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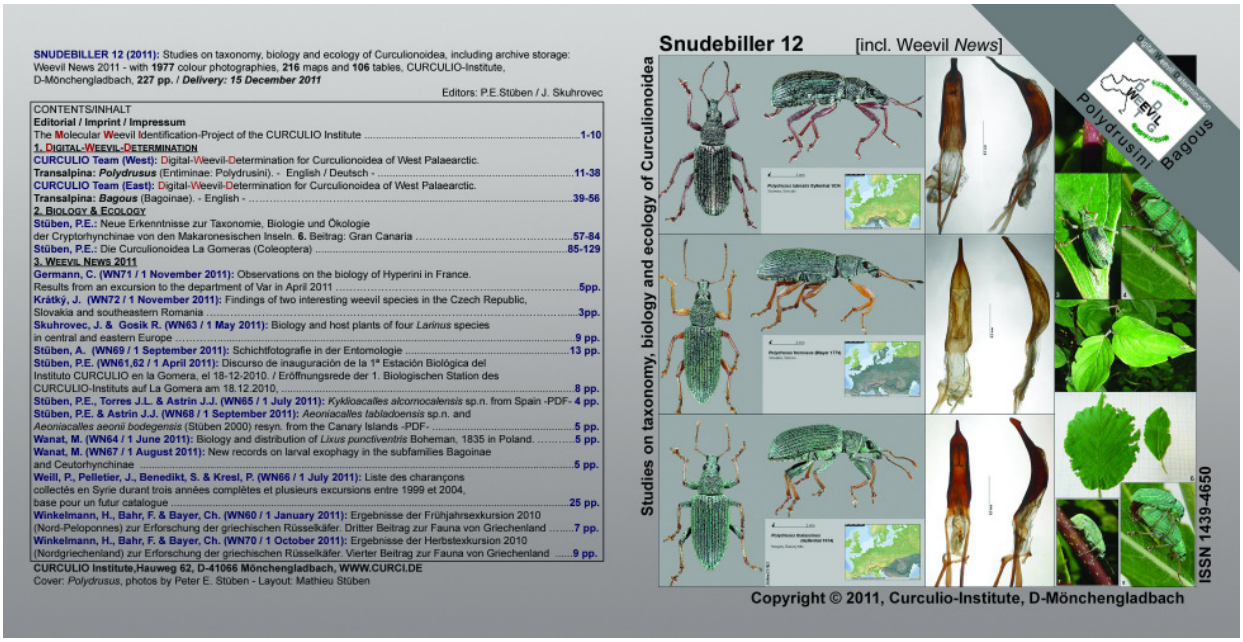

Editorial

The **M**olecular **W**eevil **I**dentification-Project of the CURCULIO-Institute (CURCI, Germany: Mönchengladbach)
- in close cooperation with the Zoologisches Forschungsmuseum Alexander Koenig (ZFMK, Germany: Bonn)

by Peter E. Stüben, Germany: Mönchengladbach

This project is a further, significant step towards 'integrative taxonomy' [Will et al. 2005; Astrin et al. in press]. The reader of the 12th edition of SNUDEBILLER will already be able to see the results of its pilot phase. There are in the truest sense genetic and morphological aspects to the aim, which is to assemble molecular (CO1 'Barcodes') and photographic databases of the **European Curculionoidea** (some 6000 species). The processing of the material is in accordance with this dual principle: tissue will be collected for DNA extraction (in ethanol) and – hand in hand with this – a reference collection will be assembled of specimens from the same locality and population ('1&1 practice'). Even our experts in the CURCULIO-Institute may make mistakes when identifying specimens and gene banks that use only references without providing comparative specimens are handicapped. Confidence in the expertise of colleagues is good, but it is better to be able to confirm identifications independently, even decades later.

Our aims are not new, but they are decidedly different! International barcoding-networks were established long ago. They are used as databases and online tools in the (re-)identification of animals and plants. In insects the usefulness of COI-Gen (Cytochrome c-Oxidase 1) has been shown, for instance, in the international Barcode of Life project

(iBOL) as well as in the regional project of the Free State of Bavaria, the *Barcoding Fauna Bavarica*. And now also in our project, the *German Barcode of Life* (GBOL) of the Federal Ministry of Education and Research?

