

Acarological Research in Republic of Congo: Advances and Challenges in Understanding Phytoseiidae and Tetranychidae Diversity

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Abstract

Mites comprise a highly diverse component of tropical agroecosystems, and phytophagous and predatory species play essential roles in crop health and the ecological balance. Despite their ecological and economic importance, the acarofauna of the Republic of the Congo (RC) remains unclear. This study provides the first comprehensive synthesis of plant-inhabiting mites reported in the country between 1980 and 2025. A narrative bibliographic review was conducted across three major databases (PubMed, Semantic Scholar, and Web of Science) using keywords related to Phytoseiidae, Tetranychidae, host plants and biodiversity. Ten publications met the inclusion criteria and corresponded to field and laboratory studies conducted in southern Congo, mainly around Brazzaville. In total, 22 mite species were identified, including 10 from Phytoseiidae and 12 from Tetranychidae, primarily associated with cassava (*Manihot esculenta*), okra, tomato, pepper, and eggplant. *Euseius fustis* and *Amblyseius sundi* were the most frequently recorded predatory mites, whereas *Mononychellus progresivus* and *Oligonychus gossypii* were the predominant phytophagous mites. Recent studies have incorporated molecular tools (12S rRNA and Internal Transcribed Spacer gene sequences), indicating a methodological transition toward integrative taxonomy. The occurrence of *Eutetranychus orientalis* on cassava is the first record of this species in the RC. Overall, acarological research in the country remains fragmented and geographically restricted. This review highlights the need to expand mite inventories, strengthen the use of molecular approaches, and promote coordinated national programmes dedicated to acarological biodiversity and sustainable

pest management.

Keywords

Predatory Mites, Spider Mites, Plant-Inhabiting Mites, Agroecosystems, Biological Control, Integrative Taxonomy

1. Introduction

Mites (subclass, Acari) constitute one of the most diverse and ecologically significant groups within the class Arachnida, occupying nearly every terrestrial habitat and playing crucial roles in ecosystems as decomposers, parasites, and plant associates [1]. Plant-inhabiting mites represent a particularly important ecological guild, comprising both phytophagous species that feed on plant tissues and may act as pests and predatory species that regulate populations of phytophagous mites and small arthropods [2] [3]. The interactions between these two functional groups are central to maintaining ecological balance and crop productivity, especially in tropical agroecosystems [4].

Phytophagous mites, including those belonging to the families Tetranychidae (spider mites), Tenuipalpidae (flat mites), and Eriophyidae (gall and rust mites), are among the most damaging arthropod pests in agriculture. They attack various crops, including cassava, tomato, citrus, cotton, and coffee, and cause significant yield losses through direct feeding and indirect physiological effects on plants [5]. Members of Tetranychidae are particularly destructive owing to their rapid reproductive cycles and ability to develop resistance to acaricides [5]. In contrast, Phytoseiidae, a family of predatory mites within the order Mesostigmata, plays an essential role in natural and applied biological control by feeding on pest mites, thrips, and whiteflies [6]. Accordingly, their efficacy and specificity make them cornerstone organisms in integrated pest management programs worldwide. The most commercially significant Phytoseiidae species include *Amblyseius swirskii*, *Phytoseiulus persimilis*, *Neoseiulus cucumeris*, and *Neoseiulus californicus*. These predatory mites are primarily used to control spider mites (e.g. *Tetranychus urticae*), thrips, and whiteflies on vegetable, ornamental, and fruit crops. Moreover, their high reproductive rate, prey specificity, and adaptability to various environments make them effective in both augmentative and conservation biological control programs.

In sub-Saharan Africa, the most studied plant-inhabiting mite system is the cassava green mite complex, which has attracted extensive research since its introduction in the 1970s. The pest species *Mononychellus tanajoa* (Bondar) and *Mononychellus progresivus* Doreste (Acari: Tetranychidae) cause severe damage to cassava (*Manihot esculenta* Crantz), a staple crop for millions of people in the region [7]. The introduction of predatory mites (Phytoseiidae) from South America into Africa by the International Institute of Tropical Agriculture is one of the

most successful examples of classical biological control against phytophagous mites. This program, implemented across West and Central Africa, demonstrated the effectiveness of natural enemies in restoring ecological balance and improving food security.

