

Broad mites: tiny terrors in protected structures - A scoping review of its identification, abundance, and management strategies

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ABSTRACT

Broad mites are serious pests of capsicum cultivated under protected structures in Fiji. Being a cosmopolitan and polyphagous pest, studies have been done in other countries. Still, no data is available on identifying the local broad mite species and its relationship to environmental factors under protected structures. Consequently, appropriate management is limited in the country. This paper aims to provide a comprehensive summary of existing knowledge on broad mite identification, abundance, and holistic management, describe the methodologies used in previous broad mite studies, and identify research gaps and limitations to serve as a basis for broad mite research and management in Fiji. The study used the checklist provided by the PRISMA extension for scoping reviews (PRISMA-ScR). The data set included 52 peer-reviewed Web of Science and ProQuest articles published between 2000-2024. The review showed that although broad mite studies have been done in other parts of the world, there is no current literature on the species of broad mite in Fiji, its abundance, and management under protected structures, which are identified as research gaps that need further studies for successful management of broad mites in Fiji.

KEYWORDS: *Broad mites, capsicum, Fiji, protected structures, identification, management*

INTRODUCTION

Broad mites are important pests in crops cultivated under protected structures globally (Grinberg et al., 2005; Luypaert et al., 2015; Luypaert et al., 2014; Weintraub et al., 2003; Z.-Q. Zhang, 2003) including in Fiji (Jovicich et al., 2016). The introduction of protected structures in Fiji was aimed at enhancing year-round production of high-value crops like capsicum (*Capsicum annuum* L.) by optimizing environmental conditions, has also led to an increase in pest infestations, particularly broad mites, which severely impact crop yield and quality (Australian Centre for International Agricultural Research, 2021; Reddy, 2016). Broad mites have greatly affected capsicum production under these structures, leading to reduced yields (Jovicich et al., 2016).

Broad mites thrive under these high humidity and temperature conditions (Mani, 2022). Their small size, rapid reproduction, and quick resistance to pesticides make them a significant threat to capsicum cultivation, causing severe damage such as leaf distortion, stunted growth, and fruit deformities (Cloyd, 2010; Peña & Bullock, 1994). While broad mites are well-studied pests in other regions, there is limited information about Fiji's agricultural context. This scoping review aims to 1) summarize existing knowledge on broad mite identification, abundance, and management and (2) identify research gaps and limitations to guide future research on broad mite management in capsicum cultivated under protected structures in Fiji.

This scoping review used peer-reviewed and early-access journal articles, conference proceedings, theses,

and book chapters published from 2000 to 2024. These articles focused on broad mite identification,

abundance studies, and management practices. A systematic search was conducted using Web of Science and ProQuest. PRISMA-ScR guidelines were used for data extraction.

This review synthesized current knowledge and provide critical insights for researchers, agricultural stakeholders, and policymakers to improve capsicum production in Fiji through sustainable and effective pest management strategies tailored to local conditions.

METHODOLOGY

This review followed the scoping review framework outlined by Arksey & O'Malley (2005) and Mak & Thomas (2022) and is reported according to PRISMA-ScR (PRISMA scoping review) reporting guidelines and checklist (Haddaway et al., 2022; Page et al., 2021). We identified and designed the research questions, discussed relevant studies using inclusion and exclusion criteria before commencing, selected the studies to be included, charted the data, collated, summarized, and reported the results.

Identifying the research question

This review was driven by the following research questions: (1) what is the current state of knowledge in broad mite identification, abundance, and holistic management? and (2) what are the current gaps in the literature that warrant further research?

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Inclusion and exclusion criteria

The review focused on journals covering broad mite identification methods, taxonomy, biology, abundance related to abiotic factors, management practices, and soil nutrient amendment. The criteria included articles written in English from 2000 to 2024, available as open access with no geographical limitations. Sources included peer-reviewed and early-access articles, conference proceedings, theses, and book chapters. The databases used were the Web of Science and the Agricultural and Environmental Science collection from ProQuest, following the search syntax in Table 1.

Table 1. The search syntax used in the Web of Science and Agricultural and Environmental science collection-ProQuest

Databases	Search syntax
Web of Science	Results for "Polyphagotarsonemus latus" (Title) OR "Broad mite" (Title) AND "Polyphagotarsonemus latus identification" (Title) AND "Polyphagotarsonemus latus characteristics" (Title) AND "Polyphagotarsonemus latus abundance under protected structures" (Title) OR "Broad mite seasonal variation" (Title) AND "Soil nutrient amendment under protected structures" (Title) AND "Soil nutrient amendment" (Title) and English (Languages) and Meeting Abstract or Data Paper or Letter (Exclude – Document Types)
Agricultural and Environmental science collection - ProQuest	abstract(("Polyphagotarsonemus latus")) OR abstract(("broad mite")) AND abstract(("Polyphagotarsonemus latus Identification")) AND abstract(("Polyphagotarsonemus latus abundance under protected structures")) OR abstract(("Broad mite seasonal variation")) AND abstract(("protected structures")) AND abstract(("Broad mite management")) OR abstract(("Broad mite control")) OR abstract(("soil nutrient amendment under protected cultivation")) AND abstract(("nutrient amendment"))

