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Diversity of praying mantises (Mantodea) of Mbalmayo Region, Cameroon, with DNA barcoding and morphological data

MASTER'S THESIS

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Declaration

I hereby declare that I have done this thesis entitled “Diversity of praying mantises (Mantodea) of Mbalmayo Region, Cameroon, with DNA barcoding and morphological data” independently, all texts in this thesis are original, and all the sources have been quoted and acknowledged by means of complete references and according to Citation rules of the FTA.

In Prague 22.04.2022

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Valeriy Govorov

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Abstract

Praying mantises (Mantodea) is an order of predatory insects with about 2500 described species. The highest diversity is accumulated in tropical regions, and one of richest is in equatorial Africa. It is likely linked to Congo Basin rainforest, second largest contiguous zone of lowland moist forests of the planet. One of the countries of Congo Basin with high species densities is Cameroon, however, the region is generally overlooked for insect diversity, especially Mantodea. In this study, we evaluated the diversity of praying mantises in south of Cameroon, using morphological and molecular means of identification. A total of 40 species was recovered using traditional taxonomic method, with 10 newly recorded for the country and 3 are probably undescribed. Analyzing of COI gene and comparison of barcodes with existing libraries in GenBank and BOLD supported morphological identification in more than 60% of the samples, others being either potential new taxon or species not present in the libraries. Direct comparison of obtained barcodes with sequences from neighboring CAR and Gabon using maximum likelihood phylogenetic trees and pairwise distances point out possible populations' structures in *C. caudata*, *M. preussi*, *S. ziela* and *O. sigma*, while revealing blank spots in known biology and ecology of *Chrysomantis* and *Panurgica*. DNA barcodes could be useful in examination of groups with complicated taxonomy, as well as in identification of immature individuals.

Key words: barcoding, biodiversity, Cameroon, Mantodea, morphology

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COI	cytochrome c oxidase subunit I
CAR	Central African Republic
PCR	polymerase chain reaction
BOLD	Barcode of Life Data System
DNA	deoxyribonucleic acid

1. Introduction and Literature Review

1.1. Introduction

Mantodea is an order of predatory insects, currently consisting of about 2500 valid species (Otte *et* al. 2005) in 29 families. Their peculiar morphological adaptation of raptorial front legs for grabbing and retaining the prey, as well as sit-and-wait hunting tactic make these insects charismatic and well-recognizable.

Figure 1. Typical appearance of a praying mantis, *Tismomorpha vitripennis* (Bolivar, 1908)

Despite the distinctive appearance (Fig. 1), the group remains understudied. The early studies (Thunberg 1815, Saussure 1872ab, Stål 1877, Giglio-Tos 1927, etc.) attempted to assess the taxonomic diversity of the group focused exclusively on external morphology. This approach proved to be inaccurate, as some of the taxa, living in the same ecological conditions, developed similar traits as a case of convergent evolution.

Starting (Chopard) 1920, in addition to habitus morphology, male genitalia structure was used. It allowed to correct previous taxonomical consensus, notably splitting some of the visually similar taxa with completely different geographical origins. In addition to traditional taxonomical means of identification, in recent decades it became possible to conduct molecular analyses of the specimens. Relatively widespread methodology of sequencing the conservative segment of the mitochondrial gene cytochrome c oxidase subunit 1 (COI) opened, among others, the possibility for detection of cryptic species. Despite being a popular modern approach for examining biodiversity, it remains seldomly used for Mantodea, with just a handful publications dealing with it (Moulin 2017, Moulin & Roy 2020, Varela-Hernández *et* al. 2022).

Praying mantises are widely distributed around the world, however, the highest diversity is accumulated in tropical regions. One of the hotspots are rainforests of equatorial Africa, with roughly 1000 species recorded. Being one of the biggest blocks of rainforest, only surpassed by the Amazon basin (UNEP 2008), Central African forests remain relatively undisturbed. They serve as a host for a substantial percentage of worldwide biodiversity, as well as an irreplaceable part of climate regulation. Better understanding and deepening existing knowledge of natural mechanisms within this vast but fragile region are closely interconnected with surveying the biodiversity of different groups of organisms. As praying mantises play an important role as consumers, recognizing their species diversity would contribute to further understanding of the ecosystem flow of the region.