The laboratory work will be done by the 'Centre of molecular Research on Biodiversity' of the ZFMK, Bonn. The mission of the CURCULIO-Institute is the acquisition of the material – here weevils – and its determination.

The molecular approach has provoked criticism from detractors, whose "quo vadis?" sometimes suggests confusion (see [Klausnitzer 2010]). The concerns are quickly summarised as the absence of experts and consequent lack of reliably determined reference-specimens, and a critique of DNA-barcoding reductionism: "A sad vision, if the unlimited diversity of our world full of miracle would be reduced to the miserable standard of a till in a supermarket!" [Klausnitzer 2010].

But it is the other way round. There are still a small number of experts, morphologists and taxonomists who are able to confidently identify their species. If we are going to hand over 200 years of entomological knowledge and morphological experience to the new molecular age by using **specific epithets**, then **today** it is more than ever up to these experts to provide assistance whilst students are still willing to go through years of training before they get to grips with the first 300-400 species of a taxonomic group.
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This confronts us with the two contrasting criticisms above: the number of described species was such an obstacle to classical taxonomists that even a key to the European Curculionoidea was not conceivable, whereas an avalanche of barcoding projects was triggered due to the discrepancy between the large number of species and the paucity of experienced taxonomists. Eventually, the sceptics of the 'museum approach' and classical taxonomists converged to resolutely reject the new and quick digital techniques of publication (i.e., the internet) based on the argument that it endangers the stability of scientific names and is a frontal attack on the International Rules of Zoological Nomenclature [Klausnitzer 2010].

Today, sceptics of the molecular approach simultaneously face extinction and caution us about a supposed 'barcoding hubris', but our work is in fact intended to further understand our planet's biodiversity in a more efficient manner. We are perhaps still in time to do so but climate change, species' extinction and environmental devastation will not slow down and patiently wait whilst we finish cataloguing the biodiversity of our planet at snails' pace. Faced with these problems, we should welcome **all** methods, especially those that accelerate the process.

The contribution of the molecular technique to accuracy of identification and reliability of phylogenetic classification, and the often evoked amazement, delight, relief and increase of knowledge following the observation and abundance of life (Klausnitzer) are not exclusive of each other. Far from it! As soon as we succeed in discouraging young people from the description-mania that has been conducted by a few taxonomists over the last two centuries, we will be able to tackle more important tasks, namely evolution, phylogeny, biology, ecology and most notably the protection of species. Only then will

systematics and taxonomy regain the importance that it is not currently afforded by sceptics.

And the question as to what constitutes a species will certainly not be decided at the till of the molecular supermarket. No p-distance will ever resolve where the 'intraspecific' ends and the 'interspecific' begins (thereto [Stüben & Astrin 2012]). DNA-based methods of barcoding have nothing to do with the definition of a 'species' which, as is well-known, is an arbitrary construct of the human mind. Species concepts, of which there are some two dozen [Wägele 2005], shall and must always be discussed. Only the most naive among us would believe that species' delimitations are a concrete and purely natural phenomenon.

Finally, we are calling for participation in this work on integrative taxonomy by the CURCULIO Institute. The laboratory work will be carried out by the 'Centre of molecular Research on Biodiversity' (Zentrum für Molekulare Biodiversitätsforschung) of the ZFMK, Bonn, whilst the role of the CURCULIO-Institute is the acquisition of weevils and their identification. Contributors that have submitted 96 specimens or more will receive a **neighbour-joining tree** of their samples (via email), once these have been analysed. This will provide evidence of genetic distances and phylogenetic relationships between a contributor's species. Those who want to carry out the sequencing themselves may request the **CO1-barcode** of their samples prior to publication in the online database. Furthermore, we intend to provide high quality, image-stacked photographs of specimens and aedeagi to all voluntary contributors who request them. The work will range from initial descriptions of species to revisions of genera! If you want to contribute please send a request to the CURCULIO Institute.