Early acarological research followed a similar trajectory in the RC. The initial studies were mainly descriptive and focused on phytophagous mites associated with cassava. The pioneering work of Bonato and his collaborators, carried out in the 1990s [8], provided the first detailed inventory of tetranychid mites in the country, particularly those infesting cassava crops in the southern regions (Kouilou, Bouenza, Pool, and Plateaux). Seven Tetranychidae species were recorded, among which *Mononychellus progresivus* and *Oligonychus gossypii* were identified as the main phytophagous species of agronomic importance. In parallel with the study of phytophagous mites, Guttierrez and Bonato (1994) identified several species of predatory mites belonging to the family Phytoseiidae, which are known for their crucial roles in the natural regulation of Tetranychidae populations. Their survey identified six major species belonging to the genera *Euseius*, *Typhlodromalus*, *Neoseiulus*, and *Amblyseius*. These observations represent the first record of Phytoseiidae in the RC and highlight the presence of predatory fauna that is potentially useful for the biological control of cassava mite pests.

Guttierrez and Bonato (1994) relied exclusively on morphological criteria for mite identification, which was the standard approach used at the time [8]. In parallel, Navajas *et al.* (1994) introduced the first molecular approaches applied to cassava mites, revealing intraspecific genetic diversity within *M. progresivus* [9]. This methodological transition has provided a foundation for integrating molecular markers to assess the taxonomy and ecology of phytophagous mites. However, despite the foundational nature of these morphological and molecular studies, no research has been published based on data collected from plant-inhabiting mites in the RC. Moreover, a prolonged period of low scientific output occurred between 1994 and 2018 with regard to plant-associated acarofauna in the RC. In the absence of biodiversity surveys conducted at the national scale during this interval, a few sporadic contributions, mostly of regional or taxonomic scope, nevertheless relied on congolese material, notably the redescription of *Typhlodromalus aripo* by Moraes *et al.* (2006) based on specimens originating from the RC [10]. Although limited in scope, these studies contributed to updating the available knowledge on plant-inhabiting mites in the RC. Research specifically dedicated to the inventory of plant-inhabiting mite biodiversity resumed with a Master's thesis completed in 2018. This thesis is mentioned here to document the re-emergence of acarological research in the RC but was not included in the narrative review, which was restricted to peer-reviewed publications. The scientific valorization of these results in an international peer-reviewed journal in 2020 highlighted the need to address existing knowledge gaps for this taxonomic group and encouraged

the initiation of new national-scale inventory projects. Accordingly, only the 2020 peer-reviewed article derived from this work was included in the present narrative review [11]. This study aimed to clarify the taxonomic status of several *Euseius* populations collected from cassava, okra, and chili using a combination of morphometric and molecular analyses (12S rRNA and ITS genes). These recent investigations mark a turning point in the adoption of integrative taxonomy in Congolese acarology, bridging the gap between traditional morphology-based studies and modern molecular narratives.

Therefore, a narrative literature review is timely and necessary to establish a baseline for acarological research in the RC. By consolidating and critically analysing existing data, this study aimed to clarify the current state of knowledge, highlight research gaps, and guide future investigations toward integrative approaches that combine morphological and molecular. The main objective of this study was to provide an updated synthesis of research on plant-inhabiting mites in the RC between 1980 and 2025. Specifically, the aims were as follows: 1) compile all available scientific literature on Tetranychidae and Phytoseiidae reported from the country; 2) identify the main species and their host plants, as well as their geographic distribution; 3) analyse the methodological evolution from morphological to molecular and integrative approaches; and 4) proposed research and management perspectives to strengthen acarological knowledge and promote the use of predatory mites in biological control programs in the RC.

2. Methodology

This narrative review was designed to compile, evaluate, and synthesise existing scientific knowledge on plant-inhabiting mites (families, Phytoseiidae and Tetranychidae) reported in the RC from 1980 to 2025. This review followed the Preferred Reporting Items for Narrative Reviews and Meta-Analyses (PRISMA) principles, emphasising transparency, reproducibility, and comprehensive data retrieval.

