Newsletter

ISSUE No. 6

BioFresh's papers & papers!

BioFresh is entering its last project phase and it is by all means a definitive year. It is time to remember the major goals of BioFresh set at the beginning of the project. BioFresh aims to improve the capacity to protect and manage freshwater biodiversity by building an information platform, do scientific analyses, increase the awareness for freshwater biodiversity and support the European Union and other bodies' environmental policies with our knowledge and results. Since the beginning of the project, we have made important progress in building the platform and doing science.

Indeed, whilst our last BioFresh newsletter was dedicated to data mobilisation/acquisition, data publishing and the platform, this newsletter features some of the many scientific outcomes of BioFresh. Several excellent papers have been published recently under BioFresh partners' lead or with BioFresh's remarkable contribution and we predict that many more are to be published.

However, to fulfil its long-term goals, BioFresh is strongly investing major efforts in raising awareness for the critical situation of freshwater biodiversity with the wider public and engaging in policy dialogue interface. BioFresh's dissemination experts are discussing implementation steps to communicate research results for non-scientists and feed results into policy processes. During this last year, BioFresh came in contact with EU policy makers , stakeholders and other EU projects to present the BioFresh results. Major results of policy relevance, as the information platform, the Global Freshwater Biodiversity Atlas, the freshwater Key Biodiversity Areas (KBAs) and BioFresh's predictive models are perfect to be advertised. Consequently, the BioFresh project, together with thematically related projects, will organise a Science-Policy Symposium in Brussels in 2014. The aims and structure of this conference will be a major topic at our 2013 annual meeting to be held in Leipzig, 15-19th April.

Naturally, our annual meeting is not only aimed to update each other on the progress and next steps in the project. Its aims are to discuss ongoing tasks, projects and results and it is also an event to meet again personally and discuss face to face. It's a major occasion to meet friends!

Enjoy BioFresh's scientific results!

Jörg Freyhof
IGB

BioFresh Coordination Team

BioFresh in Hydrobiologia

Fish-SPRICH: an open access database of freshwater fish species richness throughout the world

The Fish-SPRICH database provides richness data for freshwater fishes, which, with more than 13,000 described species, represent a quarter of all vertebrate species. This database was compiled as a collaboration between Université Paul Sabatier and Institute pour la Recherche et Development. It is based on an extensive literature survey of native, non-native (exotic) and endemic freshwater fish species richness. The resulting database, called Fish-SPRICH, includes data from more than 400 bliographic sources including published papers, books and grey literature sources. Fish-SPRICH contains richness values at the river basin grain for 1,054 river basins covering more than 80% of the earth's continental surface. This database is currently the most comprehensive global database for native, non-native and endemic freshwater fish richness available at the river basin grain. The Fish-SPRICH database and the corresponding metadata have been published (Brosse et al. 2013) and both database and metadata will soon be integrated in the BioFresh data portal.

Reference: Brosse S., Beauchard O., Blanchet S., Dürr H.H., Grenouillet G., Hugueny B., Lauzeral C., Leprieur F., Tedesco P.A., Villeger S. & Oberdorff T. 2013. Fish-SPRICH: a database of freshwater fish species richness throughout the World. Hydrobiologia 700: 343–349.