1.2. Literature Review

1.2.1. Praying mantises of Central African subregion

Biodiversity of Mantodea in some countries of the Central African subregion was assessed starting from the end of previous century.

Roy (1972) provides a comprehensive categorization of praying mantises of Gabon. Extensive material was collected since 1962 by Biological Mission in Gabon, and was combined with earlier, less voluminous sample collection efforts, deposited in National Museum of Natural History in Paris, dating as far back as 1863. Collection sites were situated in forested areas of the country, such as Oyem, Libreville, the Monts

de Cristal. Roy reports 77 collected species of 4 families and 42 genera, out of which 25 species are considered endemic to central-western forest sector, a portion of rainforests constrained by lower course of the Niger River, the lower courses of the Congo River and the tributary of the Oubangui river. The forest sector is especially diversified in Mantodea because broad rivers with fixed course create an impassable obstacle for the majority of species, as most adult females are not capable of long flights. In addition, overcoming such obstacles would mean exiting the favorable forest environment. Above mentioned collection efforts resulted in a considerable representation of Mantodea fauna of rainforests of Gabon; however, Roy (1972) suggests, that further research should be pursued in savannah biomes. Additionally, since the main collecting method was attracting the insects to a light trap, most of the specimens were adult males. Combining this method with manual collection and vegetation sweeping can greatly enhance the catch rate of females and nymphs, and would further improve the understanding of the ecology, behavior and taxonomy in praying mantises of the region.

Next study of biodiversity of Mantodea of Central African subregion was conducted more recently by Tedrow *et* al. (2015). The research was focused on several national parks of Rwanda. Four locations included several distinct habitats: mountain rainforests in Nyungwe National Park; savannahs, wetlands and mountains in Akagera National Park; elevated forest with closed and open canopies in Volcanoes National Park and semi-artificial environment of monoculture plots in Arboretum de Ruhande. Large variety of microhabitats allowed the researchers to sample the biodiversity more thoroughly, resulting into 41 collected species of 9 families and 28 genera. Sampling methods included vegetation sweeping, manual collection and light trapping. Authors also note that a few species of genus *Miomantis* were abundant at almost all sampling sites, owing to their relatively high habitat plasticity, while other taxa, such as *Idolomorpha* and *Oxyelaea* were sampled at lower numbers and in isolated localities. Several taxa were not identified to species level, such as *Compsothespis*, *Galepsus* and *Polyspilota*. Tedrow *et* al. pointed out the necessity of taxonomical revision of these groups, requiring more sampling efforts in Rwanda and neighboring regions.

Research carried out by Moulin *et* al. (2017) is the only published material dealing with barcoding of the diversity of Mantodea in Central Africa. Sampling was conducted a part of the territory of the Sangha Tri-National UNESCO World Heritage

Site in the Central African Republic (CAR), including the special forest reserve of Dzanga-Sangha, the Dzanga-Ndoki National Park. The region is covered in rainforests, with two main types: dryland forest with open and mixed canopy and semi-evergreen swamp-forest areas along the rivers with closed canopy formations. Being a refuge for local rich biodiversity, it is a subject for scientific investigations. Authors report the diversity of Mantodea of the region based on the collection efforts dating since 1984. While some of the material could not have been examined due to poor storage conditions, the team covers all species found throughout the decades of collecting trips. They also point out imperfections of systematics of some taxa, such as *Cataspilota*, *Plistospilota*, *Miomantis*, *Entella*. In addition to examining existing museum material, scientists organized several trips to Dzanga-Ndoki National Park. Collecting methods included traditional light trapping using mercury vapor bulbs, sweeping vegetation and manual search, and were complimented by visual collecting while climbing trees, remote canopy trap and aerial interception trap. Wide selection of collection techniques allowed for capture of specimens from different microhabitats, as well as nymphs and females, which are not usually attracted by light. Selected 171 samples were subject to DNA extraction, polymerase chain reaction (PCR) and sequencing. Analysis of standardized segment of the mitochondrial cytochrome c oxidase subunit I (COI) gene was performed. Resulted data were submitted and being managed at Barcode of Life Database (BOLD, Biodiversity Institute of Ontario, Canada; boldsystems.org). Sequences were used to build phylogenetic trees. The authors' efforts resulted into 94 sequences from 119 specimens, the genetic information was found to be in accordance with species limits accepted by traditional taxonomy. In total, 71 species in 36 genera of 7 families were listed for Sangha-Mbaere region and by extension for CAR. DNA barcodes obtained allowed the establishment of an irreplaceable reference database for future research. Several years later, Moulin (2020) published a description of a new cryptic species of *Chlidonoptera*, collected at the same site in Dzanga-Sangha Special Reserve, CAR. The new lineage was uncovered by DNA barcoding, reiterating the importance of this method, coupled with traditional taxonomical approaches. New species is distinguished by, aside from barcoding analysis, a larger size, genitalia morphology and isolated geographical location.