2.1. Literature Search Strategy

A structured bibliographic search was conducted using three major international databases: PubMed, Semantic Scholar, and Web of Science. These platforms were selected for their complementary coverage: PubMed for biological and ecological studies, Semantic Scholar for interdisciplinary and grey literature, and Web of Science for taxonomic and agronomic journals indexed globally. Searches were performed in English and French to identify regional publications and reports written by Congolese researchers. The search strings used Boolean operators (AND and OR) and combined taxonomic, ecological, and geographical keywords. The main query was as follows: (“acariens” OR “mites” OR “Phytoseiidae” OR “Tetranychidae”) AND (“plantes hôtes” OR “plant hosts”) AND (“République du Congo” OR “Republic of the Congo” OR “Congo-Brazzaville”). To ensure ex-

haustiveness, additional searches were performed using related terms such as “predatory mites” and “cassava green mite”. The reference lists of the retrieved articles were manually screened to identify any additional relevant studies that were not indexed in the databases.

In addition, we consulted dedicated taxonomic databases compiling mite fauna: for Phytoseiidae, the Phytoseiidae Database, which provides updated taxonomic information on described species and is largely based on Moraes *et al.* (2004) [6]; and for Tetranychidae, a reference database largely derived from the compilations of Bolland and colleagues [5].

2.2. Inclusion and Exclusion Criteria

Articles were included in the review if they met the following conditions: the study was conducted within the RC [12]; the research explicitly dealt with plant-associated mites (phytophagous or predatory); identification methods were described (morphological, molecular, or integrative); the article was peer-reviewed and the full text is available. Some studies were excluded for the following reasons:

- Studies that focused exclusively on veterinary or soil-dwelling mites, because our review targets agricultural pest species relevant to cassava and other crops.
- Studies conducted in neighbouring countries (e.g., Democratic Republic of the Congo, Gabon, and Cameroon) were excluded to maintain geographic relevance to the RC [13].
- Publications lacking sufficient methodological or locality information were excluded to ensure the reliability and traceability of the data included in our synthesis.
- Unpublished reports or theses not accessible through institutional repositories were excluded, as the full text could not be verified or reviewed for methodological rigor.
- Studies addressing life history traits [14], distribution of pest mites on cassava [15] and impact [16] of these pest mites were not considered. Our review emphasizes species occurrence and identification rather than ecological or biological traits.

2.3. Data Extraction and Organisation

A total of ten publications were retained, including two papers published in 1994, and one paper each published in 1989, 2001, 2006, 2014, 2015, 2020, 2022 and 2024. For each eligible article, data were extracted manually into a standardised template including: 1) publication details (year, reference and DOI when available); 2) taxonomic information (family and the genus/species reported, including records identified only at the generic level, *i.e.* sp. or spp.); and 3) methodological information (traditional or integrative taxonomy), as summarised in **Table 1** and **Table 2**.

Table 1. Tetranychidae species reported on cassava in the Republic of Congo, with associated methodological approaches.

Year	Reference	DOI	Genus and species reported	Methods
1994	Gutierrez & Bonato	—	<i>Mononychellus progresivus</i> , <i>Tetranychus kanzawai</i> , <i>Eutetranychus cratis</i> , <i>Oligonychus coffeae</i> , <i>O. gossypii</i> , <i>Tetranychus neocaledonicus</i> , <i>T. sayedi</i>	Field survey and collection; traditional taxonomy
1994	Navajas <i>et al.</i>	10.1007/BF00116316	<i>Mononychellus progresivus</i>	Molecular analyses (mitochondrial and nuclear DNA); cross-breeding experiments
1998	Navajas <i>et al.</i>	10.1046/j.1365- 2540.1998.00349.x	<i>Tetranychus kanzawai</i>	Molecular analyses (mitochondrial and nuclear DNA)
2015	Migeon	doi.org/10.3897/zookeys. 489.9292	<i>Oligonychus thelytokus</i> , <i>Oligonychus (Reckiella) grypus</i> , <i>Tetranychus evansi</i> , <i>Tetranychus urticae</i> .	Traditional taxonomy
2024	Okassa <i>et al.</i>	10.4314/rafea.v7i4.14	<i>Oligonychus gossypii</i> ; <i>Mononychellus progresivus</i> <i>Mononychellus sp.</i> ; <i>Oligonychus sp.</i> ; <i>Eutetranychus orientalis</i>	Field sampling; traditional taxonomy; discussion on molecular barcoding

Notes: Traditional taxonomy refers to species identification based exclusively on morphological characters. Molecular analyses were not used unless explicitly stated.

Table 2. Phytoseiidae species reported from the Republic of Congo and related taxonomic studies.

