

Forum Herbulot 2014 statement on accelerated biodiversity assessment
(Community Consensus Position)

Forum Herbulot is a research initiative, founded in the year of 2000, with approx. 150 members from 42 countries. Most are renowned experts in Lepidopterology (with a main focus on the largest family, Geometridae). During the 8th congress of the Forum Herbulot, held between June 30th and July 5th at the Nature Conservation Centre of the Ore Mountains in Schlettau, Germany, attendants joined a general discussion of the topic "How to accelerate the inventory of biodiversity" and decided to publish the following declaration:

(1) Forum Herbulot (FH) highlights that global biodiversity assessment needs to be accelerated, through

- extensive sampling projects, especially in tropical and subtropical regions where a large part of Lepidopteran diversity remains undescribed,
- species descriptions and
- interim-assessments and characterization of diversity (e.g. DNA Barcoding; collection management; databasing)

To achieve this goal we urge national and international funding agencies, as well as decision-makers to provide substantial support and financial resources to projects involving sampling, DNA barcoding, and taxonomic research. WE NEED TO consider that mankind is facing, within the next few years, its biggest environmental crisis ever, i.e. the definitive and irreversible loss of a considerable part of biodiversity on earth. Species on Earth are disappearing at an alarming rate and it will soon be too late to perform research on (and subsequent conservation of) Life's most precious heritage: biodiversity. FH urgently asks national and international authorities to endorse and support biodiversity research by adopting collecting/exportation regulations in fact facilitating, rather than obstructing, research on biodiversity, along the lines of Article 8a of the Nagoya Protocol on Access and Benefit Sharing.

(2) FH highlights the need of formally described species within the universally adopted Linnean system, but also recognizes the urgent need to develop and integrate the use of interim DNA-based systems to characterize species. Such an interim system can be generated, for instance, by the use of DNA barcoding, and of automatically assigned Barcode Index Numbers (BIN), in the Barcode of Life Datasystems (BOLD). Therefore we welcome

- (a) the forthcoming online documentation of BIN history in BOLD
- (b) DNA barcoding programs focusing on unnamed species (suspected to be new) in collections
- (c) projects of DNA barcoding of type specimens. National funding agencies and decision-makers should commit themselves quickly to provide substantial support and financial resources to generate DNA-barcodes for all type specimens deposited in their national collections.

(3) FH acknowledges the advantages of modern tools for species descriptions, and supports/encourages:

- electronic publication of species descriptions linked to online databases
- development of interfaces linking DNA barcode data (e.g. BOLD), online publishing tools and other online databases (e.g. GenBank, GBIF, EOL, etc.)
- registration in Zoobank as a standard for all new nomenclatural acts

- DNA barcoding of holotypes as best practice for all newly described species.

(4) FH recommends, for species descriptions, the following minimum quality standards (in addition to the minimum requirements of the Code):

- information on wing pattern

- internal morphological features (usually genitalia)

- genetics (preferably the standard DNA barcode, i.e. the 5' 658bp of the COI gene) when available

- differential diagnosis from the closest related species

FH encourages careful and thorough differential diagnoses, as well as full bibliographic references to the original descriptions of all mentioned species names in taxonomic publications whenever possible.

(5) Common resource data: FH supports the Bouchout Declaration

(<http://bouchoutdeclaration.org/>) for open access to biodiversity data and thus strongly encourages opening for free use the online access to key biodiversity data including sequences (along with access numbers on BOLD and GenBank / EMBL / DDBJ published in the original descriptions), taxonomic names, descriptions, occurrence data, images, ecological data, habitats, biological traits and data.

The Forum Herbulot.

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