State of the diversity of praying mantises in Gabon was updated by Moulin (2018), based on unpublished collection data and new field collections. The checklist of

species from the original publication by Roy (1974) was complemented by studying contributions to National Museum of Natural History in Paris, as well as material from several entomological surveys carried out over the last 20 years in different localities of the country. The current faunistic record is comprised of 112 valid species, while the classification was updated according to current consensus.

1.2.2. DNA barcoding in biodiversity assessment and identification

DNA barcoding is a popular tool for evaluation of biodiversity and improving taxonomy of the studied group. It can also give an important set of tools for species identification and has gained a strong interest on the international level with the foundation of such project as Barcode of Life Data System (https://www.boldsystems.org). Although having its drawbacks (Moritz & Cicero 2004), barcoding promises to be of significant help to the Central African scientific community because of its utility as a rapid identification tool and ability to indicate specimens that require more taxonomic investigation.

Barcoding already has a reputable track record in research dedicated to Central African biodiversity. For example, Jordaens *et* al. (2015) worked on assessing Afrotropical hoverflies (Insecta: Diptera: Syrphidae), a taxonomically difficult group with very limited recent revisions. Identification keys are not present for most of the Afrotropical Syrphidae, and for the existing ones, it was estimated that approximately 60% of the known fauna could be keyed out. This is connected with the number of species in one genus, the higher the number, the greater the chance the key will not work. Producing an updated identification key is complicated by original descriptions being too brief or vague, sometimes only one sex is described. Current identification tools based solely on morphology are insufficient for Afrotropical hoverflies, therefore the authors suggest creating a more accurate identification system based on molecular analysis. A total of 513 out of 640 individuals collected at various sites in Ghana, Togo, Benin and Nigeria were sequenced. The success rate of about 80% is explained by the imperfect condition of some samples: they were dried and pinned, some were older than 10 years, which allowed the DNA to degrade significantly. As the authors point out, the best option for preserving samples for further DNA extraction is to store them in ethanol. As a result, it was possible to identify 90 Afrotropical hoverfly species using

DNA barcoding. The database covers just a portion of the extensive diversity of hoverflies in the region (more than 600 species described), but it serves as an important reference for future studies and may boost the taxonomic research of the group.

Another example of successful implementation of DNA barcoding in research is shown by Deichmann *et* al. (2017). In the course of investigating the potential impacts of road development projects on local anuran community in the buffer zone of Moukalaba-Doudou National Park, Gabon, the team encountered difficulties with morphological identification of amphibian species because of their taxonomic uncertainty. To improve quality and accuracy of species inventory, a DNA barcoding library was created based on samples collected in field (Nyanga Province, Gabon) and reference specimens from the collection of the United States National Museum. Reference specimens consisted of amphibian fauna of Gabon, as well as neighboring Republic of Congo. DNA sequence data was obtained from 540 specimens and resulted into 72 species of anurans of 21 genera in 12 families. Sequences were compared with the existing ones in GenBank and were deposited there as well as to the BOLD database. In addition, species richness estimations were produced via sample-based rarefaction curves. The verification of species identification in the field using molecular analysis demonstrated that relying only on data from morphological assessment would overestimate the species diversity by approximately 70%. DNA barcoding allowed the team to reveal the errors and make corrections to the species richness variable. The authors also point out that barcoding should be used together with other types of data e.g., with collection specimens and tissue samples with lasting and detailed records, as well as audio recordings. The reference library created is an important tool for reduction of the number of errors in future studies.