Year	Reference	DOI	Genus and species reported	Methods
1989 a	Moraes <i>et al.</i>	-	<i>Euseius fustis</i> and <i>Amblyseius saltus</i>	Field survey and collection; traditional taxonomy
1994	Gutierrez & Bonato	-	<i>Amblyseius saltus</i> , <i>Amblyseius sundi</i> and <i>Euseius fustis</i>	Field survey and collection; traditional taxonomy
2006	de Moraes <i>et al.</i>	-	<i>Typhlodromalus aripo</i>	Field survey and collection; traditional taxonomy; regional synthesis
2014	Demite <i>et al.</i>	10.11646/zootaxa. 3795.5.6	<i>Amblyseius sundi</i> , <i>Euseius baetae</i> , <i>Euseius fustis</i> , <i>Euseius neodossei</i> , <i>Ueckermannseius saltus</i>	Field survey and collection; traditional taxonomy
2020	Okassa <i>et al.</i>	10.11646/zootaxa. 4768.4.2	<i>Euseius fustis</i> and <i>Euseius</i> spp.	Integrative taxonomy: morphological and molecular approaches
2022	Okassa <i>et al.</i>	10.30564/jzr.v4i4. 3854	<i>Amblyseius swirskii</i> , <i>Amblyseius</i> spp., <i>Paraphytoseius horrififer</i> , <i>Euseius fustis</i> , <i>Iphiseius</i> <i>degenerans</i> and <i>Phytoseius amba</i>	Field inventory; traditional taxonomy

Notes: Traditional taxonomy refers to morphological species identification only. Integrative taxonomy combines morphology with molecular evidence (e.g. DNA sequencing) to support species delimitation and identification.

2.4. Quality Assessment and Limitations

The methodological quality of each publication was evaluated based on sample size, identification accuracy, and clarity of host-mite association. Studies relying solely on morphological identification without voucher specimens or molecular validation were considered to have low reliability, whereas those combining morphology and genetics were classified as highly reliable. It is important to note that no quantitative meta-analysis was performed because of the heterogeneity of the data formats, inconsistent reporting of abundance, and descriptive nature of most studies. Nevertheless, the narrative synthesis presented here offers the first consolidated overview of acarological research in the RC and serves as a foundation for future comparative and experimental studies.

3. Results

3.1. Diversity of Mites

All validated records of plant-inhabiting mites were then synthesised in a summary table (**Table 1**), which lists for each species its family, scientific name, main host plants, known localities in the RC, key references and the method used for identification.

3.1.1. Tetranychidae

A study conducted by Gutierrez & Bonato (1994) on cassava (*M. esculenta*) in several localities in the RC revealed a remarkable diversity of spider mites (Tetranychidae), which was previously underestimated in this region [8]. Seven species belonging to four genera were identified: *M. progresivus*, *Tetranychus kanzawai*, *Tetranychus neocaledonicus*, *Tetranychus sayedi*, *O. gossypii*, *Oligonychus coffeae*, and *Eutetranychus cratis*. These findings formed the basis of acarological knowledge in the country for nearly three decades. Recently, a study [17] confirmed these species and reported, for the first time, the occurrence of *Eutetranychus orientalis* on cassava in Brazzaville, thereby increasing the number of confirmed species associated with this crop to eight. In addition, the European and Mediterranean Plant Protection Organization database lists [18] *Tetranychus evansi*, a highly polyphagous species known to infest Solanaceae species, such as tomato, chili, and eggplant, as present in RC. In addition, Migeon (2015) reports records from the Jean Gutierrez spider mite collection [19]. Considering this record, the total number of Tetranychidae species known in the RC is currently twelve, when all cultivated hosts are considered.

3.1.2. Phytoseiidae

Acarological studies conducted in the RC have led to the identification of several species belonging to the family Phytoseiidae, which are associated with various host plants, particularly cassava (*M. esculenta*). Six species have been reported in the literature and confirmed in the regional database [20]: *Amblyseius sundi* Pritchard & Baker, observed in Odziba; *Euseius neodossei*, recorded without de-

tails on the host or locality; *Euseius fustis*, collected on cassava in the Brazzaville and Loudima areas; *Euseius baetae*, for which synonymy with *Euseius kangwanensis* has been proposed; *Typhlodromalus saltus*, found on cassava in Loubomo; and the Mayombe region and *Typhlodromalus aripo* found on cassava in Brazzaville. These records mainly originated from the works of Gutierrez & Bonato (1994) and Moraes *et al.* (1989-2001), which contributed to refining the distribution and narratives of the Central African Phytoseiidae [10] [21].