Selecting studies, charting the data, and reporting results

The articles were downloaded into EndNote bibliographic software and uploaded into Covidence for screening and data extraction. Duplicates were removed, and screening followed the predefined inclusion and exclusion criteria outlined above. Titles and abstracts were reviewed, and eligible papers with full texts were assessed. Using the PRISMA flow diagram (Figure 1), 78 relevant studies were identified, with 46 studies from the Web of Science and 32 from the ProQuest: Agricultural and Environmental Science collection. After screening and removing duplicates, 52 final articles were included in this scoping review. The data was extracted following the Population, Concept, and Context (PCC) Framework guidelines described by Pollock et al. (2023) and amended based on the aim of this review. The literature was organized and reported in a narrative format with three thematic areas, namely (a) broad mite identification, (b) broad mite abundance studies, and (c) broad mite management. The results

were organized into five subsections. The first subsection provides the quantitative description of the 52 studies, followed by three sub-sections that describe the three thematic areas mentioned above and the fourth subsection highlights the current research gaps.

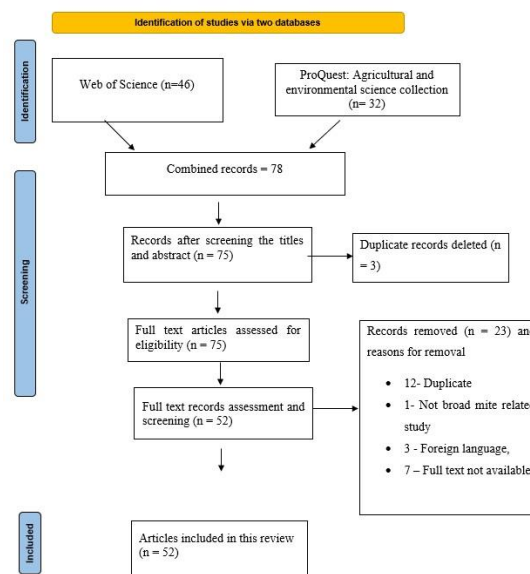


Figure 1. Screening of articles derived from Web of Science and ProQuest showing the data search and extraction process.

RESULTS

Description of the selected studies

A total of 16 countries were represented in the articles of this review (Figure 2). The three countries with the highest number of publications were Brazil (n=15), India (n=10) and Israel (n=6). There is none from the Pacific region. The highest number of studies were published between 2011 and 2015 (13 articles), 2021 and 2024 (13 articles), while the lowest studies were published between 2000 and 2005 (4 articles) (Figure 3). Of the 52 studies, 51 were published in 34 journals, while one article was from Research Square, an online preprint platform. Almost all the articles were primary research articles (n=51) except one article, which was a report. The studies were carried out in various settings (Figure 4), including open field (12), under protected structures (4), in the laboratory (17), or a combination of any of these sites.

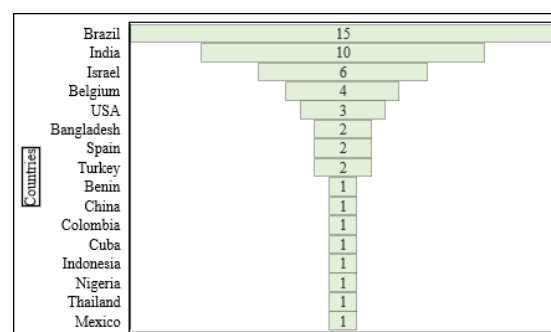


Figure 2. The number of studies on broad mite per country.

Based on the thematic areas, 71% (n=37) of the studies were focused on broad mite management, 15% (n=8) on abundance studies, and 12% (n=6) fell into the category of others. In comparison, only 2% (n=1) focused on broad mite identification (Figure 5). The top five types of studies were biological control studies (n=15), host plant resistance (n=11), abundance studies (n=8), and biological and chemical control studies (n=5 each). Some studies were a combination of multiple focus areas. Most of these studies were products of experiments with different experimental designs, while five (5) were surveys, one (1) was a report, and a laboratory protocol (Figure 6).

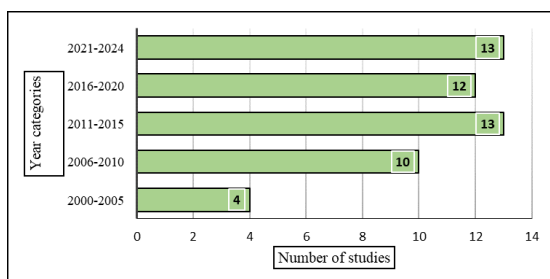


Figure 3. Number of articles published on broad mites from 2000 to 2024.

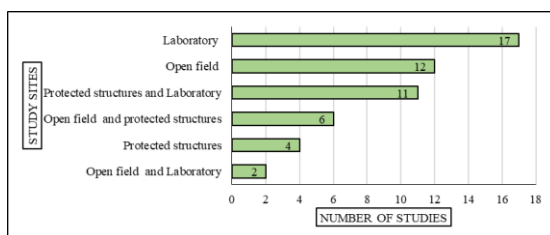


Figure 4. Sites where the broad mite studies were carried out.

