



Milestones and Future Directions in the Taxonomy of Phytoseiid Mites (Acari: Mesostigmata) in Taiwan

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ABSTRACT

Phytoseiid mites (Acari: Mesostigmata), the predators of phytophagous insects and mites, are a diverse group of biological control agents. However, their correct identification is essential for establishing successful pest management strategies. Integrating molecular data with morphological analysis can help identify and classify species and explore their evolution. Ongoing research has made major contributions to the taxonomy, conservation, and sustainable management of phytoseiids in Taiwan, enriching our understanding of their diversity and ecological roles. To date, 69 species have been recorded from Taiwan and associated islands; however, knowledge gaps remain, including the existence of unexplored regions, the presence of intraspecific variations, and the introduction of exotic predators. Future studies on these mites should focus on exploring new regions, incorporating molecular, assessments, evaluating ecological roles, and developing improved classification tools. These efforts will enhance the potential use of phytoseiids in pest management and advanced biological control strategies.

Key words: predatory mites, Taiwan, fauna, biological control

Introduction

Phytoseiid mites (Acari: Phytoseiidae) play vital roles in pest control as natural enemies of phytophagous mites and small arthropods in various agricultural and ecological systems (Huffaker *et al.*, 1970; McMurtry *et al.*, 1970, 2013, 2015). With more than 2,700 species

recorded worldwide, the taxonomy of phytoseiids has received considerable attention (Chant and McMurtry, 2007; Demite *et al.*, 2023) because taxonomic evaluation not only facilitates their correct identification but also clarifies their diversity, ecological roles, evolutionary relationships, and geographic distributions. However, many domains of specific knowledge

about phytoseiids in Taiwan remain unexplored (Liao *et al.*, 2020b). By elucidating the taxonomy and distribution patterns of phytoseiids in Taiwan, researchers can contribute to developing effective pest management strategies and gain insight into the ecological dynamics of mite populations. In this study, we investigated the status of the taxonomy of phytoseiids in Taiwan. Our findings guide future research studies on the potential applications of these mites in pest management alongside the use of conservative biological control.

Status of phytoseiid mite taxonomy in Taiwan

Research on plant-inhabiting mites in Taiwan and affiliated islands began in the 1930s, initially focusing on the non-economically important spider mites (Kishida, 1935; Anonymous, 1937; Shiraki, 1937; Takahashi, 1938; Ho, 2000). However, after the emergence of pesticide-resistant spider mites in the 1950s, various biological control strategies, specifically those involving the use of phytoseiids, were investigated. Ehara (1970) and Lo (1970) were among the first to study phytoseiids in Taiwan. Subsequently, Yi-Hsiung Tseng conducted comprehensive surveys in the 1970s and 1980s, identifying numerous species and discovering 20 new species (Tseng, 1972, 1973, 1975, 1976, 1983; Chang and Tseng, 1978). Ho and Lo (1989) reported five *Paraphytoseius* species from Taiwan, and Ho *et al.* (2003) recorded eight species on Matsu Islands. Tseng studied phytoseiids and other taxonomic groups, including Cheyletidae, mushroom mites, Tetranychidae, and Oribatida (BAPHIQ, 2009). However, the collections and type specimens deposited by Tseng at the Tainan Branch of the Bureau of Commodity Inspection and Quarantine have been lost. Efforts to locate these specimens have been unsuccessful, except for one specimen deposited in H. A. Denmark's collection (in Florida) (BAPHIQ, 2009; Liao *et al.*, 2017b; Liao *et al.*, 2020b).

Since 2009, our group has conducted extensive studies on phytoseiids in Taiwan. Liao *et al.* (2013) provided a checklist of 53 species of Taiwanese phytoseiids. Later, we reported the Taiwanese *Euseius* species (Liao *et al.*, 2017a), a

new *Typhlodromus* species in the coastal area of Lanyu Island (Liao *et al.*, 2017c), and provided information on the genera *Euseius* and *Gynaeseius* (Liao *et al.*, 2018). In their review of the subgenus *Anthoseius*, they redescribed six species that were previously described by Tseng as well as three newly recorded species (Liao *et al.*, 2019). Liao *et al.* (2020b) published a book on phytoseiid fauna, raising the number of species to 64. Subsequently, Liao *et al.* (2021a) reported phytoseiid fauna in the Penghu Islands, documenting two new species and three newly recorded species, bringing the total number of recorded phytoseiid species in Taiwan to 69.