The mite species recorded between 2020 and 2022 included *A. swirskii*, *Amblyseius* spp., *E. fustis*, *Iphiseius degenerans*, *Paraphytoseius horrifera*, and *Phytoseius amba*. Mites were collected from cassava (*M. esculenta*), tomato (*Solanum lycopersicum*), aubergine (*Solanum melongena*), okra (*Abelmoschus esculentus*), and chili (*Capsicum* spp.). For example, *A. swirskii* was mainly found on tomato, chili, cassava, and okra; *E. fustis* was found exclusively on cassava; *I. degenerans* was present on chili, okra, cassava, and aubergine; and *P. horrifera* and *P. amba* were mostly associated with aubergine and okra.

3.2. Identification Methods

The identification of spider mites belonging to the family Tetranychidae and Phytoseiidae collected in the RC was based on a combination of morphological characteristics observed under a compound microscope at high magnification (400 - 1000×).

3.2.1. Morphological Characteristics of Phytoseiidae

Mites of the family Phytoseiidae, which are natural predators of Tetranychidae, exhibit distinct morphological traits that are adapted to predation. Their bodies are oval, translucent, and covered by a single dorsal shield bearing a set of setae, the number, presence or absence of certain pairs, and relative length, which are essential diagnostic features. A detailed examination of the dorsal and ventral chaetotaxy provides key taxonomic information, as some species are characterised by the absence or reduction of setae, such as z6, s6, or r3. The structure of the ventral shield, which can be subtriangular or pentagonal in shape, also varies among species in terms of size, ornamentation, and number of setae. Additional diagnostic characteristics include morphology of the spermatheca (shape of the vesicle, canal, and atrium), dentition of the chelicerae (usually one to three teeth on the movable digit), and chaetotaxy of the legs. Species records from the RC, such as those of *A. sundi*, *E. fustis*, and *T. saltus*, primarily rely on a combination of morphological traits, particularly the arrangement and relative length of the dorsal setae, structure of the ventricular shield, and shape of the spermatheca.

3.2.2. Morphological Characteristics of Tetranychidae

These phytophagous mites are typically small (0.2 - 0.6 mm), with oval, finely striated bodies and colours ranging from yellowish green to reddish-brown, depending on the host plant and physiological state. The diagnostic criteria include the arrangement and shape of the dorsal setae, structure of the empodium (simple,

claw-like, or with several rays), and configuration of the peritremes, which may terminate in a loop or hook. The dorsal striation pattern, number and position of the dorsal setae (vi, ve, sci, sce, c1, c2, d1, e1, f1, and h1), and the structure of the genital plates are key features for distinguishing these species.

In female specimens, the ornamentation of the dorsal integument, configuration of the genital area, and shape of the peritreme are particularly useful for differentiating genera such as *Tetranychus*, *Oligonychus*, *Mononychellus*, and *Eutetranychus*. In the congolese fauna, species such as *M. progresivus*, *T. neocaledonicus*, and *O. gossypii* have been identified primarily based on their morphological features [8]. The combination of dorsal chaetotaxy, empodium morphology, and peritreme structure remains the most reliable set of morphological criteria for identifying Tetranychidae species found on cassava and other host plants in RC.

3.3. Limitations and Observations

Despite recent progress, research on plant-inhabiting mites in the RC remains scarce, sporadic, and geographically restricted, mainly to the southern departments (Brazzaville, Pool, and Plateaux). Most studies have been short-term and have focused on only a few key crops. Moreover, molecular tools remain underutilised, and no national reference collection has yet been established.

4. Discussion

Acarological research in the RC has evolved substantially over the past four decades, progressing from the early descriptive inventories of the 1980s to a more integrative and biodiversity-oriented phase since 2020. The pioneering work provided the first detailed account of plant-inhabiting mites in the country, focusing mainly on cassava (*M. esculenta*), a major subsistence crop [8]. Morphological surveys identified seven species of Tetranychidae and three species of Phytoseiidae (*E. fustis*, *A. sundi*, and *T. saltus*), providing a foundation for congolese acarological taxonomy. Later revisions [20] expanded this faunal list to include *E. baetae* and *E. neodossei*, whereas recent investigations [11] [22] confirmed six Phytoseiidae species on cassava and associated crops in the Brazzaville region. Collectively, these findings illustrate a gradual transition from morphology-based inventories to integrative approaches that combine morphological and molecular diagnostics.