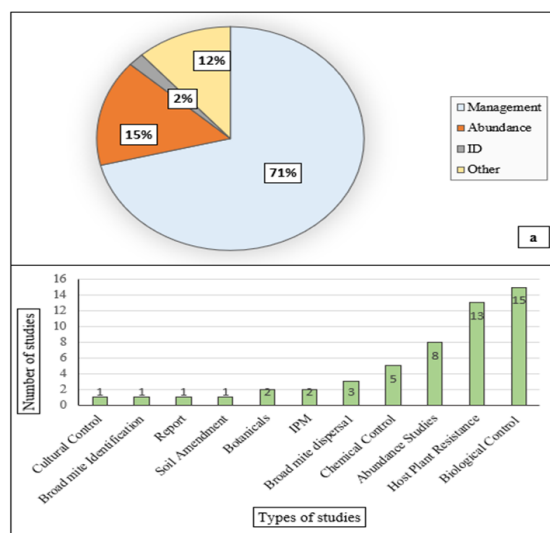


Figure 5. Types of broad mite studies recorded in this review. (a) Studies based of thematic areas, (b) categories of studies.

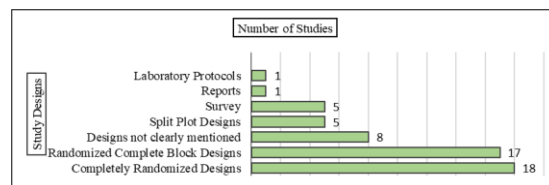


Figure 6. Types of experimental designs used in these broad mite studies.

Broad mite taxonomy

Methods of broad mite field collection

Methodologies involved in broad mite identification were presented in several studies included in this review and can be simplified in three steps (Leus et al., 2022). Firstly, infested young leaves were collected from the field or greenhouse and stored in vials with ethanol or paper bags placed in a cooler (Bala & Karmakar, 2022; Leus et al., 2022; Ovando-Garay et al., 2022; Rodriguez et al., 2017; Silva et al., 2016; van Maanen et al., 2010). Next, samples observed under a stereomicroscope in the laboratory (Silva et al., 2016) were extracted using the sieving and vacuum filtration methods (Leus et al., 2022). Finally, samples were either stored in 70% ethanol for later slide mounting (Bala & Karmakar, 2022; Leus et al., 2022; Silva et al., 2016) or in 100% ethanol for identification under the standard electron microscope (SEM) and molecular identification (Ovando-Garay et al., 2022).

Broad mite identification

Of 52 studies included in this review, only one detailed broad mite identification of two Mexican populations. This highlights the importance of accurate identification for successful broad mite management (Ovando-Garay et al., 2022). Identification methods include morphological (Bala & Karmakar, 2022), molecular, or integrating both (Ovando-Garay et al., 2022), with the latter due to morphological variation and the lack of identification keys. Research opportunity also lies in the broad mite's genetic and molecular characteristics, which remain poorly understood (Ovando-Garay et al., 2022).

All 52 studies referred to the species as *Polyphagotarsonemus latus* Banks (Table 2), commonly known as broad mites, yellow mites, and white mites, depending on the geographical locations (Table 3). Despite this confirmation, significant morphological (70% for females, 53% for males) and molecular variations (83-86% similarity with Indian sequence; 99% similarity within Mexican populations) exist between populations, suggesting the presence of species-complex (Ovando-Garay et al. 2022).

Morphological and molecular identification process of broad mites

The broad mite mounting and identification process, detailed in Figure 7 requires prior knowledge of basic broad mite morphology to ensure correct species is mounted using either Hoyer's (Cañarte et al., 2022;

Ovando-Garay et al., 2022; Renkema et al., 2017; Silva et al., 2016) or modified Berlese's medium (Bala & Karmakar, 2022) onto the slide (Ovando-Garay et al., 2022). For SEM, samples were dried in 99.9% Hexamethyldisilazane, mounted onto cylindrical aluminum mounting stubs with conductive carbon tape, and coated with a 70 nm layer of gold/palladium using a sputter coater. The specimens were then examined following the morphological criteria listed in Table 4 (Ovando-Garay et al. (2022)). The steps in molecular identification of broad mites using the primers LCO1490 and HCO2198 are described in Table 5 (Ovando-Garay et al., 2022).

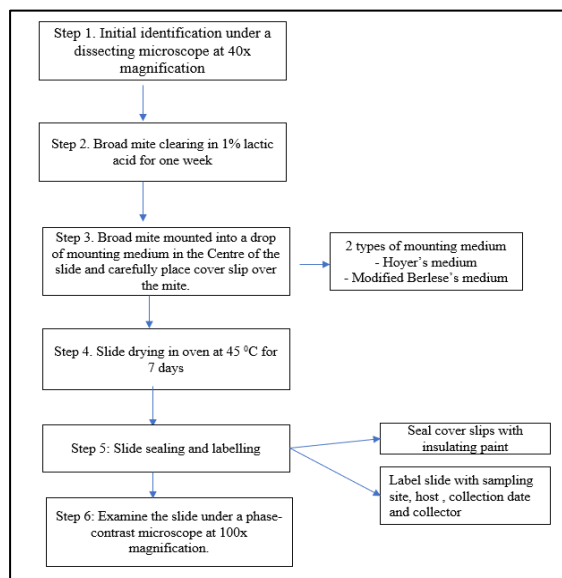


Figure 7. Steps in broad mite slide mounting as described by Ovando-Garay et al. (2022).