Barcoding can be an irreplaceable tool in situations when traditional taxonomical methods are of little use. In case of Mantodea, identification using morphology is only reliable when adult individuals are used. Nymphs may possess underdeveloped body characters important for identification e.g., wings, body coloration, while oothecae of different taxa may look identical and are in general almost never described. However, Wang *et* al. (2015) applied the barcoding technique in an attempt to identify the species to which the oothecae belonged to. Based on the obtained COI sequences, they uncovered 4 species of praying mantises commonly used in

traditional Chinese medicine. This research is particularly intriguing, as ootheca identification is a rather complicated endeavor, requiring special export and import permits, incubation of the clutch, rearing the nymphs till imago and, finally, applying traditional identification. Sequencing the DNA of ootheca and comparing the result with existing database might be a better solution in this case. Scherrer (2014) used same approach in his revision of *Miobantia*, a genus of Thespidae family, notoriously known for its high levels of sexual dimorphism and most species known only by one sex, usually male. Scherrer barcoded the DNA of a representative selection of 923 specimens studied and attempted to associate the females and nymphs with their corresponding conspecific males. In the analysis, first he calculated intra- and interspecific genetic distances for males only, and then used all sequenced males, females and nymphs to calculate pairwise distances. Achieved associations allowed to identify the expected limits of morphological variation among dimorphic sexes and permitted a more confident morphological investigation. The author notes that while his association of males, females and immature stages was successful, it may not be as effective with a smaller sample size or with missing species.

1.2.3. Congo Basin rainforests

Diversity of Mantodea in Central Africa was investigated by just a handful of abovementioned publications. Nevertheless, it is estimated to house around 1000 species of praying mantises (Tedrow *et* al. 2015). Rich diversity is most likely connected to the Congo Basin forests of Central Africa the world's second largest contiguous zone of lowland tropical moist broadleaf forests, surpassed only by Amazon. These forests (Fig. 1), located approximately 7° south and north of the equator, cover a massive expanse of over 180 million ha, distributed unevenly among six Central African countries: Cameroon, the Central African Republic, the Republic of Congo, Equatorial Guinea, Gabon, and the Democratic Republic of Congo. The Congo Basin forests account for roughly 20% of the world's remaining tropical rainforest (UNESCO 1978, Justice et al. 2001), as well as 70% of the continent's total plant cover (CBFP 2005, CBFP 2006).

