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and traditional taxonomy represents a very powerful approach for detection and description of cryptic species, as well as addressing synonymy issues. The ability to recover DNA barcodes from very old types is presented, emphasizing its potential for solving some of the most difficult taxonomic problems.

DNA barcodes and monitoring forest health

Jeremy R. deWaard & Leland M. Humble

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The economic, sociological and biological value of Canada's forests makes their sustainability essential to our well-being. To ensure their sustainability, it is critical to regularly and effectively monitor forest health. Genetic approaches, in particular DNA barcoding, have the potential to revolutionize the practice of forest biomonitoring. We describe how barcoding is being utilized in several ongoing projects concerning the Geometridae and other forest Lepidoptera in Western Canada. Firstly, a barcode library for geometrids is near completion and is currently being employed in a pilot project for the detection and surveillance of invasive defoliators. Our reliance on natural history collections for construction of this reference database, as well as the resultant discovery of invasive species and regional records, are described. Secondly, genetic methods are being applied to monitoring the diversity effects of anthropogenic disturbances (e.g. silviculture) and natural modifications (e.g. native pest outbreaks) in Canada's forests. The combined application of DNA barcoding with a North American geometrid phylogeny and a rapidly evolving marker (informative at the population level) is described, allowing the measure of multiple levels of diversity across varying treatments of disturbance. Lastly, an outline of how barcoding is facilitating the generation of regional faunal inventories is given, highlighting how a provincial geometrid checklist is being refined, while a moth inventory for one of North America's largest urban parks is being defined.

On the systematic position and molecular phylogeny of *Lythria* Hübner (Lepidoptera: Geometridae: Sterrhinae)

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The geometrid genus *Lythria*, comprising five Palaearctic species, was for long treated as a member of the subfamily Larentiinae. However, detailed investigation revealed that there are several morphological characters that link *Lythria* with the subfamily Sterrhinae. Therefore, molecular phylogenetic study was conducted on a basis of three nuclear and two mitochondrial gene sequences to find out whether *Lythria* is a larentiine or sterrhine genus. The phylogenetic analysis reliably demonstrated that *Lythria* belongs to the subfamily Sterrhinae. Unfortunately, the intrageneric relationships within *Lythria* appeared to be in conflict with morphological data, as *L. sanguinaria* grouped together with *L. purpuraria*, not with *L. cruentaria*. We therefore performed an additional analysis which included also the fourth European

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species *L. plumularia*, and *L. venustata* which is endemic to Kazakhstan. We revealed that *L. venustata* is the most basal taxon in the genus *Lythria*, and that there are two apical groupings of sister taxa: *L. cruentaria* grouped together with *L. sanguinaria*, and *L. purpuraria* with *L. plumularia*. Conflict between the results of two analyses most probably occurred because of the large amount of homoplasy in the first analysis, which was excluded by the reduction of the dataset in the second analysis.

DNA barcoding and molecular phylogeny of *Eois* moths (Geometridae) from southern Ecuador

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The genus *Eois* (Larentiinae) comprises an important part of a megadiverse assemblage of geometrid moths in the mountain rainforests of southern Ecuador. Owing to the diversity of morphotypes found in this genus, the abundance of many of its component species, and the close relationships with larval food plants in the genus *Piper*, the genus *Eois* has been chosen as a target for a more detailed investigation of local species diversity, species delimitations, and ecological segregation. COI barcode sequences (676 bp) were generated from approximately 350 individuals to establish an inventory of DNA barcodes from one study area (Reserva Biológica San Francisco). This inventory will be used to match larvae to known adult samples and will be of vital help to extend the currently very limited knowledge about food plant relationships and host specialization. Analyses of barcoding sequence divergence show that when a conservative morphology-based approach in species delimitation is used a few cases arise were maximum within-species distances exceed minimum between-species distances. However, there is a varying degree of evidence for the presence of cryptic species in all of these critical cases, as gained from analyses of elongation factor 1-alpha sequences, phylogenetic analysis and morphological reexamination. Up to 33 previously unrecognized species could be identified with the help of COI barcodes and morphological evidence in addition to at least 10 entirely new species, thereby increasing the number of *Eois* morphospecies in that small area of Andean mountain forests from 99 to 142. Notably there are no cases where two or more previously known morphospecies had to be lumped (i.e. there was no cryptic polymorphism). Morphospecies were either confirmed or evidence for cryptic species was found. We acquired elongation factor 1-alpha sequences and extended COI sequences of approximately 100 individuals representing at least 70 *Eois* species amounting to a combined sequence dataset of ~2200 bp. Maximum parsimony and Bayesian inference of phylogeny have been employed to estimate relationships within *Eois*. Phylogenetic trees reveal that all included wing-pattern types except for one evolved only once. The exception to this rule occurs in the most basal clade whose species closely resemble those in a clade higher up in the tree. This may represent an ancestral character state or the result of convergent evolution. Additionally it could be determined that species known to feed on *Piper* are spread over most of the major clades within *Eois*, indicating that the host plant relationship with *Piper* is indeed a trait found all over the neotropical members of the genus and not just certain subclades. Within the Larentiinae *Eois* has traditionally been placed close to the Eupitheciini, but there is presently no support for such a placement in our phylogenetic analyses.

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