Broad mite abundance, host range, and damage characteristics

Broad mite's sampling and monitoring methods

Broad mite abundance studies used different methods depending on the research site. Surveys were commonly used to collect data in open fields over multiple seasons to identify trends in the pest and natural enemies' population (Nasrin et al., 2021; J. Rosado et al., 2015; J F Rosado et al., 2015; Soroker et al., 2003). Sticky traps were used in the field or under protected structures to monitor pest abundance and possible phoresy (Cañarte et al., 2022; Soroker et al., 2003). Studies observing broad mite damage on crops were conducted in all research sites where host plants were first checked for symptoms of broad mite damage before sampled leaves were examined under a microscope for broad mites due to their microscopic size (Bala & Karmakar, 2022; Cañarte et al., 2022; Nasrin et al., 2021; Rodriguez et al., 2017; Rosado et al., 2015; Rosado et al., 2015; Sarkar et al., 2023; Soroker et al., 2003; Umeh et al., 2007). In Brazil, Geographical Positioning Systems (GPS) were used to map broad mite damage by pinpointing their spread

pattern within a 30-meter diameter in open fields (J F Rosado et al., 2015).

Broad mite sampling methods vary between systematic, random, and purposive sampling depending on the study's objectives. Data collected included (1) broad mite abundance in relation to environmental parameters, (2) broad mite damage symptoms on host plants, and (3) broad mite dispersal (Nasrin et al., 2021; Rosado et al., 2015; Rosado et al., 2015; Soroker et al., 2003). Some studies also integrate abundance studies and host plant resistance, which will be discussed in detail in the broad mite management section.

Factors affecting broad mite Abundance

Environmental factors influence the broad mite population abundance, which varies in different cultivation systems. Optimum conditions for broad mites in the protected structure are 25 °C and 80% relative humidity, 16:8 h (L:D) photoperiod length, and 80 to 100 $\mu\text{mol m}^{-2} \text{s}^{-1}$ light intensity. Minimum and maximum temperature thresholds are 10-36 °C; anything below these values is harmful to broad mites (Luypaert et al., 2014). The ideal temperature range in open fields is 23-28 °C with minimum and maximum thresholds of 14 to 25 °C (Rosado et al., 2015). Records show that even below these temperatures, mites can still cause damage to physic nut (*Jatropha curcas*) in Brazil (Rosado et al., 2015). In Bangladesh, the highest broad mite population on chili was recorded at 26.8 °C and 84% relative humidity (Nasrin et al., 2021), while in Nigeria, Umeh et al. (2007) recorded the highest broad mite count on oranges at 26.2°C. Laboratory studies where broad mites caused damage were at 24-25 °C (Cabedo-López et al., 2021; Palevsky et al., 2001; Soroker et al., 2003).

Host range and damage characteristics

Thirteen plant families were described as host plants in the reviewed literature. The most studied plants were from the Solanaceae family including capsicum (*Capsicum annuum*), chili (*C. frutescens*), balloon pepper (*C. baccatum*), potato (*Solanum tuberosum*), Gboma egg plants (*S. macrocarpon*), egg plants (*S. melongena*) and tomato (*S. lycopersicum*) (Alagarmalai et al., 2009; Bala & Karmakar, 2022; Breda et al., 2016; Grinberg-Yaari et al., 2015; Lopez et al., 2017; Martins et al., 2016; Nasrin et al., 2021; Onzo et al., 2012; Ovando-Garay et al., 2022; Palevsky et al., 2001; Silva et al., 2016). The Citrus family included Valencia orange (*Citrus sinensis* 'Valencia'), sweet orange (*C. sinensis*), mandarin orange (*C. reticulata*), sour orange (*C. aurantium*) and Cleopatra mandarin (*C. reshni*) (Cabedo-López et al., 2021; Puspitarini et al., 2022; Rodriguez et al., 2017; Umeh et al., 2007). While from the Cucurbit family, the hosts were watermelon (*Citrullus lanatus* var. *lanatus*) and cucumber (*Cucumis sativus*) (Alagarmalai et al., 2009; Grinberg et al., 2005; Kousik et al., 2007; Palevsky et al., 2001; Soroker et al., 2003).

Table 2. Review literature that mentioned broad mite as *Polyphagotarsonemus latus*

Authors
(Akyazi et al., 2019; Akyazi et al., 2022; Alagarmalai et al., 2009; Augustine et al., 2023; Bajya & Ranjith, 2016; Bala & Karmakar, 2022; Breda et al., 2016; Breda et al., 2017; Britto et al., 2012; Cabedo-López et al., 2021; Cañarte et al., 2022; de Souza Deise et al., 2021; Evaristo et al., 2013; A. Ghosh et al., 2010; S. K. Ghosh, 2023; Gotyal et al., 2016; Grinberg-Yaari et al., 2015; Grinberg et al., 2005; Humberto Godoy et al., 2021; Kousik et al., 2007; Leus et al., 2022; Lopez et al., 2017; Luypaert et al., 2015; Luypaert et al., 2017; Luypaert et al., 2014; Maketon et al., 2008; Marques et al., 2014; Martins et al., 2016; Mikunthan & Manjunatha, 2008; Mitra et al., 2015; Morell et al., 2010; Nasrin et al., 2021; Onzo et al., 2012; Ovando-Garay et al., 2022; Palevsky et al., 2001; Puspitarini et al., 2022; Rahman & Khan, 2010; Renkema et al., 2017; Rodríguez-cruz et al., 2013; Rodriguez et al., 2017; J. Rosado et al., 2015; J F Rosado et al., 2015; Sarkar et al., 2023; Sarmiento et al., 2011; Singh & Singh, 2013; Soroker et al., 2003; Umeh et al., 2007; van Maanen et al., 2010; Venzon et al., 2008; Weintraub et al., 2003; Y. N. Zhang et al., 2023)