‚ sebastien.brosse@univ-tlse3.fr

Sebastien Brosse,
UPS
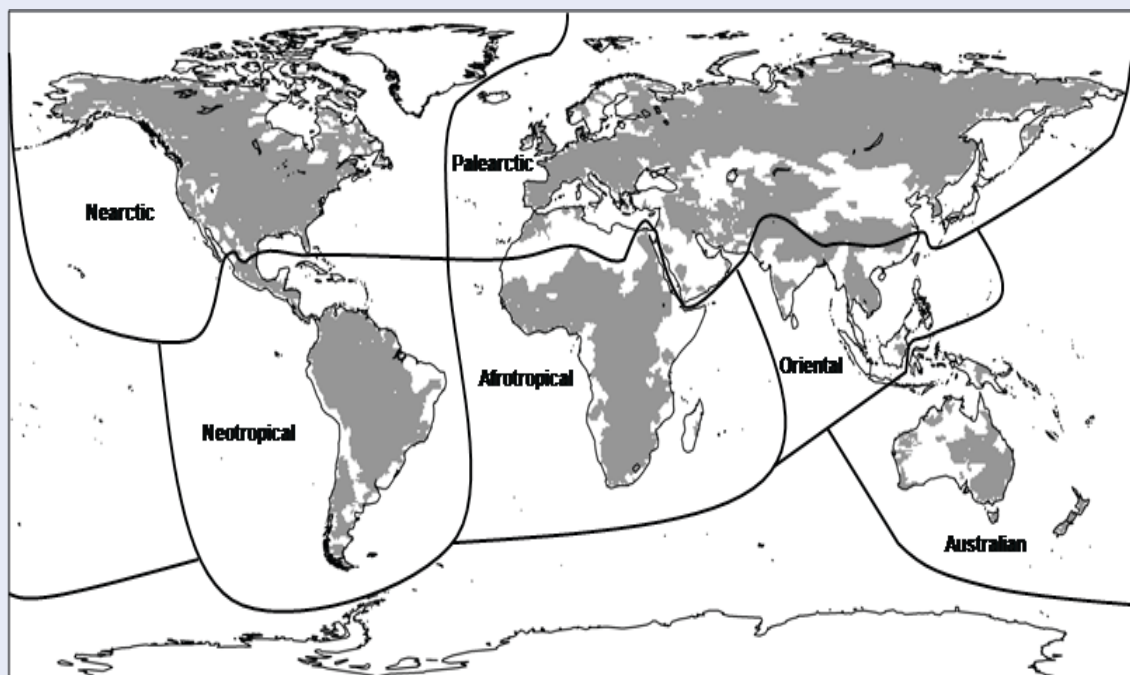
Map indicating the area covered by the 1,054 river basins considered in the Fish-SPRICH database (in grey). Note that some large areas where no basins were investigated correspond to deserts (both cold and hot) where there are no perennial rivers (e.g. northern Africa, central Australia, polar zones). Bold lines indicate realm boundaries. Map: Sebastien Brosse.

BioFresh in Ecological Indicators

A framework to measure changes in taxonomic dissimilarity following species introductions and extirpations

A recent BioFresh paper from Université Paul sabatier provided insights on how to measure changes in taxonomic dissimilarity. It proposes a complete mathematical formula to disentangle how extirpation and introduction processes affect biodiversity change.

Applying this framework to simulated data revealed that the two commonly used indices to measure changes in taxonomic dissimilarity (Jaccard and Beta-Sim) provide contrasted results, with opposite direction of changes in more than 14% of the cases. This discrepancy was attributable to the mathematical structure of the indices, the Jaccard being the one measuring change in dissimilarity whereas the Beta-Sim only estimates species turnover. As for beta-diversity, it is hence possible to decompose the changes in Jaccard's dissimilarity into changes in taxonomic turnover and changes in taxonomic nestedness-resultant components.

Under the context of global change, the framework proposed in this paper has practical applications to measure and predict human impact on biodiversity. It indeed permits to identify the determinants of biotic homogenization and differentiation, processes that currently affect most ecosystems on earth. As a support to ecologists interested in applying this framework, a R function to compute the indices presented in this paper is provided as Appendix B.

Reference: Villeger S. & Brosse S. 2012. Measuring changes in taxonomic dissimilarity following species introductions and extirpations. Ecological Indicators 18: 552-558.