During the 1980s and 1990s, the morphological approach represented the global standard for mite identification. However, this methodology has intrinsic limitations, particularly in distinguishing between cryptic and morphologically similar species. A pioneering molecular study [9] on *M. progresivus* marked a turning point in African acarology, revealing intraspecific genetic variation and partial reproductive isolation among its populations. Although this study did not specifically address congolese fauna, it established a methodological framework for future molecular studies in the region.

Following this foundational phase, acarological research in the RC entered a hiatus of nearly two decades (1994-2020). The absence of publications during this period reflects the discontinuity of local research programs and limited institutional support for taxonomic and biodiversity studies. It was not until the early 2020s that new surveys revitalised the field, emphasising biodiversity assessments, integrative taxonomy and applications in biological control. Recently, Belle Mbou Okassa *et al.* (2020-2025) [11] [22] refined the inventory of predatory mites on cassava and confirmed the presence of six Phytoseiidae species (*E. fustis*, *A. sundi*, *T. saltus*, *E. baetae*, *E. neodossei*, and *I. degenerans*). Parallel analyses updated the Tetranychidae fauna and identified *M. progresivus* and *O. gossypii* as the most prevalent phytophagous species on *M. esculenta*.

The advent of molecular biology in taxonomy has marked a major breakthrough in species identification, particularly since the pioneering work of Hebert *et al.* (2003), who introduced DNA barcoding as a reference approach to molecular narratives [23]. In acarology, the use of molecular tools has greatly contributed to resolving complex taxonomic issues, such as the validation of new species [24], and improvements in diagnostic reliability through their ability to distinguish interspecific differentiation from intraspecific variability [25]. In the congolese context, only one study has explored the potential of molecular barcoding to clarify the taxonomic status of specimens belonging to the genus *Euseius*. However, the reliability of molecular diagnoses strongly depends on the completeness and accuracy of reference databases, which remain limited for many mite taxa. This is the first study to use an integrative taxonomy approach, combining molecular analyses based on 12S rRNA and ITS gene sequences with morphological characterisation, and provides the first genetic characterisation of congolese populations of species belonging to the genus *Euseius* [11].

The faunal composition revealed by recent surveys highlights the strong biogeographical connections linking the mite communities of the RC to those of neighbouring Central African countries. Several dominant species recorded in RC, such as *M. progresivus*, *E. fustis*, and *A. sundi* are also prevalent in Cameroon, Gabon, and the Democratic Republic of Congo. This distribution pattern suggests that many species exhibit a pan-equatorial range, reflecting similar climatic conditions and widespread cultivation of cassava and other tropical crops.

M. progresivus is recognized as the primary mite pest of cassava in Central Africa and is associated with significant agronomic losses [8] [16]. Field studies have shown that infestations can reduce cassava productivity by altering dry matter allocation to storage roots, even when foliar damage appears moderate [16], with reported yield losses ranging from approximately 13% to more than 80% under severe outbreaks. *Oligonychus gossypii* is another phytophagous mite of agronomic relevance in congolese agroecosystems, infesting cassava as well as cotton and vegetable crops [8] [15] [16]. Its feeding activity causes chlorosis, premature leaf senescence, and reduced photosynthetic capacity, and recurrent infestations suggest a contribution to cumulative yield losses under favourable conditions [14]

[16].

The recent detection of *E. orientalis* in Brazzaville is noteworthy. Originally native to Asia and the Middle East, this polyphagous species has expanded across Africa and the Mediterranean Basin in recent decades. Its occurrence in the RC likely represents a recent introduction or range extension, possibly facilitated by the regional trade of citrus and ornamental plant. Given its polyphagy and defoliation potential, *E. orientalis* warrants monitoring as an emerging pest in the Congolese horticultural system.

Conversely, the relatively high diversity of Phytoseiidae, particularly within *Euseius* and *Amblyseius*, reflects favourable ecological conditions for predatory mites in humid tropical environments. These taxa are known for their adaptability to diverse microhabitats, tolerance of pollen-based diets, and persistence during periods of low prey density. Their consistent occurrence on cassava and solanaceous crops indicates a strong potential for the natural regulation of Tetranychidae populations, which merits confirmation through field-based studies on predator-prey interactions.