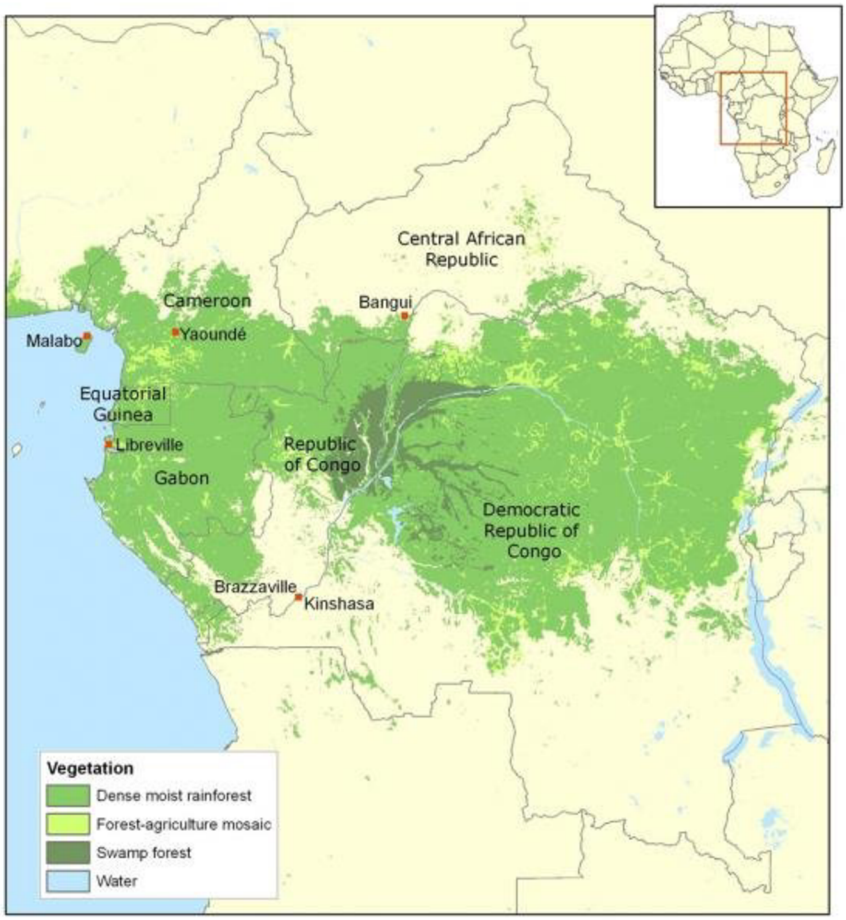

Figure 1. Map of Congo Basin rainforests. Source: World Resources Institute

Despite seeming immenseness, Congo Basin forests are vulnerable to global changes in climate, which are predicted to have a major impact on the region's biota. Increasing temperatures and shifting precipitation patterns have the potential to amplify the negative consequences of land use change, alter natural disturbance regimes, and decrease the availability of sufficient habitat for forest biota (Boko *et* al. 2007, Abernethy *et* al. 2013; James *et* al. 2013). Although it has been claimed that Congolese forests are particularly resistant to severe drought (Asefi-Najafabady & Saatchi 2013), recent research reveals that a persistent drying trend will reduce photosynthetic capacity and lead to changes in plant community composition (Zhou *et* al. 2014). According to ecological niche modeling research, if the average global temperature rises by 1.5°C, 30 percent of plant and animal species will become extinct (Thomas *et* al. 2004). Drastic changes to the environment and to species diversity call for intensification of faunistic research to better plan conservation programs. With rapid advances in sequencing

methods, more reliable multilocus phylogenies of many species groups are becoming more attainable. Robust molecular phylogenies not only help clarify the taxonomy of threatened species (http://www.iucnredlist.org/) but also facilitate species listings for monitoring and planning (Mace 2004), providing a complement to morphological assessment of poorly described taxa (Gotelli 2004). This information is essential especially in the tropics where many species lack formal description (Dick & Kress 2009, Janzen *et* al. 2009).

Sampling blind spots exist for many taxonomic groups across the Congo Basin due to the inaccessibility and political instability of this region. Detailed inventory data in particular are needed for many taxonomic groups that remain understudied, including invertebrates. Sample collection needs to cover gaps in existing inventories (Costello *et* al. 2013) and should be coordinated with biodiversity assessments both within and outside protected areas. Biodiversity inventories also need to gather geo-referenced data that can be linked to species records (Dayrat 2005).

Cameroon is one of the Central African countries on which biodiversity conservation in Africa should focus first (Doumenge 1998, Foahom 2001, Kamdem-Toham *et* al. 2006). It has one of the highest species densities of mammals (280 species) and vascular plants (9000 species) in Africa, and houses more than 40 globally threatened animals (Alpert 1993). Although few diversity studies were conducted, Cameroon also seems a biodiversity hotspot for insects. Despite brief mentions on distribution of about 155 species of praying mantises (Ehrmann 2002), research dedicated to Mantodea had never been conducted in Cameroon. The southern part of the country is located in Congo Basin, where aggressive deforestation degrades the ecological state of the region, making the exploration of the understudied biodiversity of any taxon an increasingly elusive task.

2. Aims of the thesis

We evaluated the diversity of Mantodea of the Mbalmayo region and produced for the first time a database of DNA barcodes of praying mantises of Cameroon.

We focused on following aims:

1. Identification of collected samples using diagnostic characters: external morphology, color patterns, morphology of the male genitalia.

2. Evaluation of the taxonomic identity of the samples by analyzing the conservative segment of the mitochondrial cytochrome c oxidase subunit I (COI) gene.

3. Review and assessment of the diversity of Mantodea of the area studied, by comparison of the resulting barcodes with the databases existing for neighboring countries (CAR, Gabon: Moulin *et* al. 2017; N. Moulin, unpubl. data).