In addition to domestic species, exotic phytoseiids in Taiwan need further confirmation for previous releases in the 1980s. Lo *et al.* (1986) introduced and released three phytoseiid mite species, namely *Phytoseiulus persimilis* Athias-Henriot, *Neoseiulus californicus* (McGregor), and *Neoseiulus fallacis* (Garman), were introduced and released in various agricultural areas, including alpine orchards, strawberry fields, pear orchards, protected papaya plants, and tea plantations for classical biological control of spider mites (Lo *et al.*, 1986; Lee and Lo, 1989; Lo *et al.*, 1990; Hao *et al.*, 1996; Ho, 1990). After its release, the predator *N. fallacis* was initially observed in large numbers in the release fields, suggesting its successful establishment. However, it was absent in subsequent long-term investigations (Liao *et al.*, 2020b), suggesting a failure in its establishment. As to *P. persimilis*, there is a lack of follow-up information about its fate (Lo *et al.*, 1986; Liao *et al.*, 2020b). Based on an ecological niche modeling study, Liao *et al.* (2021b) speculated that the apparent failure in the establishment was due to unsuitable climatic conditions. Further studies should elucidate the status and effects of the introduced predators in Taiwan (Liao *et al.*, 2021b). Together, these findings underscore the complexity and challenges associated with introducing exotic predatory mites for biological control purposes. The success or failure of population establishment can be influenced by various factors, such as climatic suitability and ecological interactions. Evaluation of ongoing monitoring efforts and further research is necessary to assess the results of these introductions and their potential

benefits within integrated pest management strategies. In summary, research on the taxonomy of phytoseiids in Taiwan has a rich history and has significantly expanded our understanding of their diversity and relationships with environmental factors. The recorded species and their distribution patterns may guide future taxonomic and ecological studies as well as facilitate the applications of plant-inhabiting mites in pest management and ecological conservation.

Species diversity and occurrence patterns

Phytoseiid mites have attracted considerable attention as biological control agents against phytophagous mites and other arthropods (Huffaker *et al.*, 1970; McMurtry and Croft, 1997; McMurtry *et al.*, 1970, 2013, 2015). More than 2,700 species and 90 genera have been recorded worldwide (Demite *et al.*, 2023). In Taiwan, phytoseiid species have been collected mainly in urban and suburban regions with high levels of agricultural activity, but some have also been from forest and mountainous regions (Ehara, 1970; Lo, 1970; Tseng, 1972, 1973, 1975, 1976, 1983; Chang and Tseng, 1978; Liao *et al.*, 2017a, 2017c, 2018, 2019, 2020b, 2021a). The distribution patterns and diversity of phytoseiids in Taiwan are closely associated with their preferred host plants and habitats. For example, some species, such as *Neoseiulus baraki* (Athias-Henriot) and *N. taiwanicus* (Ehara), have strong associations with monocotyledonous plants and are often found in the leaf sheaths of rice plants (Muma and Denmark, 1967; McMurtry *et al.*, 2013). Other phytoseiids occupy specific plant structures, such as domatia and trichomes. The presence of phytoseiids in various plant habitats contributes to their species diversity in Taiwan. Altitude is an important factor influencing their distribution. Certain species, such as *Scapulaseius tienhsianensis* (Tseng), exhibit preferences for specific altitudes, with observations made over 2,000 m in mountainous regions (Tseng, 1983). Geographic locations and associated environmental conditions influence phytoseiid distribution (Ho *et al.*, 1995). For instance, *Amblyseius largoensis* (Muma) is found

only in southern Taiwan (Liao *et al.*, 2020a), whereas *Neoseiulus longispinosus* (Evans) is found primarily in southern Taiwan (Ho *et al.*, 1995). Temperature is another key factor influencing phytoseiid distribution, with the most suitable temperatures range being 10 to 30°C. Taiwan has a subtropical and tropical climate, which is favorable for the proliferation of phytoseiids, and extreme weather events can affect mite density. Notably, a cold snap from the winter of 2010 to the spring of 2011 reduced the density of phytoseiid mites (Liao *et al.*, 2020b), making it challenging to collect even common species, such as *Amblyseius herbicolus* (Chant) and *Euseius ovalis* (Evans). Together, these findings improve our understanding of the diversity of phytoseiids in Taiwan and highlight the need for further research and exploration to uncover their ecological roles and potential applications in pest management and ecological conservation.

Challenges and future directions

Unexplored regions and ecosystems in Taiwan

Phytoseiid mites inhabit diverse plants, such as crops, weeds, and bushes, extensively utilizing foliage habitats (Chant, 1985; McMurtry and Croft, 1997; Chant and McMurtry, 2007; Wu *et al.*, 2009). They can be found in various plant parts, including flowers and leaf domatia (Walter and Proctor, 2013). Some species are soil-dwelling, occupying habitats ranging from the tundra to tropical rainforests (Chant, 1985, 2007; Chant and McMurtry, 2007). Although aquatic mesostigmatids and mites living in rocky shores or wetland habitats have been reported, no swimming phytoseiids have been discovered (Krantz, 1974; Walter and Proctor, 2013; Stathakis *et al.*, 2016; Liao *et al.*, 2017c). Phytoseiids have also been observed in unique environments, such as pitcher plants (Muma and Denmark, 1967). However, not all regions and ecosystems in Taiwan have been explored, offering opportunities for future studies on these mites.