Overall, these findings provide a comprehensive overview of the current state of acarological research in the RC. They highlight both the scientific progress achieved and the persistent challenges that must be addressed. The transition toward integrative taxonomy represents a decisive step forward, aligning local acarological studies with international standards and providing a foundation for sustainable pest management and biodiversity conservation across Central African agroecosystems.

Perspectives

Future research in acarology in the RC should focus on three complementary axes: expanding taxonomic knowledge, strengthening molecular identification tools, and establishing scientific networks dedicated to mite biodiversity. In particular, large areas of northern Congo remain virtually unexplored from an acarological perspective, and baseline surveys in these regions would substantially improve current knowledge of species distributions and host associations.

From a methodological perspective, the generalization of DNA barcoding approaches [23] represents a major advance in improving the reliability of taxonomic diagnostics and resolving the morphological ambiguities that remain common among Phytoseiidae and Tetranychidae. Since the late 2000s, several studies have defined genetic divergence thresholds that serve to distinguish intra- from interspecific variation in mites. For Phytoseiidae, analyses based on mitochondrial genes such as COI and 12S rRNA have shown that intraspecific divergences are generally below 2%, while interspecific divergences often exceed 8% - 12%, confirming the existence of a barcoding gap that can be used for species delimitation and molecular diagnosis [11] [24]-[27]. Priority should be given to genera already reported from the country and suspected to include cryptic species complexes, such as *Euseius*, *Typhlodromalus* and *Amblyseius* among Phytoseiidae, and *Mononychellus*, *Oligonychus* and *Tetranychus* among Tetranychidae. These thresholds now

represent key benchmarks for the molecular validation of species boundaries.

However, the performance of DNA barcoding strongly depends on the completeness and quality of reference databases used for sequence comparison. Insufficient taxonomic or geographic coverage can lead to misidentifications or ambiguous assignments, thus limiting the ecological interpretation of results [28] [29].

In this context, the establishment of regional barcode libraries integrating morphologically validated and georeferenced specimens is a priority. As emphasized by [30] the effectiveness of barcoding depends not only on the number of available sequences but also on their traceability, the quality of associated metadata, and the inclusion of voucher specimens preserved in reference collections. Such an approach would ensure the reproducibility of analyses and enhance comparability among laboratories.

The creation of a national reference database for the acarofauna of the RC would therefore represent a strategic step forward. This database could rely on standardized gene sequences (COI, 12S rRNA, ITS) obtained from local populations, coupled with detailed morphological and ecological data. Ultimately, such an infrastructure would help fill existing gaps in international databases like BOLD [31] or GenBank [32] where African fauna remains largely underrepresented.

Finally, the development of training programs and regional collaborations involving congolese institutions, African research centers, and international partners is essential to ensure the sustainability of these initiatives. Strengthening expertise in integrative taxonomy, bioinformatics, and molecular biology will anchor congolese acarology within global biodiversity research networks. In the short term, these efforts would primarily support accurate species identification and biodiversity assessment, while in the longer term they would provide a robust framework for ecological studies and sustainable pest management strategies.

In summary, the combination of morphological, molecular, and ecological approaches, supported by reliable databases and strong institutional partnerships, will pave the way for a deeper understanding and sustainable management of phytophagous and predatory mites in Central African agroecosystems.

5. Conclusions and Recommendations

Over the past four decades, acarological research in the RC has progressed from descriptive inventories to integrative studies combining morphology and molecular tools. The synthesis of available data revealed 22 species of plant-inhabiting 10 mites of Phytoseiidae and 12 of Tetranychidae mainly associated with cassava and other economically important crops. Among these, *E. fustis* and *I. degenerans* have emerged as key predatory species with potential applications in biological control, whereas *M. progresivus* remains the dominant phytophagous pest.

Despite these advances, significant gaps persist, particularly regarding the northern and central regions of the country, molecular phylogenetic data, and long-

term monitoring of predator prey dynamics. Strengthening acarological research will require the establishment of specialised laboratories, the development of reference collections, and training of new experts in integrative taxonomy. Beyond its agronomic implications, studying mites in the RC contributes to a broader understanding of tropical biodiversity and ecosystem functions. By linking taxonomy, ecology, and applied research, acarology can play a pivotal role in promoting sustainable pest management and biodiversity conservation in Central African agroecosystems.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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