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Prospective

Filling the Gaps on Trophic Interactions between Lepidoptera and Hymenoptera using Information Retrieved from Interlinked and Integrated Taxonomic Datasets

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BACKGROUND

The fragmented natural biotopes and the modern agro-ecosystems can be perceived as a simplification of natural ecosystems where a few plant species predominate [1-4]. It was historically assumed that the food chain: host plant – lepidopteran species– hymenopteran species can describe the trophic relationships. In reality a multiple complex of food web interactions is involved. However, predicting analysing and identifying these ecological multi-trophic interactions using classical methods such as dissection is time-consuming and inefficient. The automatized surveys in tropical biotopes of pest control areas yielded an enormous amount of insects which need to be processed. Molecular tools implemented for species recognition and to analyse lepidopteran DNA as pests of plants as well as the DNA of parasitoids within their hosts assisted a lot in the fast automatized processing of data and helped to understand the multi-trophic interactions [5]. However, incompleteness of DNA reference libraries, the complexity of pest species agglomerates feeding on the same host plants, technical and clerical inconsistencies cause serious impediments in understanding multi-trophic interactions and evaluating the biological control methods. In this prospective paper I am presenting a summarized review of the scientific literature published between 1758 and 2016 on the model leaf mining group Gracillariidae (Lepidoptera) and interrelated Hymenoptera species for using literature data as a predictive approach and filling the gaps in missing data on trophic interactions [6]. A total of 633 articles were found and the amount of published papers steadily increases the volume of the literature, especially in recent years. 1988 gracillariid species (73.24%) have at least one host plant record while only 356 gracillariid species (13.12%) have parasitoid records. Based on the analysis of those publications I propose future avenues in which automatized molecular tools, in correlation with accumulating new data by empiric field surveys, can contribute to understand the complexity of trophic interactions and suggest that the text mining approach related to host plants, Lepidoptera and Hymenoptera species could help design the models of trophic systems.

LITERATURE TEXT-MINING

Text mining has been actively studied in the biological domain [7,8]. Among the various text-mining applications are online and offline systems, which aim to extract species as facts reported in the biology literature. Hymenoptera trophic information has been tackled as one of the targets for integrated datasets. Beside the Chalcidoidea database [9], which gives unstructured information on the hosts of Hymenoptera species there have been only a few other efforts to summarize the extracted information on trophic relationships of Hymenoptera.

The Global Gracillariidae dataset, containing data on 4,200 records on hymenopteran parasitoids, developed a rule-based system to structure multi-level data and to extract it in a simplified way. It then applies to hand-coded patterns and reveals the target relationships, e. g. the lepidopteron –hymenopteran relationship. The system has been also applied for tri-model groups of organisms: plants, lepidopterans and hymenopterans and it uses the semantic approach on observation and rearing, published in literature. The link to the molecular dataset at BOLD is in development (http://www.boldsystems.org/). The main difference of the Global Gracillariidae database from other databases is the use of a name-related recognition method based on searchable taxonomic, subject and geographical keywords. It focuses on the curation of model groups, including Hymenoptera. The tool applies a filter to identify and report the potentially relevant interactions. This filtering process was evaluated by many years of online use with regular subsequent updates. The precision of information is high.

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CRITERIA OF VERIFICATION

The proposed patterns for trophic relationships between specific model groups of gracillariid lepidopteran – parasitoid hymenopteran species can be widely used for the concept of reusing similar patterns to resolve similar problems. I attribute four verification criteria of text-mined data 1) Functionality; 2) Completeness; 3) Consistency, and 4) Reliability (Figure 1). Without these four criteria mentioned above, the process of identification of species becomes worthless and loses its utility. Speculative species delineations should be discouraged since in this way the conceptual understanding of lepidopteran/hymenoptera species enters more a fiction field rather than answering to a precise qualitative/quantitative query.

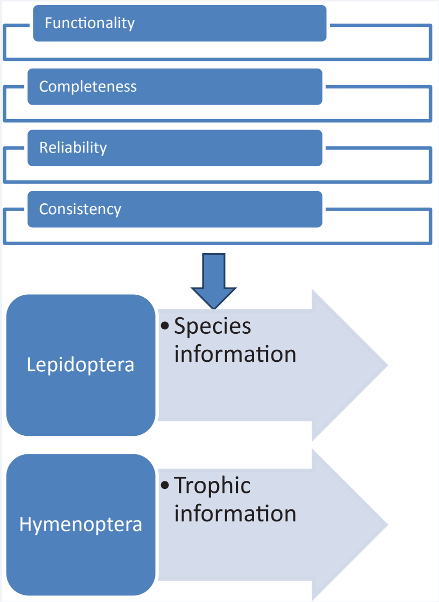

Figure 1 Criteria of verification in the web of species trophic interactions.

FUTURE CHALLENGES

The present knowledge on lepidopteran-hymenopteran trophic relationship is still in the initial stadium of investigation. The method to fill the gaps using text-mining approaches and based on empirical and experimental observation seems to be plausible. Based on the case study, the interlinked information stored in the Global Gracillariidae database, the future challenges are to evaluate the text-mined information, implement the feedback and suggestions from users and experts and to improve and continuously complete the contentsof information.

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