3. Methods

Data collection was conducted in July-August 2021, in the village Ebogo II, south Cameroon, 3°23'15.8"N 11°27'59.8"E. Ebogo II is located in the northern part of the Congo Basin at an elevation around 650 m asl., with a mean annual temperature of 24.3°C. The landscape is relatively flat, with homogeneous natural conditions, originally covered by tropical rain forest. The rainfall, of about 1700 mm on an annual basis, is distributed mostly in two rainy seasons between March and June, and between September and October, respectively.

Most specimens were collected using a light trap, consisted of a white sheet illuminated by UV mercury vapor lamp OSRAM HWL (MBFT) 160W during the night. In addition, manual collection efforts were organized in surrounding forest, and included visual examination of vegetation, tree climbing and net sweeping. Insects were killed using ethyl acetate vapor jar, preserved in 80% ethanol or dried on cotton wraps.

Identifications follow the most recent taxonomical revision of the order (Schwarz & Roy 2019) and were done using dichotomous keys whenever available, in comprehensive monographs (Giglio-Tos 1927, Roy 1973) and dedicated taxon revisions (Roy 1967, 1996, etc.). Species that had no recent literature references were identified by studying their original descriptions (Rehn 1949, La Greca 1967, Roy 2010, etc.). When required, male genitalia were separated from the specimens, macerated in 10% KOH solution for 4–36 h and rinsed with water and ethanol afterwards. Prepared male genitalia are stored in microvials with glycerol together with corresponding specimens. External morphology and male genitalia were studied using Leica M205 C stereo microscope (Wetzlar, Germany). Photographs of the live specimens were made with Sony Alpha a6000 digital camera (Tokyo, Japan) and Sony SEL30M35 30mm f/3.5 macro lens.

DNA barcoding was performed for a representative number of specimens (n=45), by diversity and material quality criteria. DNA was extracted from tissue (meta- or mesothoracic leg) using DNEasy Blood & Tissue kit (Qiagen), the isolates were checked for quality and quantity on NanoDrop spectrophotometer. Samples with high DNA concentration (>20-25 ng/µL) were diluted with water until optimal concentration. PCR was done using COH6 (5'- TAD ACT TCD GGR TGD CCA AAR AAY CA -3')

and COL6b (5'- ACA AAT CAT AAA GAT ATY GG -3') primers (Mantellato *et* al. 2016), the thermal cycle and PCR composition are presented in Table 1 and 2 respectively. The amplified products were visualized in 1% agarose gel, purified using Gel / PCR DNA fragment extraction kit (Geneaid) and sequenced by capillary electrophoresis in Genetic Analyzer (Applied Biosystems, USA) with forward primer at Biology Section, Faculty of Science, Charles University. Raw sequences were edited in Geneious v10.2.6 (https://www.geneious.com) software and aligned by ClustalW approach (Thompson, Higgins & Gibson 1994) as implemented in Geneious. Resulted sequences in fasta format were blasted in GenBank using "Nucleotide BLAST" online tool and in BOLD version 4 "Identification" section.

Public DNA barcodes from samples collected in CAR (n=84) were obtained from BOLD. In addition, several unpublished sequences from Cameroon (n=10) and Gabon (n=6) were provided by Nicolas Moulin (Muséum national d'Histoire naturelle, Paris, France). Raw chromatograms were used for editing the sequences and aligned together with sequences from Ebogo II using same software tools as described above.

Table 1. Temperature cycling profile

Stage	Temperature, °C	Time, min	# of cycles
Initial denaturation	94	5	1
Denaturation	94	1	30
Annealing	55	1	
Extension	72	1	
Final extension	72	10	1

Table 2. PCR composition

Component	Volume, µl
DNA	2
COH6 forward primer (10 µM/ µl)	1
COL6B reverse primer (10 µM/ µl)	1
PPP mix (Top Bio)	12
Nuclease free water	9
Total	25

Pairwise distances and maximum likelihood trees were calculated in IQTREE 1.6.12 using following command:

"iqtree -s inalignment.fasta -bb 1000 -bnni -alrt 1000 -abayes -nt AUTO"

-s specifies input alignment file

-bb specifies number of bootstrap replicates (>=1000)

-bnni performs an additional step to further optimize UFBoot trees by nearest neighbor interchange (NNI) based directly on bootstrap alignments

-alrt specifies number of replicates (>=1000) to perform SH-like approximate likelihood ratio test (SH-aLRT)

-abayes performs approximate Bayes test

-nt specifies the number of CPU cores

The best model according to Bayesian information criterion was GTR+F+I+G4.