➲ sebastien.villeger@univ-tlse3.fr

➲ sebastien.brosse@univ-tlse3.fr

Sebastien Villeger
Sebastien Brosse,
UPS
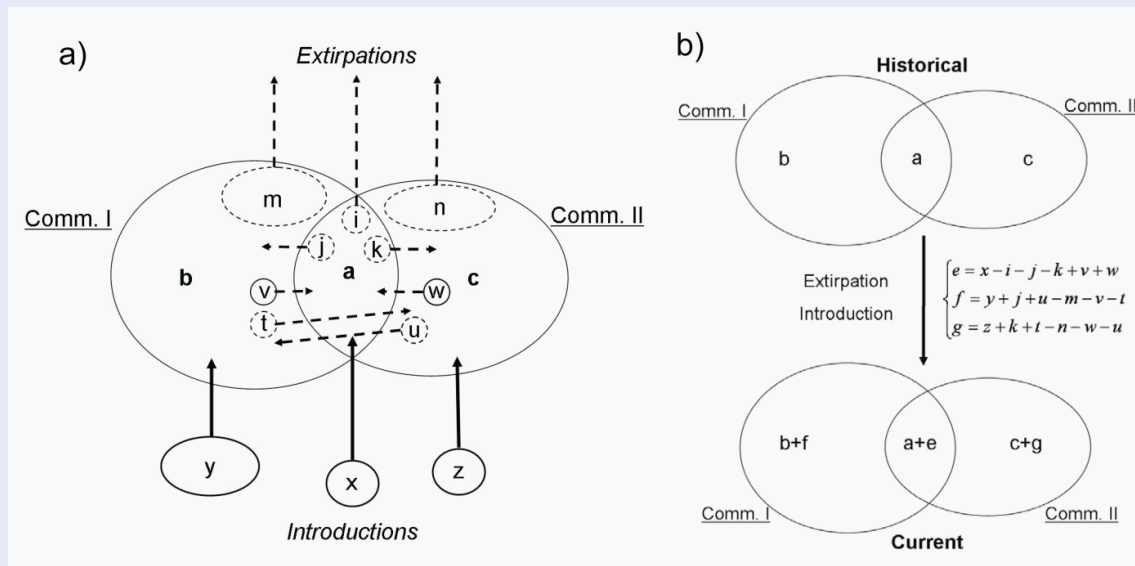
Conceptual framework of how species extirpation and introduction affect the taxonomic dissimilarity between two communities. (a) Schematic representation of the taxonomic dissimilarity between two communities. Species pools from the two communities are represented by the two ovals, their intersection symbolizing the species shared by the two communities. Letters represent the number of species initially present (a–c), introduced (t–z) or extirpated (i–n) from the communities. (b) Change in taxonomic dissimilarity from "historical" to a "current" situation following species introductions and extirpations. Comparisons between two past periods or between current situation and future simulated communities are also possible. Letters e, f and g represent changes in the number of species shared by the two communities or not after changes in species composition. Figure: Sebastien Brosse.

BioFresh in PLoS One

How to predict species invasions using species distribution models?

Species distribution models (SDMs) are widespread in ecology and conservation biology, but their accuracy can be lowered by non-environmental (noisy) absences that are common in species occurrence data. Those noisy absences are particularly abundant when considering non-native species which are usually not in equilibrium with their environment. In this paper we propose an iterative ensemble modelling (IEM) method to deal with noisy absences and hence improve the predictive reliability of ensemble modelling of species distributions.

In the IEM approach, outputs of a classical ensemble model (EM) were used to update the raw occurrence data. The revised data was then used as input for a new EM run. This process was iterated until the predictions stabilized. The outputs of the iterative method were compared to those of the classical EM using virtual species. The IEM process tended to converge rapidly. It increased the consensus between predictions provided by different methods as well as between those provided by different learning data sets. Comparing IEM and EM showed that for high levels of non-environmental absences, iterations significantly increased prediction reliability measured by the Kappa and TSS indices, as well as the percentage of well-predicted sites. Compared to EM, IEM also reduced biases in estimates of species prevalence. IEM thus constitutes a promising way to increase the accuracy of EM predictions of difficult-to-detect species, as well as of non-native species that are not in equilibrium with their environment.

