FRB
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POUR LA RECHERCHE
SUR LA BIODIVERSITÉ

CESAB
CENTRE FOR THE SYNTHESIS AND ANALYSIS
OF BIODIVERSITY

Project summary

ACTIAS

Global patterns of insect diversity, distribution and evolutionary distinctness. What can we learn from two of the bestdocumented families of moths?

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Start and finish: 2016-2019

Large-scale analyses are key to understanding spatial and temporal dynamics of biodiversity, and – as a corollary – to its conservation. The ACTIAS project aimed at proposing, through synthesis at CESAB, the first insect model for analysing species diversity at global scale.

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Context and objectives

The ACTIAS project stemmed from the observation that large-scale studies carried out to document spatio-temporal patterns of terrestrial biodiversity and to understand its origin and fate are biased toward vertebrates and plants (*e.g.* 1, 2), leaving insects – despite representing the vast majority of multicellular organisms – largely untouched at that scale. Yet, insects are key organisms in ecosystems and we only recently started to measure how severe are the impacts of global changes on their species and populations (3, 4).

Large-scale biodiversity studies have built on the outstanding development in the recent past of infrastructures, methods and tools to manage and analyze very large datasets. "Big Data" analyses stimulated invaluable advances in the field of macroecology, biogeography and evolutionary biology, and have fueled better informed conservation policies in a world that we unfortunately now understand as entering what has been termed its "sixth extinction" period.

Our project aimed at (a) erecting a set of two families of moths – *Saturniidae* and *Sphingidae* – as the first models for large-scale diversity studies in insects, at (b) carrying out the first large-scale investigation of macroecological patterns and of the processes governing them, and ultimately at (c) informing the fate of insect diversity and help design adapted conservation strategies.

(1) Jetz *et al*. 2012. *Nature* **491**: 444-448 (2) Pimm *et al.* 2014. *Science* **344**: 1246752 (3) Fonseca 2009. *Cons. Biol.* **23**: 1507-1515 (4) Hallmann *et al*. 2017. *PloS one* **12**: e0185809

Methods and approaches used for the project

After having identified the challenges and solutions to gather, structure, combine and analyze sets of relevant data, our group focused on building the three main pillars of the ACTIAS database: (a) an assessment of species diversity and of the representativeness of our data; (b) our capacity to combine records from diverse sources using a dedicated workflow handling taxonomical and geographical issues; (c) the integration of life-history traits as key explanatory variables.

We then devised and carried out macroecology analyses at global scale, documenting spatial patterns of species richness and range size, and investigating how these relate to environmental variables, species life-history traits, or evolutionary history.

Principal conclusions

Saturniidae and *Sphingidae* are now being established as new models for the study of biodiversity patterns at global scale. They are the first and unique groups of insects whose species diversity has been comprehensively documented, building on the integration of more than 80K records with DNA barcodes and 200K occurrence records from databases, natural history collections and literature.

One major challenge against assembling a large database from different sources was the validation and reconciliation of taxonomy, as well as completing and validating geographical data. This is critical in groups like insects with a strong taxonomic impediment, and ACTIAS produced a dedicated workflow, applicable to any taxon and that can be parameterized to formally and objectively process records from multiple sources.

Global analysis of species richness revealed patterns following a clear latitudinal gradient in both families, with diversity reaching its maximum in the inter-tropical region. Contrasted patterns exist however within and between the two families and can be related to both evolutionary history and life-history traits (e.g. dispersal capacity).

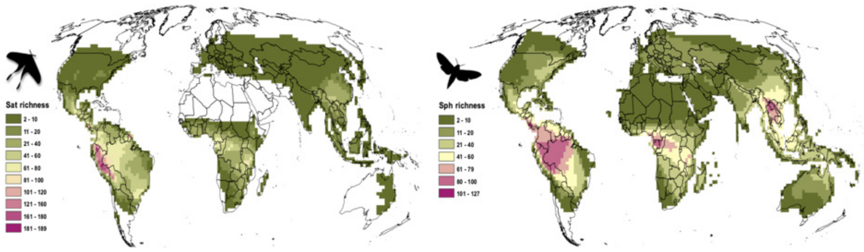

Fig. Distribution of species richness in Saturniidae (left) and Sphingidae (right) derived from overlapping distribution ranges of over 5K species from the ACTIAS database.

Anticipated (or actual) impact of these results for science, society, and public and private decision making

Our group, through synthesis of existing data and synergy between researchers with expertise in various fields of biology, created a database of nearly 300K records covering the diversity of two families of moths. Macroecology analyses will inform areas of the world that concentrate richness of insect species and of species with small ranges, as well as where evolutionary uniqueness and phylogenetic diversity are highest. This will offer the first opportunity to evaluate the fit of current conservation policies and then to devise and implement new and better strategies toward insect conservation.

Through the integration of life-history traits and phylogenetic information, it is expected that the ACTIAS database will also deliver important scientific advances thanks to a better understanding of the processes that have generated and are maintaining the diversity of insect species. These include for instance the development and application of better predictive models that are key to designing sound and sustainable environmental policies (e.g. preserving ecosystem services, mediating diversity losses, anticipating or preventing species invasions or range expansions, etc.).

Furthermore, the workflow developed within ACTIAS is expected to be of much broader use to the community of biodiversity scientists. It can be applied to any group of organism, but we expect that its use will specifically encourage the generation of other global scale insect databases, thus enhancing the generalization of our findings and further improving our understanding of these dominant yet poorly known organisms.

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