4. Results

4.1. Taxonomic checklist

A total of 45 specimens (8 families, 34 genera, 41 males, 4 females) were examined, with 40 species recovered using morphological identification and shown in a list below. Detailed list of species with label data and distribution is presented in Appendix 1. Photographs of most abundant species are shown on Fig. 2.

1. *Amorphoscelis grisea*
2. *Amorphoscelis lamottei*
3. *Bolivaroscelis carinata*
4. *Caudatoscelis caudata*
5. *Maculatoscelis ascalaphoides*
6. *Negromantis lutescens*
7. *Negromantis sp.*
8. *Tarachodes (Tarachodes) feae*
9. *Galepsus (Galepsus)* sp.
10. *Miomantis preussi*
11. *Sibylla (Sibylla) dolosa*
12. *Sibylla (Sibyllopsis) griffinii*
13. *Chlidonoptera vexillum*
14. *Chloroharpax modesta*
15. *Panurgica feae*
16. *Panurgica rehni*
17. *Chrysomantis cachani*
18. *Chrysomantis speciosa*
19. *Oxypiloidea (Catasigerpes) margarathae*
20. *Anasigerpes bifasciata*
21. *Dactylopteryx flexuosa*
22. *Theopompella aurivillii*
23. *Stenopyga (Stenopyga) extera*
24. *Stenopyga (Stenopyga) ziela*
25. *Deromantis limbalicollis*
26. *Omomantis sigma*
27. *Polyspilota aeruginosa*
28. *Polyspilota* sp.
29. *Plistospilota* cf. *P. maxima*
30. *Prohierodula laticollis*
31. *Prohierodula picta*
32. *Prohierodula viridimarginata*
33. *Cataspilota calabarica*
34. *Cataspilota lolodorfana*
35. *Alalomantis muta*
36. *Sphodromantis aureoides*
37. *Sphodromantis balachowskyi*
38. *Sphodromantis lineola pinguis*
39. *Sphodromantis* sp.
40. *Tismomorpha vitripennis*

Figure 2. Live habitus of common Mantodea collected in Ebogo II, Cameroon. A – *Alalomantis muta*; B – *Caudatoscelis caudata*; C – *Chlidonoptera vexillum*; D – *Negromantis lutescens*; E – *Anasigerpes bifasciata*; F – *Polyspilota aeruginosa*; G – *Progierodula laticollis*; H – *Miomantis preussi*; I – *Dactylopteryx flexuosa*

4.2. DNA barcodes

Obtained sequences (n=44, Table 3) are compared with traditional taxonomic identifications and existing barcodes libraries in GenBank and BOLD. Out of 38 species, 25 sequences matched with sequence in the database (i.e, the similarity percentage was >95±1%) with same taxonomical identification. In 3 cases, samples matched to correct genus level and 12 others returned results with obviously incorrect taxonomic reference, e.g., from other family and geographical location. In the latter case, the similarity percentage never exceeded 90%, so it was considered a mismatch.