➲ christine.lauzeral@cict.fr

➲ sebastien.brosse@univ-tlse3.fr

Christine Lauzeral
Sebastien Brosse,
UPS
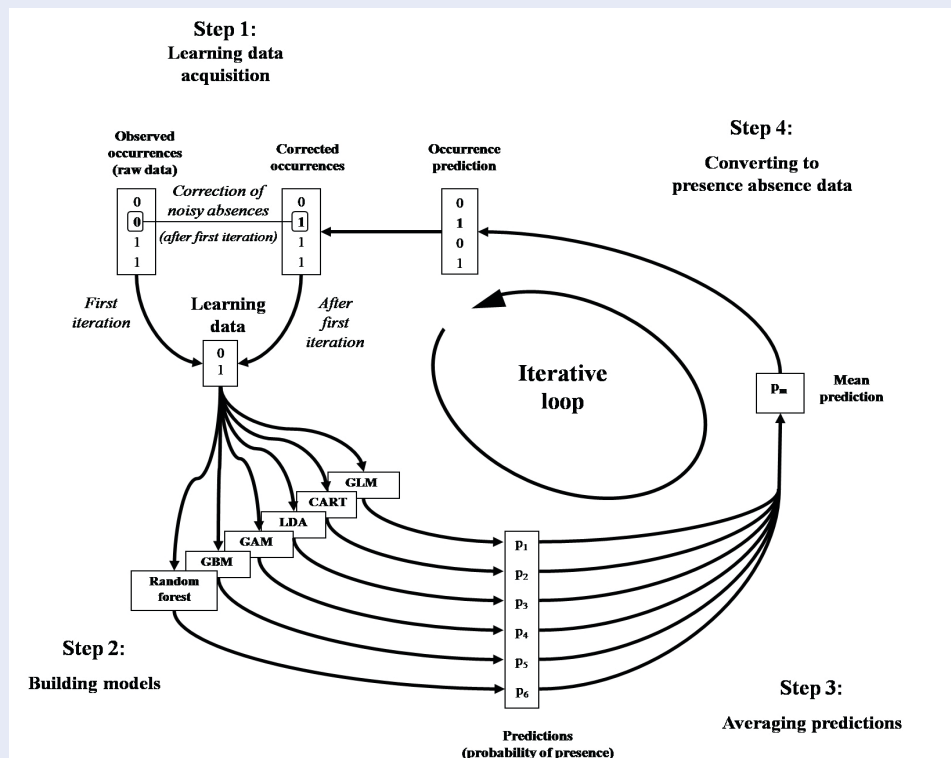
A schematic representation of the iterative ensemble modelling method.

Figure: Sebastien Brosse.

BioFresh in Global Change Biology

How would climate change affect European stream macroinvertebrates' distributions?

A recently published paper led by Sami Domisch (BiK-F, Frankfurt) and in collaboration with the Bio-Fresh partner UB (University of Barcelona) is online in Global Change Biology. It explores the possible future patterns of stream macro-invertebrates' distributions across Europe under warming climates. In the study, the authors analysed potential shifts of suitable climatic conditions for a variety of 191 species, as well as for specific trait-based sets.

Using an ensemble of bioclimatic envelope models and future climate scenarios, the paper shows that suitable climatic conditions would remain for nearly 99% of the modelled species in Europe until the year 2080. Nevertheless, a decrease in the amount of climatically suitable areas was projected for 57–59% of the species, while losses could be of 38–44% on average. Especially cold-adapted species were projected to lose climatically suitable areas, while gains were expected for warm-adapted species. In addition, endemic species of the Alps and the Iberian Peninsula were projected to lose significantly larger amounts of suitable climatic areas than non-endemic species.

The results highlight the vulnerability of freshwater organisms to climate change and the need to understand the consequences for ecological functioning and biodiversity conservation. In particular, future research on the combination of limited and fragmented habitat availability under warming climates and species' dispersal abilities is required.