This much can be said in favour of the project: The "**1&1 practice**" (double samples) means that for each ethanol-specimen there is at least one complementary mounted specimen (male) **from the same location and date** and this will enable re-identification in case of noticeable molecular results. This is the most unique feature of this project!

We thank Christoph Bayer (Berlin) and Dr. Keith Bensusan (Gibraltar) for their help in translation.

Literatur

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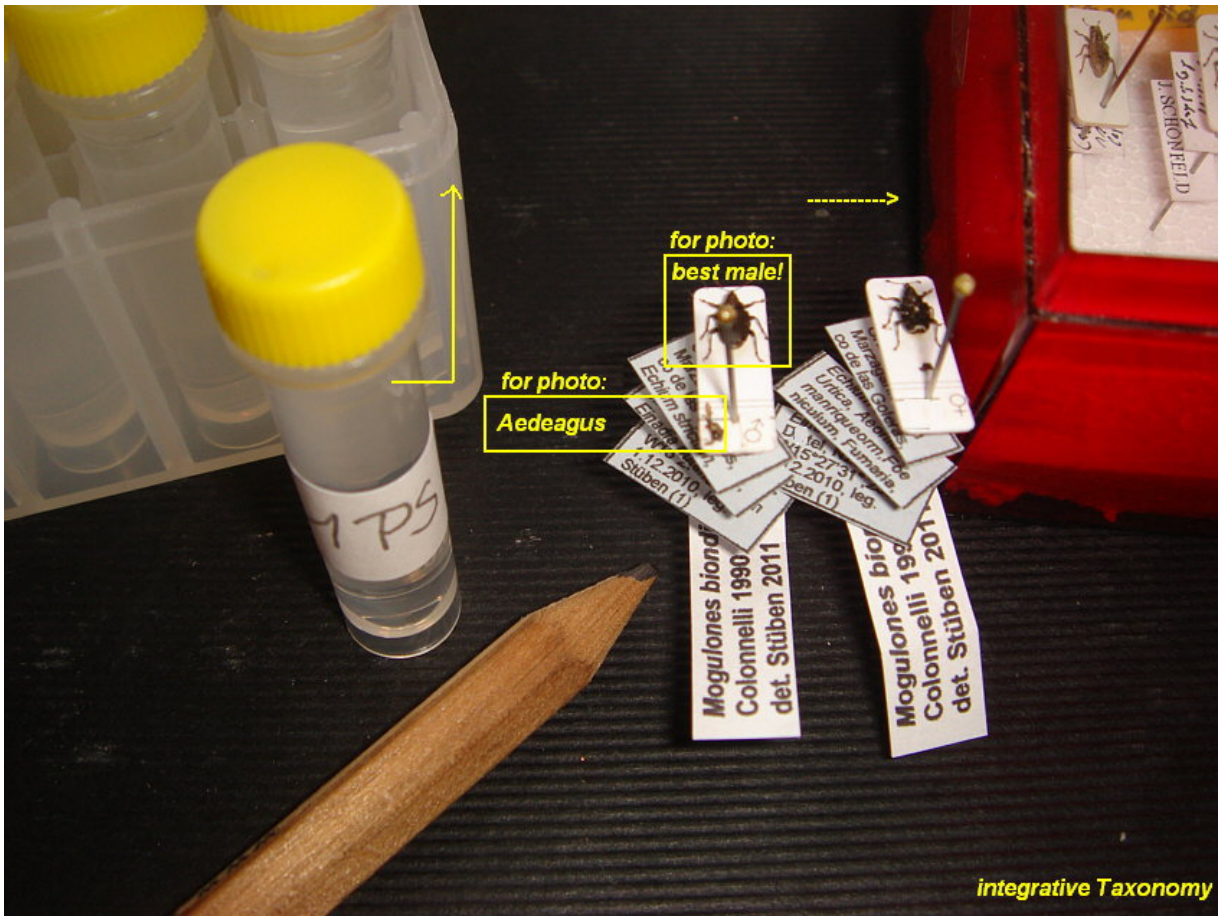
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best male!
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integrative Taxonomy