With its diverse and ecologically rich landscapes, Taiwan has unique habitats that have not been thoroughly investigated; these

include specific mountain ranges, islands, coastal regions, forests, and agricultural landscapes beyond the commonly studied regions. For example, forest regions on the main island and various offshore islands, apart from Penghu Islands, Orchid Islands, and Matsu Islands, remain understudied (Liao *et al.*, 2020b). Exploring these unexplored regions in Taiwan for several reasons. First, targeted surveys and sampling in these habitats can lead to discovering new phytoseiid mite species, contributing to our overall understanding of their diversity. Additionally, these unexplored regions may harbor unique habitats and ecological characteristics, offering valuable insights into the ecology and distribution of phytoseiids in Taiwan. By bridging the knowledge gaps through exploring these habitats, researchers can clarify the diversity of phytoseiids and contribute to broader ecological research. In summary, exploring the unexplored regions in Taiwan presents an exciting opportunity to study phytoseiid diversity. Thus, researchers can discover new species, uncover unique ecological interactions, and facilitate the conservation and management of these valuable ecosystems while also evaluating the potential of these mites in biological pest control in agricultural fields.

Tseng's specimen mystery

Yi-Hsiung Tseng made significant contributions to the taxonomy of mite fauna and established a foundation for mite research in Taiwan. He described 47 phytoseiid species. However, the absence of Tseng's collection and type specimens poses hindrances to the validation of the identity of species described by Tseng. Liao *et al.* (2020b) surveyed Taiwan and affiliated islands to collect the species described by Tseng. However, because of the typographical errors or ambiguous English translations of localities and the changes in landscape over the years, some species could not be found; these species included *Amblyseius trisetosus* Tseng, *Proprioseiopsis pubes* (Tseng), *Neoseiulus monomacrosetus* (Tseng), *Neoseiulus spineus* (Tseng), *Okiseius formosanus* Tseng, *Scapulaseius vestificus* (Tseng), *Phytoseius rugatus* Tseng, and *Typhlodromus (Anthoseius) eleglidus* Tseng. Liao *et al.* (2020b) redescribed these species

based on their original descriptions. Given Tseng's limited and vague descriptions and the loss of his specimens, a new type designation for all species he described may be necessary to clarify their species status. However, the designation of a new type should be made per Article 75.3.4 of the International Code of Zoological Nomenclature (International Commission on Zoological Nomenclature, 1999) and not simply as a routine curation procedure. Efforts such as collaboration among researchers and institutions should be made to rediscover Tseng's lost specimens and provide additional descriptions and illustrations.

Application of molecular data in the identification of species and evolutionary relationships

Because of the small size and limited morphological characteristics of mites, the integration of molecular data is crucial for taxonomic and evolutionary studies (Navajas *et al.*, 1999; Navajas and Fenton, 2000; Cruickshank, 2002; Vicente dos Santos and Tixier, 2017). Molecular methods clarify more characteristics and objectivity to classify species and resolve evolutionary relationships. Molecular studies in Phytoseiidae have mainly focused on the identification of species by using markers, such as 12S rDNA, CytB mtDNA, COI mtDNA, and ITSS (Navajas *et al.*, 1999; Li *et al.*, 2011; Vicente dos Santos and Tixier, 2017). Very few studies have explored the higher-level relationships (e.g., genus) (Kanouh *et al.*, 2010; Tsolakis *et al.*, 2012). Moreover, preserving voucher specimens after DNA extraction to confirm morphological characteristics remains challenging. The problems of misidentification and unstable distinguishing characteristics may be resolved using a molecular approach. For example, the *A. largoensis* species group requires further investigation (Liao *et al.*, 2020b). Additional research is also warranted to distinguish closely related species, such as *Neoseiulus womersleyi* (Schicha) and *N. longispinosus* (Ho *et al.*, 1995; Liao *et al.*, 2020b; Negm *et al.*, 2021). In summary, integrating molecular and morphological assessment is crucial for mite taxonomy and evolutionary studies. Given the small size and limited characteristics of the Phytoseiidae family,

molecular markers, such as COI, appear promising tools for identifying taxonomic and phylogenetic relationships (Vicente dos Santos *et al.*, 2017).