Reference: Domisch, S., Araújo, M. B., Bonada, N., Pauls, S.U., Jähnig, S.C., Haase, P. (2013). Modelling distribution in European stream macroinvertebrates under future climates. Global Change Biology, doi: 10.1111/gcb.12107

✆ sami.domisch@senckenberg.de

Núria Bonada,
UB
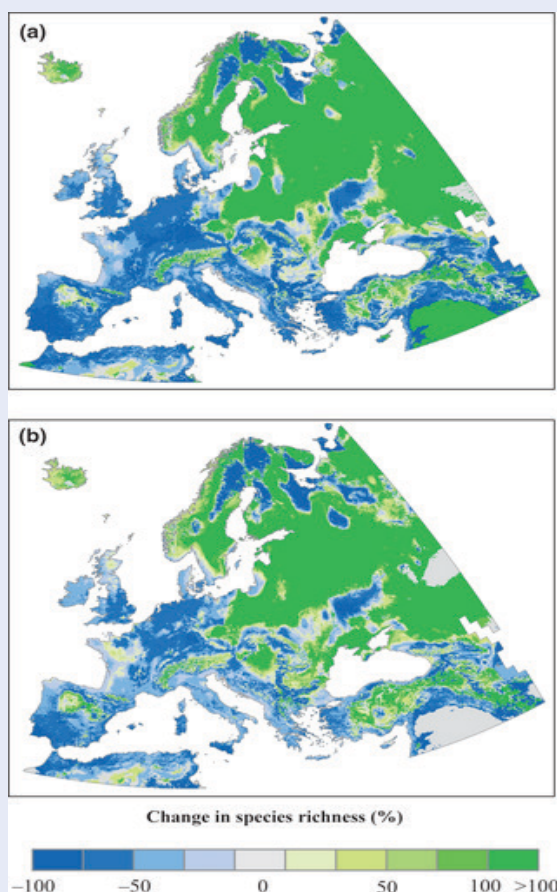
Relative changes in the number of species for each grid cell for which climatically suitable areas (CSA) were projected under the A2a (a) and the B2a (b) climate warming scenarios compared with the baseline.

Map: Sami Domisch.

BioFresh in Systematic Biology

Diversification dynamics in groundwaters

A key challenge for biologists is to document and explain global patterns of diversification in a wide-range of environments. Within the framework of BioFresh, the authors of a recent paper in Systematic Biology explored patterns of continental-scale diversification in a groundwater species-rich clade, the super-family Aselloidea (Pancrustacea, Isopoda; see Figure panel a).

The data set comprised a total of 114 Aselloidea morphospecies collected at 300 sites spanning a wide range of freshwater habitats in Europe and the USA. In the literature, two major hypotheses have long been debated to explain how reproductive isolation of groundwater colonizers from surface freshwater populations could lead to diversification in groundwater. According to the adaptive shift hypothesis (ASH), species diversification depends primarily on species evolvability: diversification occurs because of contrasted selective pressures between surface freshwater and groundwater. ASH is thus expected to result in a constant pattern of diversification rate. In contrast, the climatic relict hypothesis (CRH) assumes that diversification proceeds because major physical perturbations acting over broad geographic regions interrupt synchronously gene flow among many groundwater populations by driving surface water populations to extinction. Consequently, many isolated groundwater populations undergo synchronous speciation, leading CRH to predict large shifts in diversification rates associated with physical perturbations at large spatial scale.

