

recent burst in activity of specific transposable elements. The genomic data also indicate a deeper divergence than previous estimates based on mitochondrial DNA, and we found no evidence of post-divergence gene-flow between any species pair, despite observations of hybridization in nature. We found that genomic differentiation is heterogeneous between species, with limited evidence of parallelism and significant differentiation associated with chromosome number changes within *L. sinapis*. Both the genome-scan approach and a complementary expression analysis revealed candidate loci for lineage specific adaptations.

[From subtribal classification to cryptic species delimitation: progress in clarifying the systematics of the diverse *Euptychiina* butterflies \(Nymphalidae, Satyrinae\)](#)

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The mostly small, brown butterflies of the satyrine subtribe *Euptychiina* occur throughout temperate and tropical North and South America, in fields, grasslands and savannah, as well as rain forests and cloud forests. Although often common, many species are difficult or impossible to identify, due to wing patterns that may vary substantially within species but minimally between species, morphological homogeneity, a poor understanding of species relationships and generic limits, and, historically, a lack of taxonomic work. The last couple of decades, however, have seen a renaissance in euptychiine research, with work on the higher-level phylogenetics as well as generic revisions, by dozens of collaborators in Europe and the Americas. The Lamas (2004) checklist recognized 400 species (described and undescribed) in 40 genera; currently, we estimate the group to contain 542 species in 72 genera, with 76 species and 7 genera described since 2004. An estimated 137 species and 24 genera are still to be described. Focusing mainly on work done over the last five years at the McGuire Center for Lepidoptera and Biodiversity, one of several institutions currently collaborating in euptychiine research, we summarize some of our ongoing molecular phylogenetic and taxonomic revisionary research.

[Patterns of biodiversity of butterflies and diurnal moths in the monsoon tropics of northern Australia](#)

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Northern Australia is a vast region that includes the Kimberley, the Top End, the Gulf Country and Cape York Peninsula. Collectively, these areas comprise the Australian Monsoon Tropics biome, a distinct geographical region renowned internationally for its large and relatively intact natural landscapes, high biodiversity and strong Indigenous culture. We

compiled a comprehensive inventory of the butterflies and diurnal moths of the western portion of this region to determine the composition, distribution, relative abundance, breeding status and conservation status of the fauna. The overall goal was to assess how well the fauna is represented in the conservation reserve system and to identify ‘hotspot’ areas. Such information is vital for conservation management and provides a baseline against which the extent and direction of change can be assessed in future. Our dataset comprising approximately 23,500 records based on field observations (61%), museum specimens (28%) and literature (11%) represents 4,352 sites and spans more than 110 years of recording effort. These data indicate that 166 taxa representing 163 species (132 butterflies and 31 diurnal moths) have been recorded from the study region. Broad patterns of species richness, endemism, key threatening processes and priority areas for conservation across the study region will be discussed.

[Host repertoire evolution and diversification of butterflies](#)

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The diversification of herbivorous insects is often explained by the parasitic use of host plants, as plants represent a great diversity of resources. In their classical paper, Ehrlich and Raven assumed that a trait that allows an individual organism to explore a novel niche also promotes diversification, as the new niche would equate to a new adaptive zone, relatively free of competition. However, the mechanism connecting the increase in individual fitness to an increase in cladogenesis was not specified. Even though this gap in how micro- and macroevolution are connected resulted in a range of proposed mechanisms, little consensus has been achieved. One of the main standing questions is the relative frequency of host colonisations with and without changes in host specificity (host range expansion vs. host shifting), and their importance for diversification. To tackle this problem, we combined various methods to study the origins of macroevolutionary patterns of host use and parasite diversity. From the mechanisms that allow a parasite to expand its host range (coupled with expansion of overall niche breadth), to the effects that evolution of host-parasite interactions has on diversification. For example, we are developing a Bayesian inference method to reconstruct the host repertoire of parasite lineages (that can be applied to other ecological interactions). We also suggest a new approach that combines network and phylogenetic analyses to assess how insect-plant interactions changed through evolutionary time, and how that relates to host-associated diversification. Based on changes in network structure through time, we propose the integration of alternative explanations to the evolution of insect-plant interactions into a single process. With the recent recognition that host-parasite and herbivorous insect-plant systems have much in common, this unified explanation likely

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