Development of improved taxonomic and identification tools

The development of artificial intelligence-based identification tools can revolutionize the field of mite taxonomy and identification. The conventional methods rely on microscopic images and human expertise, which can be time-consuming, particularly considering the small size and complex morphological features of mites (Tixier, 2012; Liao *et al.*, 2020a). By training the algorithm on a large data set of morphological features of specimens from different countries, Liao *et al.* (2020a) achieved impressive classification accuracy and identified intraspecific variations, thus developing a semi-automated identification of the system for phytoseiids. Their innovative approach simplified the identification process and reduced reliance on human expertise. However, although dorsal setae are crucial for identifying phytoseiid mites (Tixier, 2012), other morphological features should also be considered, particularly when dealing with different groups of mites. The accuracy and reliability of AI-based identification tools for mite identification should be improved by overcoming challenges related to slide preparation, measurement errors, and the effect of mounting media on determined lengths. Developing fully automated identification systems will advance taxonomic and ecological studies, pest management, and conservation efforts.

Implications for pest management and ecological conservation

Since 1970, many studies worldwide have explored the roles of phytoseiids as biological control agents, making them one of the most important mite groups researched globally (Huffaker *et al.*, 1970; McMurtry *et al.*, 1970, 2013, 2015). Taiwan has made considerable achievements in the taxonomy of phytoseiids; several introduced and local mite species with biological control potential have been identified in various agricultural systems (Liao *et al.*, 2020b). Notable species include *N. californicus*,

N. fallacis, *P. persimilis*, *N. longispinosus*, *N. womersleyi*, *Neoseiulus barkeri* Hughes, and *Proprioseiopsis asetus* (Chant). Both laboratory and field studies exhibit substantial effectiveness in controlling various pests, including thrips, phytophagous mites such as *Tetranychus urticae* Koch and *Polyphagotarsonemus latus* (Banks), aphids, and whiteflies. Specifically, *N. barkeri* can effectively control thrips, and *Prop. asetus* exhibits potential agents against phytophagous mites (Ho and Chen, 2001).

Incorporating phytoseiids into integrated pest management programs as alternatives to chemical pesticides promotes safe and sustainable agricultural practices, manages pest populations, and ultimately improves crop health and yields. Reserving natural habitats is essential for conserving native phytoseiid species in Taiwan and other countries. Protecting the diversity and ecological roles of native phytoseiids supports sustainable agriculture and contributes to broader ecological conservation efforts. Taiwan has major potential for phytoseiid mite research in terms of exploring new habitats, studying mites' interactions with host plants and other organisms, and applying innovative techniques. International collaboration, data sharing, and interdisciplinary approaches are vital in advancing phytoseiid mite research and promoting sustainable pest management practices.

Conclusion

Many studies have focused on the taxonomy of phytoseiid mites in Taiwan, considerably expanding our knowledge in this field. Researchers, particularly Y. H. Tseng, have made notable contributions by identifying and documenting numerous mite species, providing valuable insights into their diversity and distribution patterns, and offering comprehensive species lists, redescriptions, and taxonomic revisions. However, further research and exploration of phytoseiid mite taxonomy are warranted. Unexplored regions, including remote areas and diverse ecosystems, offer opportunities for new discoveries. In-depth phylogenetic and genetic studies can improve

our understanding of the evolutionary relationships among species and populations. Investigating the ecological roles and adaptive strategies of phytoseiids in various habitats and their interactions with host plants, prey, and other natural enemies, is crucial for developing and implementing effective strategies for pest management and ecological conservation. This includes developing improved taxonomic and identification tools, such as advanced molecular techniques and data integration tools. In conclusion, although significant progress has been made in research on the taxonomy of phytoseiids in Taiwan, in addition to ongoing research, collaboration among researchers and exploring uncharted territories are warranted to deepen our understanding of their diversity, ecological roles, and potential applications in pest management. Such efforts will facilitate the sustainable development of agriculture and the preservation of biodiversity in Taiwan and other countries.

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臺灣植綫蟎（蟎蜱亞綱：中氣門目）分類學的里程碑與未來方向

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摘 要

植綫蟎（蟎蜱亞綱：中氣門目）是著名的植食性昆蟲和蟎類的捕食者，具有很高多樣性的生物防治天敵。然而，在將其用作生物防治措施之前，正確鑑定這些捕食者對於成功管理至關重要。此外由於形態鑑定存在困難，將分子數據整合到物種分類和進化研究中變得必要。在臺灣，對於植綫蟎的分類學研究豐富了我們對其多樣性和生態角色的認識。迄今已在臺灣及相關島嶼記錄了 69 個物種，但仍存在知識缺口，包括未被探索的地區、遺失標本問題、種內變異議題和外來捕食者的立足確認。未來的研究應該聚焦於探索新區域，整合分子研究，深入了解其生態角色，並發展改進的分類工具。這些努力將提升植綫蟎在害蟲管理中的潛力，並推動生物防治策略的發展。

關鍵詞：捕食性蟎類、臺灣、動物群、生物防治