meeting</i>   | 10   |
|         | All leaflets  | III Workshop sulle Ricerche Naturalistiche in Provincia di Sondrio. Museo Civico di Storia Naturale, Morbegno. 20 October 2012.  |      |
|         | All leaflets  | For distribution after the project   | 2165 |
|         | PowerPoint presentation                                   | <ul style="list-style-type: none"> <li>• DIPARTIMENTO RISORSE FORESTALI E MONTANE, Dirigente generale</li> <li>• Sulle tracce degli animali. Porte Aperte alla Fondazione Edmund Mach. San Michele all'Adige, 20 novembre 2011 – open day for at least an audience of 5000 people</li> </ul> |      |
| Finnish | Leaflet: Introduction to conservation genetics            | <i>ConGRESS national workshop</i>  | 200  |
|         |   | Minister of the environment visiting Paimio River Natura 2000 area   | 5    |
|         | Leaflet: DNA methods in species identification            | <i>ConGRESS national workshop</i>  | 200  |
|         | Leaflet: Genetics in harvesting and management of species | <i>ConGRESS national workshop</i>  | 200  |
|         | All leaflets  | For distribution after the project   | 1700 |
| German  | Leaflet: Introduction to conservation genetics            | <i>ConGRESS regional workshops, Germany, Austria, Switzerland</i>  | 900  |
|         |   | ECCB Glasgow   | 50   |
|         |   | Governmental Forest Agencies, Germany, Switzerland   | 50   |
|         |   | For distribution after the project   | 1625 |
| Czech   | PowerPoint presentation                                   | <i>Czech and Slovak workshops</i>  |      |
|         |   | Masaryk University, Molecular Ecology course   |      |
|         |   | Palacky University, Conservation Genetics course   |      |
|         | Leaflet: Introduction to conservation genetics            | <i>Slovakia and Hungary workshops</i>  | 60   |
|         | All leaflets  | PROVAZ project workshops, autumn 2013  | 560  |
|         | All leaflets  | For distribution after the project   | 500  |
| Dutch   |   | For distribution after the project   | 130  |
| French  | All leaflets  | For distribution after the project   | 550  |
| Spanish | PowerPoint presentation                                   | Universidad Pablo de Olavide, course material  |      |
|         | PowerPoint presentation                                   | 6 <sup>th</sup> World Congress on South American Camelids, Arica, Chile, November 2012   |      |
|         | All leaflets  | For distribution after the project   | 1025 |

Although the goal of ConGRESS was not to produce commercially exploitable foreground, the appropriate use of both the Sample Planning Tool and the Decision Making Tool are likely to have cost-saving implications for governments and NGOs

wishing to use genetics in their decision making because they will ensure that all projects will produce statistically significant results and because they will assist in re-evaluating previous studies to assess whether those results were fit-for-purpose for evidence based conservation. Although direct evaluation of the tools we have produced is somewhat subjective, the **Sample Planning Tool** (SPOTG - *Sample Planning Optimization Tool for conservation and population Genetics, also called Sample Planning Tool, on the web*) has been used much more extensively than other tools to date: as described below.

First, the SPOTG has already been used by Congress partners for University courses. For example, Giorgio Bertorelle and Sean Hoban taught several classes during the *Conservation Genetics* course (Masters students, University of Ferrara, December 2012). Peter Galbusera, Gernot Segelbacher and Pim Artzen similarly used SPOTG in their classes in spring 2013. Considering the online availability of this tool and the papers published and forthcoming that describe it, we expect that use of SPOTG for teaching the importance of planning a genetic study in biology conservation will spread to many universities.

In common with the rest of the portal, the impact of WP3 will be better evaluated after at least two years of online availability, i.e. by the end 2014. We predict that only at that time the community of biodiversity managers, biology conservation experts, and teachers will have had the chance to learn about this tool and possibly use it for the development of conservation plans and for teaching to a large audience of future conservation biologists the importance of a well-planned conservation genetics study. This time to measure impact is long because even though SPOTG is user-friendly and runs quickly, the full planning of a study often takes approximately six months (permits, supplies, etc.), followed by field collections, which may take another approximately six months.

However, already as a direct evidence of the likely impacts in the future, we are aware that SPOTG has already been used in real situations in at **least three cases**: i) by Margarida Fernandes from the Instituto da Conservação da Natureza e das Florestas, Lisbon, Portugal, who performed a post-study analysis of power for black stork, with the bottleneck module; ii) by Alice Laguardia from the Beijing Institute of Forestry, who used the tool to help planning a connectivity study in large cats; iii) by José Godoy, from the Estación Biológica de Doñana, Seville, who has run some analyses with the temporal module for ancient sampling with parameters suitable for the Iberian lynx. In addition, the tool has provided the basis for several discussions on the Forum.

Given the high interest already shown by end-users for testing this tool and by students in our classes for learning to use it, we are confident that the diffusion of SPOTG will have a lasting impact in biodiversity conservation planning, by favoring the implementation of genetic studies with appropriate statistical power, and helping avoid expensive studies when not necessary.

Finally, our publications record for a Coordination and Support Action project, where no new science is usually included has yielded five papers to date, including one in *Nature Reviews Genetics* (IF 41.06, ISI ranked first for genetics)