

**Symposium "Future trends of Taxonomy  
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Executive Summary**



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Understanding the origin and diversity of the living world is a cumbersome endeavour that requires a revision of traditional taxonomic practices. However, it is widely recognized that progress in the study of biodiversity in this time of crisis is hindered by a worldwide shortage of taxonomists coupled with a lack of enough funding for taxonomic study (the "Taxonomic impediment"). To overcome this impediment, it is mandatory both to adopt new technologies developed in other fields for taxonomic use, and to address the key conceptual challenges that taxonomy faces. Under the auspices of EDIT (European Distributed Institute of Taxonomy), 25 European scientists actively publishing in taxonomy, 90 EDIT members, 17 non-EDIT CETAF (Consortium of European Taxonomic Facilities) members, and 15 speakers were invited to gather in a 3-day symposium to discuss in depth future trends of taxonomy. Speakers were selected to cover a wide range of technological (first day) and conceptual (second day) topics, and the 25 taxonomists from 12 European countries were asked to provide a personal statement regarding the current status of taxonomy in their countries. The last day was devoted to a brainstorming session among the speakers to produce a scoping document summarizing the conclusions of the meeting, and providing recommendations for the future mission of EDIT (see the corresponding report).

The main questions addressed by the speakers in their presentations were the following:

"A renaissance of insect morphology -  $\mu$ -Ct and other innovative techniques" by Rolf Beutel (University of Jena, Germany). A review of the state of the art of new microscope technologies was presented and their implementation in the ongoing project "Beetle tree of life". The use of confocal laser scanning microscopy was shown for external features, coupled with low energy micro-computer tomography and 3D reconstruction for internal features. The new technologies were found to provide few new informative characters but high resolution of previous ones coupled with fast processing of samples.

"Ancient (Museum preserved) tissues and DNA" by Matthew Collins (University of York, UK). Currently available methods for DNA and RNA extraction from ancient tissues were reviewed. Most DNA was shown to disappear postmortem, and the remaining DNA is affected by oxidation, hydrolization, and cross-linking processes. Yet, DNA may survive in hidden environments such as bone or hair. Modelling decay of DNA could be a useful tool for predicting the likelihood of successful PCR amplification from Museum collections.

"Tissue & DNA storage and sharing: BRCs networking" by Manuel Morente (Cancer Research Center, Spain). The talk was centred on Biobanks as repositories of specimens or tissue and DNA samples. The importance of developing homogenous protocols for

collecting, handling and storing samples, as well as the enforcement of quality controls, and networking was particularly emphasized.

"Field work: the need to scale up and adjust to new constraints" Philippe Bouchet (MNHN, France). Fieldwork conducted specifically for taxonomical purposes essentially remains small-scale and low-tech, and not infrequently squarely unlawful. Taxonomists must scale up the way they are conducting field work and must learn how to address the Access and Benefit Sharing (ABS) requirements of the CBD. Large expeditions require a distinction between participation, right to study, and collection ownership. The future of taxonomic fieldwork is threatened by over-regulation, and the Buffon declaration called for a distinction between academic versus commercial bioprospecting.

"Environmental sequencing" by Jeroen Raes (EMBL, Heidelberg, Germany). The field of environmental sequencing is growing fast, and there are more than 100 ongoing metagenomic projects. The use of environmental sequencing has a potential interest for taxonomic studies but requires complex bioinformatic analyses.

"Phyloinformatics -- integrating everything" by Roderic Page (University of Glasgow, UK). The information link to a specimen needs to be integrated and made easily accessible to the user. Identifiers from different databases can be combined following the framework of CrossRef, which is used by publishers to integrate data and foster citations. Much of the available information in the web may be under copyright. It would be desirable to substitute current copyright rules by "creative commons", which allows specific use of data.

"Uniting supertrees and supermatrices to derive the Tree of Life" by Olaf Bininda-Emonds (University of Jena, Germany). Supermatrices and Supertrees can be now combined for analyzing large taxonomic groups. Hence, supertrees become not the final product of the analysis but they are implemented within the search strategy to speed up phylogenetic analyses and gain accuracy.

"New sequencing techniques" by Miguel Alvarez (ROCHE, Spain). Pyrosequencing (GS-FLX automated sequencers) was presented as a revolution in sequencing techniques. However, it is still too expensive, the load of data produced requires specific bioinformatic tools, and new sequencing procedures need to be adapted to taxonomic studies.

"Zoobank and Zoological Nomenclature" by Ellinor Michel (ICZN, UK). The need of supporting Zoobank as an open-access register for animal scientific names was emphasized. It was suggested that registration would be voluntary initially but likely to become mandatory in the long term. The question on whether registration equals publication was debated.

"Zoological nomenclature: some urgent needs and problems" by Alain Dubois (MNHN, France). Despite several attempts to change the Linnean code, it seems fair to maintain the status quo on the code with small adjustments to the new times. For instance, work is needed on rules for higher taxa. The increasing role of developing countries in taxonomic description was contrasted with their yet limited access to technologies.

"Developments and threats in taxonomic research: a summary from statements by leading European taxonomists and phylogeneticists" by Klauss Klass (Museum of Zoology, Dresden, Germany). The statements written by taxonomists on their view of taxonomy in their different countries were analyzed. Increasing networking and availability of new technologies were highlighted as positive developments. Yet, a warning on the declining of positions and budgets, of support to amateurs, and of taxonomic education at universities was made.

"From field records to a sustainable taxonomic knowledge base: new approaches and opportunities for efficient biodiversity inventories" by Christopher Hauser (State Museum of Natural History, Stuttgart, Germany). The talk stressed the need of sustainable data generation as one of the major challenges for taxonomy. For that, it is important to develop standards and protocols (Darwin core, Taxonomic Database Working Group –TDWG) for sharing biodiversity data generated from projects such as ATBI (All taxa biodiversity inventories). An example from the EDIT pilot study in Mercantour (Alpes Maritimes) was presented.

"DNA taxonomy" by Alfried Vogler (NHM, UK). DNA taxonomy was praised as a tool for discovering and identifying new species, and a valid replacement of the current description system based on morphology. Coalescence simulations were presented in support of the objective recognition of species based on sequence divergence. Among its advantages over other methods, DNA taxonomy has direct use in ATOL projects, surveys, species diversity and turnover.

"DNA sequences in taxonomy: empirical performance, opportunities, and pitfalls" by Rudolph Meier (National University of Singapore, Singapore). The usefulness of Barcoding as service for forensics, food determination, customs, etc was recognized, but its use in taxonomic discovery was challenged. Several analyses to determine taxonomic accuracy of Barcoding were presented. Success on species identification was found to depend strongly on the presence of singletons (good coverage), and large intra or small inter-specific divergences.

"Initiatives for Improving Systematics: Attitudes, Impediments and Opportunities" by Diana Lipscomb (George Washington University, USA). A review of the variety of research programs in taxonomy (PEET, ATOL, PBI, RevSys) sponsored by NSF (USA) was presented. It was stressed the importance of a science-driven evaluation of projects and jobs (relative irrelevance of impact factors), and the role of scientists in directly designing the funding policy (bottom-up approach).

Every day, after the talks, a round-table session with the corresponding speakers was held, establishing lively discussions with the audience. The book of the symposium (Future Trends in Taxonomy symposium booklet) including the summaries of all the talks and the statements of the 25 European taxonomists on the status of taxonomy in their countries can be found at: <http://www.e-taxonomy.eu/edit-downloads.php> under the heading of Work Package 4.