The analyses in this paper supported a constant diversification rate during most of the course of Aselloidea evolution, until 4-15 Ma when diversification rates started to decrease (see Figure panel b). This constant accumulation of lineages challenges the CRH view that groundwater species diversification in temperate regions might have been primarily driven by major changes in physical environment. Rather than acting synchronously over broad geographic regions, factors causing extinction of surface populations and subsequent reproductive isolation of groundwater populations may act in a local and asynchronous manner,
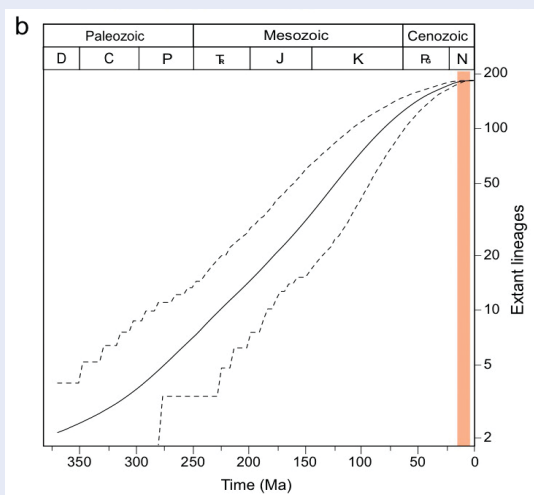
Patterns of Aselloidea diversification. a – *Proasellus valdensis* (Isopoda, Aselloidea). b – Lineage-through-time (LTT) plot. Y-axis is log-scale of extant lineage number. Solid line is the dated phylogeny LTT plot and dashed lines show 95% confidence intervals. Top boxes indicate geological periods following the FGDC Digital Cartographic Standard for Geologic Map Symbolization. Orange vertical band shows the recent shift in diversification rates inferred from diversification analyses. Figure: Theotime Colin.

thereby resulting in a constant speciation rate over time. The phylogeny in this paper also revealed several cases of parapatric distributions among closely related surface water and groundwater species suggesting that species diversification could also arise from a process of disruptive selection along the surface-subterranean environmental gradient. The results provide new informations and data about biodiversity patterns in surface and subterranean freshwater and call for reevaluating the spatial scale and timing of factors causing diversification events in groundwater.

Morvan C., Malard F., Paradis E., Lefébure T., Konecny-Dupré L., Douady C.J. 2013. Timetree of Aselloidea reveals species *diversification dynamics in groundwater in Systematic Biology, doi: 10.1093/sysbio/syt015.*

➲ claire.morvan@univ-lyon1.fr

Claire Morvan,
UCBL

BioFresh in Science

Essential Biodiversity Variables (EBVs)

Reducing the rate of biodiversity loss and averting dangerous biodiversity change are global goals, adressed by the Aichi Targets for 2020 by Parties to the United Nations (UN) Convention on Biological Diversity (CBD). However, there is still a long way to go to reach the goals and even observation of biodiversity loss is challenging, as a global, harmonized observation system for delivering regular, timely data on biodiversity change is still missing. Following the example of the Essential Climate Variables, the Group on Earth Observations Biodiversity Observation Network (GEO BON), with the contribution of BioFresh, is developing - and seeking consensus around - Essential Biodiversity Variables (EBVs). These could form the basis or at least a first discussion point to develop biodiversity monitoring programs worldwide.

Reference: Henrique M. Pereira, S. Ferrier, M. Walters, G.N. Geller, R.H.G. Jongman, R.J. Scholes, M.W. Bruford, N. Brummitt, S.H.M. *Butchart, A.C. Cardoso,N.C. Coops, E. Dulloo, D.P. Faith, J. Freyhof, R.D. Gregory, C. Heip, R. Höft, G. Hurtt, W. Jetz, D. Karp, M.A. McGeoch, D. Obura, Y. Onoda, N. Pettorelli,B. Reyers, R. Sayre, J.P.W. Scharlemann, S.N. Stuart, E. Turak, M. Walpole, M. Wegmann , 2013, Essential Biodiversity Variables, in-Science 18 January 2013:Vol. 339 no. 6117 pp. 277-278, doi: 10.1126/ science.1229931*

➲ freyhof@igb-berlin.de

Jörg Freyhof
IGB

Fourth annual meeting of BioFresh

BioFresh goes political

The fourth annual meeting of BioFresh will be held in April 15-19 at Schloss Machern in Leipzig.