Table 3. Different geographical locations where broad mites and synonyms are recorded

Synonym	Country	Authors
Broad mite	Benin, Israel, Bangladesh, Cuba, India, Spain, China, Brazil, USA, Nigeria, Thailand, Brazil and Belgium	(Akyazi et al., 2019; Alagarmalai et al., 2009; Augustine et al., 2023; Breda et al., 2016; Britto et al., 2012; Evaristo et al., 2013; Grinberg-Yaari et al., 2015; Humberto Godoy et al., 2021; Kousik et al., 2007; Leus et al., 2022; Luypaert et al., 2015; Luypaert et al., 2017; Luypaert et al., 2014; Maketon et al., 2008; Marques et al., 2014; Mikunthan & Manjunatha, 2008; Morell et al., 2010; Nasrin et al., 2021; Onzo et al., 2012; Ovando-Garay et al., 2022; Palevsky et al., 2001; Rahman & Khan, 2010; Rodríguez-cruz et al., 2013; Sarmiento et al., 2011; Soroker et al., 2003; Umeh et al., 2007; van Maanen et al., 2010; Venzon et al., 2008; Weintraub et al., 2003; Y. N. Zhang et al., 2023)
Yellow mite	India and Bangladesh	(Bajya & Ranjith, 2016; A. Ghosh et al., 2010; S. K. Ghosh, 2023; Mitra et al., 2015; Rahman & Khan, 2010; Sarkar et al., 2023; Singh & Singh, 2013)
White mite	Brazil	(Akyazi et al., 2019; Venzon et al., 2008)
Tropical mite		
Citrus silver mite		

Table 4. Broad mite morphological identification criteria as described by (Ovando-Garay et al. (2022).

Criteria	Female Parameters	Male Parameters
Total length	✓	✓
Idiosome width	✓	✓
Idiosome length	✓	✓ (with and without genital capsule)
Distance between trochanters I	✓	✓
Distance between trochanters II	✓	✓
Distance between trochanters III	✓	✓
Length of trochanter III	✓	
Length of femorogenu III	✓	
Distance between trochanters IV	✓	✓
Length of trochanter IV	✓	✓
Length of femorogenu IV	✓	✓
Length of tibiotarsus IV	✓	✓
Length of seta v" on tibiotarsus IV	✓	
Length of seta tc" on tibiotarsus IV	✓	
Gnathosoma length	✓	✓
Gnathosoma width	✓	✓
Length of claw I	✓	

Table 5. Steps in broad mite DNA extraction, amplification, and purification.

Steps	Description
Sample Selection	Collect samples from different hosts and locations.
DNA Extraction	Add 50 µL of lysis solution (25 mM NaOH, 0.2 mM EDTA, pH 12) and 3.5 µL of proteinase K (1.30 mg/mL). Incubate for three hours at 55°C, then chill for 5 minutes then mechanically lysing with glass beads. Centrifuge for 10 seconds at 2000rpm. Neutralize the isolated DNA with 50 µL of 40 Mm Tris-HCl, pH 5, precipitated with 100% alcohol, washed with 70% ethanol, dry and resuspend in 20 µL injectable water.
PCR Amplification	Primers LCO1490 and HCO2198 were used to amplify the cytochrome c oxidase subunit I (COI) gene of mitochondrial DNA (mtDNA COI). The PCR protocol included initial denaturation at 95°C for 5 minutes, followed by 30 cycles of denaturation at 95°C for 30 seconds, annealing at either 40°C or 48°C for 40 seconds, and extension at 72°C for 1 minute. The 30 µL PCR reaction used two times PCR Master Mix (2x). Amplified products were run on a 1% agarose gel stained with SYBR Green.
PCR Product Purification and Sequencing	PCR products were purified using a commercially available kit and sent for sequencing at Macrogen (Seoul, South Korea).

Other host plants include mulberry (*Morus rubra* Moraceae) (Augustine et al., 2023), strawberry (*Fragaria ananassa* Duchesne Rosaceae) (Renkema et al., 2017), physic nut (*Jatropha curcas* Euphorbiaceae) (Evaristo et al., 2013; J. Rosado et al., 2015; J F Rosado et al., 2015), common bean (*Phaseolus vulgaris* Fabaceae) (Humberto Godoy et al., 2021), pot Azalea (*Rhododendron simsii* Ericaceae) (Luypaert et al., 2015; Luypaert et al., 2014), garlic (*Allium sativum* Amaryllidaceae) (Bala & Karmakar, 2022), yellow elder (*Tecoma stans* Bignoniaceae) (Ovando-Garay et al., 2022), tea (*Camellia sinensis* Theaceae) (Akyazi et al., 2019), cotton (*Gossypium hirsutum* Malvaceae), jute (*Corchorus olitorius* Malvaceae) (Mitra et al., 2015; Sarkar et al., 2023), cauliflower (*Brassica oleracea* var. *botrytis* Brassicaceae) and cabbage (*Brassica* spp. Brassicaceae) (Bala & Karmakar, 2022).

