Integrative taxonomy of araneomorph spiders: Breathing new life into an old science

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Chapter 6

Epilogue

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General discussion

The present thesis highlights the relevance and usefulness of taxonomic literature (old and new) and exemplifies the benefits of adopting an integral approach to the description of new taxa. As mentioned in **Chapter 1**, taxonomy as a science has accumulated data and knowledge for more than 250 years. The quality and usefulness of the facts recorded in taxonomic literature have greatly improved from the early (purely) descriptive texts to the modern works that are rich in detailed and integrated data. These developments have improved the rigor of phylogenetic inference, documented distribution patterns of taxa through time and space, and revealed broad evolutionary patterns and other interesting phenomena. My work illustrates some applications of legacy data contained in literature (**Chapters 2** and **3**), and also explores an integrative perspective that involves new taxonomic descriptions and generation of phylogenetic hypotheses integrating molecular and morphological data (**Chapters 4** and **5**).

Taxonomy has provided a system under which groups of natural entities can be catalogued and biological data can be aggregated by the use of a taxonomic name (e.g. genus or species). Nevertheless, slow pace of identification, description, and categorization, plus the huge number of unknown species and human impact on natural habitats and biodiversity have made traditional taxonomy obsolete and partially unreliable. As a response to this, several authors have made patent the urgent need for taxonomy to accelerate its description and knowledge accumulation process by the change of some practices and use of new technologies [1–9]. One of the main drivers of this change involves the access to primary taxonomic literature and specimen information [1, 6]. My thesis heavily relies on the utilization of some of these "e-taxonomic" products, like the BHL [10], WSC [11], Plazi [12], and GBIF [13]; and also helps to test and collaborates on the improvement of the program Golden Gate Imagine, the software used for data mining in **Chapter 2**. Electronic access to literature is one of the primary tools in my dissertation, being fundamental for acquiring primary taxonomic data used in **Chapter 2** to analyze the distribution of the *Teutamus* group; observing the patterns and formulating an evolutionary hypotheses for the origin of genital asymmetry in spiders (**Chapter 3**); and gathering taxonomic information that helped us identify and eventually describe new species and test the phylogenies of the the spider families Hahniidae (**Chapter 4**) and the Symphytognathidae **(Chapter 5**).

The approach used in my thesis for mining and gathering specimen data from taxonomic literature —used in **Chapter 2**— proved to be a powerful tool for analyzing species distributions. Here, I applied this knowledge to plan our fieldwork targeting adult specimens of one particular group of ground dwelling spiders; however, there are many other possible uses that remain to be explored in the future. Some examples of these applications include species estimations, catalog building and taxonomic inconsistencies identification, inclusion of underrepresented taxa in global datasets, species distribution patterns detection, among other applications. This potent tool has been gaining traction among taxonomic journals and publishers (like Pensoft, Zootaxa, Zookeys, among others) in its prospective approach [14, 15]; and is also being used in projects similar to the one presented here that have extracted data and analyzed the legacy taxonomic literature of groups as diverse as on damselflies [16] and *Tyrannosaurus rex* [17, 18].

Besides the aforementioned specimen data, taxonomic literature has also linked other types of information like illustrations, photographs, and molecular data to taxonomic names. In this way, I think of taxonomic literature as a massive (yet largely unstructured) data repository. This repository has accumulated biological data in the form of text called treatments [19–21]. The quality and usefulness of some of these data greatly varies depending on the time, author and even taxonomic group, and has —without any doubt — improved with utilization of modern techniques and technologies [22]. Spider taxonomy — probably one of the best curated bodies of taxonomic literature (see Chapter 1) — has accumulated and made available thousands of taxonomic documents that represent a huge collection of species, facts, and images. Similar to other arthropod groups, spider species delimitation greatly relies on the comparative morphology of the genital characters; therefore, it does not come as a surprise that sexual characters are some of the best studied and understood, having detailed images and descriptions that might allow for the detection of interesting phenomena and broad evolutionary patterns. One example of this is the evolution of asymmetry in spider genitalia [23, 24]. For **Chapter 3**, I conducted a casual but taxonomically broad study of the evolution of this character in spiders, assigning the identified cases to traditional categories of asymmetry [23–26] and suggested the evolutionary patterns and causes behind the development of this morphological character. Moreover, I attempted to test some of these hypotheses by examining the behavioral implications of the evolution of genital asymmetry in the species *Teutamus politus*; although I collected a fair number of live specimens during our fieldwork in an attempt to observe courtship and mating, the behavioral experiments were unsuccessful. Nevertheless, ours was the most comprehensive study of asymmetry in spiders encountering dozens of species in several families that show some kind of asymmetry and had been overlooked in the scarce previous reviews on the topic.

The sampling methods I used during our fieldwork — although intended for the collection of *Teutamus* group spiders — also captured much more material. Some of these specimens were used in this thesis for **Chapters 3**, **4** and **5**; but considerably more material remains to be studied. Our sampling collected thousands of specimens from several arthropod groups including insects, millipedes, mites, Opiliones, among many others. Together with my supervisor Jeremy Miller and our collaborator Booppa Petcharad, I collected more than 4,600 spider specimens of which 1,454 were adults representing 35 spider families. Only the families Liocranidae, Hahniidae and Symphytognathidae (the latter two both new records for Thailand) were identified to species level. Still, from this relatively small selection of taxa, I described a total of five new species following the integrative approach I mentioned in the introduction and including morphological and molecular data. All of the specimens collected for the present project are now deposited in the collection of Naturalis Biodiversity Center, where they can be archived and eventually contribute to other taxonomic, systematic, ecological and evolutionary studies.

In this context, **Chapters 4** and **5** focused on the generation of new taxonomic content using the integrative approach [27–33]. In these two chapters I described five new species and made the first reports of two families for Thailand. Both families — as in the aforementioned *Teutamus* group — are ground dwelling, mostly inhabiting leaf litter. They are relatively small to tiny, ranging from less than 1 cm down to less than 0.5 mm! In fact, one of the newly described species, *Anapistula choojaiae* n. sp., could be considered among the smallest spiders ever discovered together with a couple other species in the genus *Patu* [34, 35]. Both chapters are examples of the integration of new taxonomic descriptions with high resolution photographs, molecular data and character evolution, similar to what has been done previously in other spider studies [27, 29, 31, 33]. In the case of the Hahniidae (**Chapter 4**) by reviewing what is known about the eye size reduction and eventual eye loss within this family; and for the Symphytognathidae (**Chapter 5**) by using 3D modeling to accurately document and compare the genital morphology allowing us to better circumscribe the genus *Crassignatha*, and transferring there some species previously misplaced in the genus *Patu.*

I consider that this thesis demonstrates the use of many of the new taxonomic *e-tools* like specimen information databases (e.g. GBIF) and literature repositories, and data mining and management resources (e.g. BHL, WSC, PLAZI). In this way, the present work illustrates the re-use and re-analysis of specimen data and morphological images contained in literature, and also features the use of an integrative taxonomic approach for new descriptions that allow for species documentation, as well as the inference of evolutionary hypotheses. I feel that the common use of these tools will, without any doubt, help overcome the taxonomic impediment while collaborating on the effort of describing and understanding our (greatly endangered) biodiversity.

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