This year's meeting is organised under the slogan "BioFresh goes political". Apart from discussing the work progress and preparing the last phase of the project, a full day will be dedicated to a workshop about understanding Science Policy Interface (SPI) and raising the profile of freshwater biodiversity research and its funding. This workshop should result in two main outcomes: one aim is to create a space where science and policy come together to discuss current ways to methods of science-policy communication and its best practices, its challenges and futures needs when engaging with policy makers and stakeholders. For this, BioFresh will profit from the experiences and inputs of several guests involved in other FP7 EU projects (KNEU, OpenNESS, REFORM, SPIRAL, ViBRANT, WaterD-ISS) related to freshwater, e-infrastructures, data mobilisation and publishing.

Finally, BioFresh hopes to join forces with these EU projects to design a Science-Policy Symposium on freshwater biodiversity, to be held in Spring 2014 in Brussels.

➲ www.ufz.de/index.php?en=31265

Carla Pinho
IGB

BioFresh work progress

IUCN workshop on Freshwater Key Biodiversity Areas in Bosnia and Herzegovina

Key Biodiversity Areas (KBAs) are globally important sites for the conservation of species diversity. KBAs are now specifically referred to within the Environmental Safeguards policies of many companies, donors, development agencies, and financing bodies (e.g. the International Financing Corporation). They are also specifically mentioned as sites to be included within a representative global protected areas network (CBD Target 11). All information on KBAs is currently held within the World Biodiversity Database (WBDB) and the Integrated Biodiversity Assessment Tool (IBAT) but is limited to "Important Birds Areas (IBAs)", "Alliance for Zero Extinction Sites (AZEs)" and some terrestrial KBAs – there are currently no KBAs indentified for freshwater biodiversity within the WBDB or IBAT. Therefore, freshwater KBA's are one of the most important products BioFresh is heading for. In response to this major lack of focus on important sites for freshwater biodiversity BioFresh Partner IUCN has developed a methodology for identifying Freshwater KBAs and together with WP7 partners is now running stakeholder workshops to validate and create awareness of proposed sites as identified through the regional freshwater biodiversity assessments previously completed for the Mediterranean Basin. Freshwater KBAs, once validated and refined through these stakeholder workshops, will then be entered into the WBDB enabling them to be publicly recognised alongside the IBAs, AZEs, and other terrestrial KBAs. Supported by BioFresh, the WBDB has also now been modified by Birdlife

International to accept the additional information relevant to freshwater KBAs, and the first trials are underway to import the information. This represents a most important step forwards in the protection of freshwater biodiversity in the face of development.

The first of these stakeholder workshops (11-13 December 2012) led by BioFresh and the Freshwater Biodiversity Unit of the IUCN Global Species Programme brought together a range of stakeholders to validate proposed Freshwater KBAs in the southern European part (Balkan region) of the Mediterranean Biodiversity Hotspot. In this workshop, held in Jahorina (Bosnia and Herzegovina), experts completed and validated information for a network of river or lake catchments previously proposed as freshwater KBAs for this part of theregion. For each site they also identified/validated the species present, major threats, priority actions, and potential champions (relevant organisations with a presence in the area) in a position to raise the profile of each KBA site. In each case the KBA site boundary was delineated to include a "focal area" (the location of the conservation target - such as a cave system supporting threatened or restricted range species) and the "management zone" (the connected, surrounding area that would need to be managed in order to conserve the species in the focal area). The information compiled in the workshop, for 90 freshwater KBAs, is now undergoing further work to complete the data sets for each site. This work aims to provide the foundation for creation of a representative Protected Areas network for freshwater species, as well as providing information on important sites for freshwater biodiversity for decision makers involved in the conservation and sustainable management of freshwater biodiversity in the Mediterranean Basin Biodiversity Hotspot. This first stakeholder KBA workshop, organised in collaboration with the IUCN Centre for Mediterranean Co-operation is part of the initiative "Mediterranean Biodiversity Assessment II", identification of Important Freshwater Areas, and co-funded by the Critical Ecosystem Partnership Fund, MAVA Foundation, the Spanish Agency for International Development Cooperation (AECID) and FREDIE initiative (Freshwater Diversity Identification for Europe).

➲ William.DARWALL@iucn.org

William Darwall,
IUCN