Broad mites are minute, so their presence on host plants is often indicated by damage symptoms. Damage may appear in small clusters but can rapidly spread throughout the field (Breda et al., 2016; Singh & Singh, 2013; Venzon et al., 2008). Broad mites feed on young leaves, fruits, and flower buds, leading to leaf curling, stunted growth, fruit and flower fall, flower discoloration, and scarring (Puspitarini et al., 2022). Symptoms may be similar between host plants and different plant parts.

Common symptoms on young leaves include discoloration, downward curling, necrosis and leaf bronzing were seen in eggplants (Onzo et al., 2012), strawberry (Renkema et al., 2017), oranges (Cabedo-

López et al., 2021; Rodriguez et al., 2017), chilis and capsicum (Breda et al., 2016; Singh & Singh, 2013; Venzon et al., 2008) and jute (Mitra et al., 2015). Leaf curling is a sign of heavy broad mite infestation (Breda et al., 2016; Singh & Singh, 2013; Venzon et al., 2008). In cucumber and watermelon, infested leaves tend to be smaller (Grinberg et al., 2005; Kousik et al., 2007).

Other symptoms of broad mite damage in capsicum and chili include elongated petioles, shortened internodes and increased growth of side shoots (Breda et al., 2016; Singh & Singh, 2013; Venzon et al., 2008).

Damage rating scales have been developed for chili (Mikunthan & Manjunatha, 2008), jute (A. Ghosh et al., 2010) and capsicum (Breda et al., 2016) (Table 6). The scales share common characteristics like increased severity of damage, with early stages exhibiting leaf curling or bronzing, increasing distortion of leaves and growth tips, progressing to defoliation, and considerable consequences on plant height and overall health in severe stages.

Broad mite dispersal

Phoresy is the most notable form of broad mite dispersal detailed in the literature (Alagarmalai et al., 2009; Cañarte et al., 2022; Palevsky et al., 2001; Soroker et al., 2003). Female broad mites have been observed “hitchhiking” on the tarsi of whiteflies, *Bemisia tabaci* (Alagarmalai et al., 2009). The cuticular wax secreted by whiteflies influences its detachment (Cañarte et al., 2022; Soroker et al., 2003), host type, and the broad mite’s fitness (Soroker et al. (2003).

Table 6. Damage rating scales developed for chili, jute, and capsicum

Damage Scale	Chili	Jute	Capsicum
0	Healthy	No damage	No injury
1	25% of leaves curled	Leaf base is lightly bronzed	Leaf surface slightly rough
2	26 to 50% of leaves curled and moderately damaged	Leaf base bronzed	Downward or upward leaf edge curled with light zigzag pattern on mid-vein
3	51-75% of leaf curled, buds deformed and growth stunted	Symptoms 1-2 observed plus leaf fall	Leaves and deformed with prominent zigzag patterns on leaf veins
4	>75% of leaf curled, buds severely deformed, growth stunted and defoliated	All leaves dropped, only shoot remains	Leaves severely deformed
5	NA	Apical shoot dies	NA

Management of broad mites

The highest number of papers in this review was on broad mite management, with 37 in total (Figure 8), including biological control studies (n=15), host plant resistance studies (n=13), and chemical control (n=5). There was one on soil amendment, which tackled a holistic management approach of broad mites.

Biological control

Predatory mites belong to three families: Ascidae, Blattisociidae, and Phytoseiidae (Britto et al., 2012; Marques et al., 2014; Onzo et al., 2012; Rodríguez-Cruz et al., 2013; Sarmiento et al., 2011; Silva et al., 2016; van Maanen et al., 2010; Weintraub et al., 2003;

YN Zhang et al., 2023). Only species from the Ascidae family (*Asca* species) were found on eggplants in Brazil. The soil-dwelling predatory mite *Lasioseius floridensis* (Blattisociidae) was found ineffective in managing broad mites on chili when other food sources, such as *Rhabditella axei*, were available (Britto et al., 2012).

Of these three families, the Phytoseiidae family was the most studied, particularly the genera *Neoseiulus*, *Amblyseius*, *Euseius*, *Iphiseiodes*, *Proprioseiopsis*, *Typhlodromalus*, and the *Phytoseius* spp. (Onzo et al., 2012; Silva et al., 2016; van Maanen et al., 2010; Weintraub et al., 2003). *Neoseiulus cucumeris* successfully managed a broad mite population on capsicum grown under protected

structures in Israel (Weintraub et al., 2003). *Amblyseius swirskii* thrived under connected crop canopies in protected structures (Onzo et al., 2012; van Maanen et al., 2010), and *A. orientalis* was recommended for broad mite management in China (YN Zhang et al., 2023). Other predatory mites, such as *Proprioseiopsis cannaensis*, *P. mexicanus*, *P. neotropicus*, *P. ovatus*, *Typhlodromalus aripo*, *T. manglae*, *Phytoseiulus guianensis*, and *T. peregrinus*, were also found on chili and eggplants, indicating potential for further study (Silva et al., 2016).

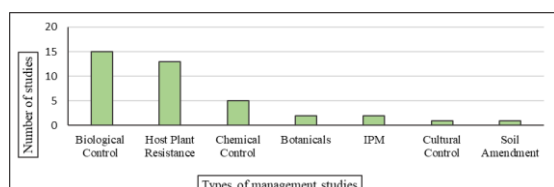


Figure 8. Types of broad mite management studies.

Entomopathogenic fungi (EPF) (Maketon et al., 2008; Puspitarini et al., 2022) were also used for the control of broad mites. *Beauveria bassiana* and *Metarhizium anisopliae* are the most studied. *B. bassiana* caused 90-100% broad mite mortality within 120 hours and, when combined with *Mimosa pudica* leaf extract (MpAE) at various concentrations, resulted in 100% mortality (Puspitarini et al., 2022). *M. anisopliae* strain CKM-048 was effective against broad mite larvae and adults but not eggs, requiring reapplication every 3-4 days for ongoing control (Maketon et al., 2008). Another EPF recorded to aid in managing broad mites in chili-cotton-chili intercrop was *Fusarium semitectum* (Mikunthan & Manjunatha, 2008). In contrast, the four soil fungal isolates, namely *Aspergillus brunneoviolaceus*, *Clonostachys chloroleuca*, *Fusarium inflexum*, and *Penicillium adametzii*, proved unsuitable as broad mite biological agents (de Souza Deise et al., 2021).

Host plant resistance

DNA markers can identify genetic variations within a plant's genera that make them resistant to pest attack (Humberto Godoy et al., 2021) through defense mechanisms, hormonal signaling pathways, and high levels of phenolic compounds in leaves. Twenty-one DNA markers in jute (*Corchorus olitorius*) were found with markers J-170, HK-89, and HK-64, offering 100% selection efficiency against broad mites (A. Ghosh et al., 2010). Hormonal signaling pathways, including the salicylic acid (SA) and jasmonic acid/ethylene (JA/E) pathways (Grinberg et al., 2005), for instance, wild tomato plants release jasmonic acid (JA) through the JA/E pathway in the early stages of broad mite infestation (Grinberg-Yaari et al., 2015) whereas SA is activated once the infestation has advanced (Leus et al., 2022). In cucumber, broad mite infestation increased the defense-related gene expressions like β -1,3 glucanase (BGL2) and lipoxygenase (LOX), which are linked to the JA/E and SA pathways. JA mainly defends against herbivores, while increased SA levels indicate a systemic defense response (Luybaert et al., 2017) which also induces high phenolic compounds

that contribute to jute (Mitra et al., 2015), capsicum (Breda et al., 2016), physic nut (Evaristo et al., 2013), watermelon (Kousik et al., 2007) and beans (Humberto Godoy et al., 2021) tolerance to broad mite feeding (Humberto Godoy et al., 2021).

Chemical control

A recent survey showed high failure rates of acaricides like piromesifen (66.67%), diafenthiuron (63.33%), fenazaquin (58.33%), dicofol (55.56%), and propargite (Augustine et al., 2023) which were linked to resistance to synthetic pesticides of mite population tested. Therefore, it is vital to find ecologically acceptable acaricide alternatives such as Abamectin and improve application techniques like the temporary withdrawal method (Augustine et al., 2023) that can be used in Integrated Pest Management (IPM). Abamectin was found effective against adults, causing 100% mortality one hour after treatment. It also kills larvae upon hatching but has low ovicidal efficacy (Akyazi et al., 2022).

Botanical acaricides like azadirachtin, neem oil, garlic bulb extract, and soft soap have become eco-friendly alternatives to synthetic pesticides. Azadirachtin gradually reduces broad mite populations, while neem oil is the most repellent formulation of neem plant extract (Breda et al., 2017). A 10% soap solution and 20% garlic + soap mixture were effective on eggs (Akyazi et al., 2022).

Cultural control

Cultural control for broad mite management in chili involved modifying the microenvironment to promote the growth of the EPF *Fusarium semitectum* through intercropping. The most effective systems were chili-sorghum, chili-cotton-chili, and chili-red gram, which increased chili yield by creating a favorable microclimate for *F. semitectum* development, aiding in the control of chili thrips and broad mites (Mikunthan & Manjunatha, 2008).

Soil amendments

Soil fertility can affect the plant's susceptibility to pests, influencing resistance or herbivore susceptibility. In the fertilizer regime at the recommended nitrogen dose (80:40:40 kg/ha), broad mite infestation was moderate, but at a higher dose (120:40:40 kg/ha), mite populations increased (Gotyal et al., 2016).

Integrated pest management (IPM)

There is a developed IPM program for broad mites on tea (*C. sinensis* L.) and jute (*C. olitorius*), but none on capsicum. This program has six modules focusing on insects, mites, and nematodes at various growth stages of jute (Figure 9). Module 3 proved to be the most cost-effective strategy for managing jute pests (Rahman & Khan, 2010) and can be a model for developing an IPM program for capsicum. The IPM module includes

predatory mites (*A. californicus* and *A. swirskii*), micronized sulphur, garlic bulb extract, tobacco leaf extract, and soft soap (Akyazi et al., 2019).

Module	Description	Practices
M1	Against nematodes only	1. Seed treatment with carbosulfan (2.5 g/kg). 2. Soil application with carbofuran (1 kg/ha) before sowing.
M2	Against insect and mite pests	1. Remove early instar bihar hairy caterpillars manually. 2. Spray neemazal (1 ml/l) for other insects. 3. Spray dicofol (185 g/ha) for mites.
M3	Against insect, mite, and nematode pests	Combine M1 and M2 practices.
M4	Recommended practices	1. Remove early instar bihar hairy caterpillars manually. 2. Spray endosulfan (350 g/ha) for other insects and mites.
M5	Farmer practices	1. Broadcast sowing method. 2. Spray endosulfan (350 g/ha) twice, 15 days apart, for pests.
M6	Untreated control	No treatments applied.

Figure 1. Summary of the IPM Modules used management of jute pests (Rahman and Khan 2010).

Research gaps in broad mite studies in Fiji

This review found no studies explicitly addressing broad mite issues in Oceania and Fiji. However, broad mites have been reported in Australia, New Zealand, Papua New Guinea, Guam, Samoa, Solomon Islands, American Samoa, Kiribati, The Marianas, New Caledonia, Wallis and Futuna, Tonga, Hawaii, Palau, and Fiji (CABI, 2022; Hamasaki et al., 2008; Jovicich et al., 2016; Naituku et al., 2017).

The importance of research on broad mites infesting high-valued crops like capsicum in Fiji is highly relevant and needed since the pest thrives in tropical and sub-tropical climates and in warm and humid greenhouse conditions (Zhang, 2003). In Fiji, broad mites are present year-round in open fields and protected structures (Australian Centre for International Agricultural Research, 2019), and have significantly reduced capsicum yields under these environments (Jovicich et al., 2016). The climatic conditions in Fiji are ideal for broad mites to thrive, with optimum temperatures around 25°C and relative humidity at 80% (Luybaert et al., 2015; Zhang, 2003), similar to those recorded in the protected structures (Breda et al., 2016). Therefore, determining the optimum temperature and humidity for broad mite density is essential for developing effective cultural management strategies.

Studies suggest that broad mites (*Polyphagotarsonemus latus* Banks) showed variations within populations, potentially consisting of closely related subspecies with slight morphological or genetic differences, which could be the case for Fiji species. Facilities and capacity-building for molecular and morphological techniques (Ovando-Garay et al., 2022) have been one of the priorities in Fiji, which is crucial for accurate species identification and effective pest management programs.

The available feeding damage rating scale from previous studies on different crops could be valuable tools for researchers in Fiji to adapt and improve to overcome the difficulty due to their microscopic size. This rating scale helps detect and estimate the mites' density on leaves because it correlates with visible plant symptoms (Fasulo, 2000; Montasser et al., 2011).

Another important finding from this review is that out of the 60 known plant families that are hosts of broad mites worldwide, 13 were discussed, with one of these families being Solanaceae. In Fiji, high-value solanaceous crops include capsicum, tomato, chilies, and eggplants. Capsicum, in particular, is highly susceptible to broad mites under protected structures (Jovicich et al., 2016). Also, understanding the relationship between broad mites and other arthropods is also important as studies have shown that broad mite movements involved phoresy with whitefly (Palevsky et al., 2001; White et al., 2017; Alagarmalai et al., 2009; Cañarte et al., 2022; Malumphy, 2009; Palevsky et al., 2001, thrips and aphids (Palevsky et al., 2001).

This review highlights the importance of IPM, with 71% of studies dedicated to it. IPM targets overall crop health (Akyazi et al., 2019; Rahman & Khan, 2010), suggesting that strategies for broad mites and associated pests could also be developed for Fiji.

The reported broad mite management practices such as chemical, cultural, botanical, and biological control are also used to manage other crops' pests and diseases in Fiji. Chemical control is the most common method Fijian farmers use to manage broad mites, but many of these recommended pesticides are insecticides that may not effectively target broad mites. Successful pest management in Fiji requires a holistic approach that includes selective pesticides and soil nutrient amendments to slow down the build-up of chemical resistance, as this is becoming an issue in managing broad mites (Augustine et al., 2023).

Timing and options for management are critical because broad mites can cause severe crop damage due to their lack of effective natural enemies, high fecundity, short development times, parthenogenetic capability, adaptability to new environments, and rapid resistance to pesticides (Chong, 2022). In this review, we identified environmentally friendly alternatives, such as abamectin and sulfur (Akyazi et al., 2022; Akyazi et al., 2019), biological control, host plant resistance, and botanicals that can also be adopted for broad mite management in Fiji. Modified cropping systems should be incorporated to create a microclimate for EPF or predatory mites to manage broad mites (Mikunthan & Manjunatha, 2008). Soil amendment or fertilizer regime can also be incorporated into IPM programs for Fiji to maintain soil health in intensive capsicum cultivation under protected structures (Gotyal et al., 2016).

Conclusion

This scoping review was conducted to summarise the existing information on broad mites. It highlights the economic importance of these pests due to their cosmopolitan and polyphagous nature, as well as the need for comprehensive information on their effective management in Fiji. The identified research gaps and limitations provide a foundation for developing broad mite management strategies in the country. Several potential research areas have been identified, including

the integrated identification of broad mite species, studying their abundance on capsicum and other related hosts in relation to weather parameters, exploring the potential for broad mite phoresy on whitefly species in Fiji, and adopting a holistic approach that incorporates selective acaricides, host plant resistance, integrated pest management (IPM), and soil nutrient amendments.

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