Table 3. List of obtained DNA barcodes

Name of the sequence	Identification based on morphology	Similarity match with sequence from the database, %
GOV-1_Plistospilota_sp	*Plistospilota* cf. *P. maxima*	no match
GOV-2_Sphodromantis	*Sphodromantis lineola pinguis*	94.44
GOV-3_Prohierodula_laticollis	*Prohierodula laticollis*	98.16
GOV-4_Omomantis_sigma	*Omomantis sigma*	99.22
GOV-5_Alalomantis_muta	*Alalomantis muta*	99.84
GOV-7_Prohierodula_viridimarginata	*Prohierodula viridimarginata*	95.85
GOV-8_Prohierodula_picta	*Prohierodula picta*	96.36
GOV-10_Polyspilota_aeruginosa	*Polyspilota aeruginosa*	99.19
GOV-11_Polyspilota_black	*Polyspilota* sp.	100, match as *P. aeruginosa*
GOV-12_Cataspilota_sp	*Cataspilota lolodorfana*	97.28
GOV-13_Cataspilota_sp	*Cataspilota calabarica*	97.85
GOV-17_Anasigerpes_bifasciata	*Anasigerpes bifasciata*	100
GOV-18_Sibyllopsis_griffinii	*Sibylla (Sibyllopsis) griffinii*	no match
GOV-19_Chlidonoptera_sp	*Chlidonoptera vexillum*	99.09
GOV-20_Stenopyga_sp	*Stenopyga extera*	no match
GOV-21_Stenopyga_sp	*Stenopyga ziela*	95.79
GOV-22_Miomantis_preussi	*Miomantis preussi*	98.87
GOV-23_Deromantis	*Deromantis limbalicollis*	no match

GOV-24_Chloroharpax_modesta	*Chloroharpax modesta*	99.34
GOV-26_Negromantis_sp	*Negromantis* sp.	no match
GOV-27_Sphodromantis_sp_BF	*Sphodromantis* sp.	no match
GOV-29_Sphodromantis_sp	*Sphodromantis balachowskyi*	98.22
GOV-30_Tismomorpha_vitripennis	*Tismomorpha vitripennis*	98.37
GOV-32_Galepsus	*Galepsus (Galepsus)* sp.	no match
GOV-34_Panurgica_sp	*Panurgica feae*	no match
GOV-35_Panurgica_sp	*Panurgica rehni*	97.22
GOV-41_Chrysomantis_sp	*Chrysomantis speciosa*	match to genus
GOV-42_Amorphoscelis_sp	*Amorphoscelis grisea*	97.31
GOV-43_Amorphoscelis_sp	*Caudatoscelis caudata*	99.15
GOV-44_Maculatoscelis_sp	*Maculatoscelis ascalaphoides*	99.43
GOV-45_Amorphoscelis_sp	*Amorphoscelis grisea*	no match
GOV-48_Amorphoscelis_sp	*Amorphoscelis lammotei*	no match
GOV-50_Dactylopteryx_sp	*Dactylopteryx flexuosa*	88.99
GOV-51_Oxypiloidea_sp	*Chrysomantis cachani*	95.22
GOV-53_Amorphoscelis_nymph	*Bolivaroscelis carinata*	no match
GOV-56_Maculatoscelis_sp	*Maculatoscelis ascalaphoides*	99.34
GOV-57_Tarachodes_sp	*Tarachodes feae*	98.38
GOV-58_ Oxypiloidea_sp	*Chrysomantis cachani*	95.40
GOV-59_Stenopyga_nymph	*Stenopyga* sp.	no match
GOV-60_Theopompella_sp	*Theopompella aurivillii*	no match
GOV-61_Sphodromantis_aureoides	*Sphodromantis aureoides*	match to genus
GOV-62_ Oxypiloidea_sp	*Oxypiloidea (Catasigerpes) margarathae*	99.64
GOV-63_Sibylla_dolosa	*Sibylla (Sibylla) dolosa*	97.19
GOV-CL3_Negromantis_sp	*Negromantis* sp.	no match
GOV-CL5.1_Negromantis_sp	*Negromantis* sp.	no match

4.3 Phylogenetic trees and pairwise distances

Maximum likelihood trees were built using sequences from samples collected in Ebogo II and joined with available DNA barcodes from CAR, Cameroon and Gabon. Samples from subfamily Amorphoscelinae were used to root the main tree (Figure 3.1 and 3.2) as it is the most basal taxon available, while for subfamily Tenoderinae (Fig.4) *T. vitripennis* was used as an outgroup from Hierodulinae.

DNA barcodes obtained from Ebogo II samples are highlighted in red on figures 3.1, 3.2 and 4, targeted groups of sequences are numerated and commented in Discussion. Bootstrap supports are given in percent. Pairwise distances for all sequences used are presented in Appendix 2 on attached CD.

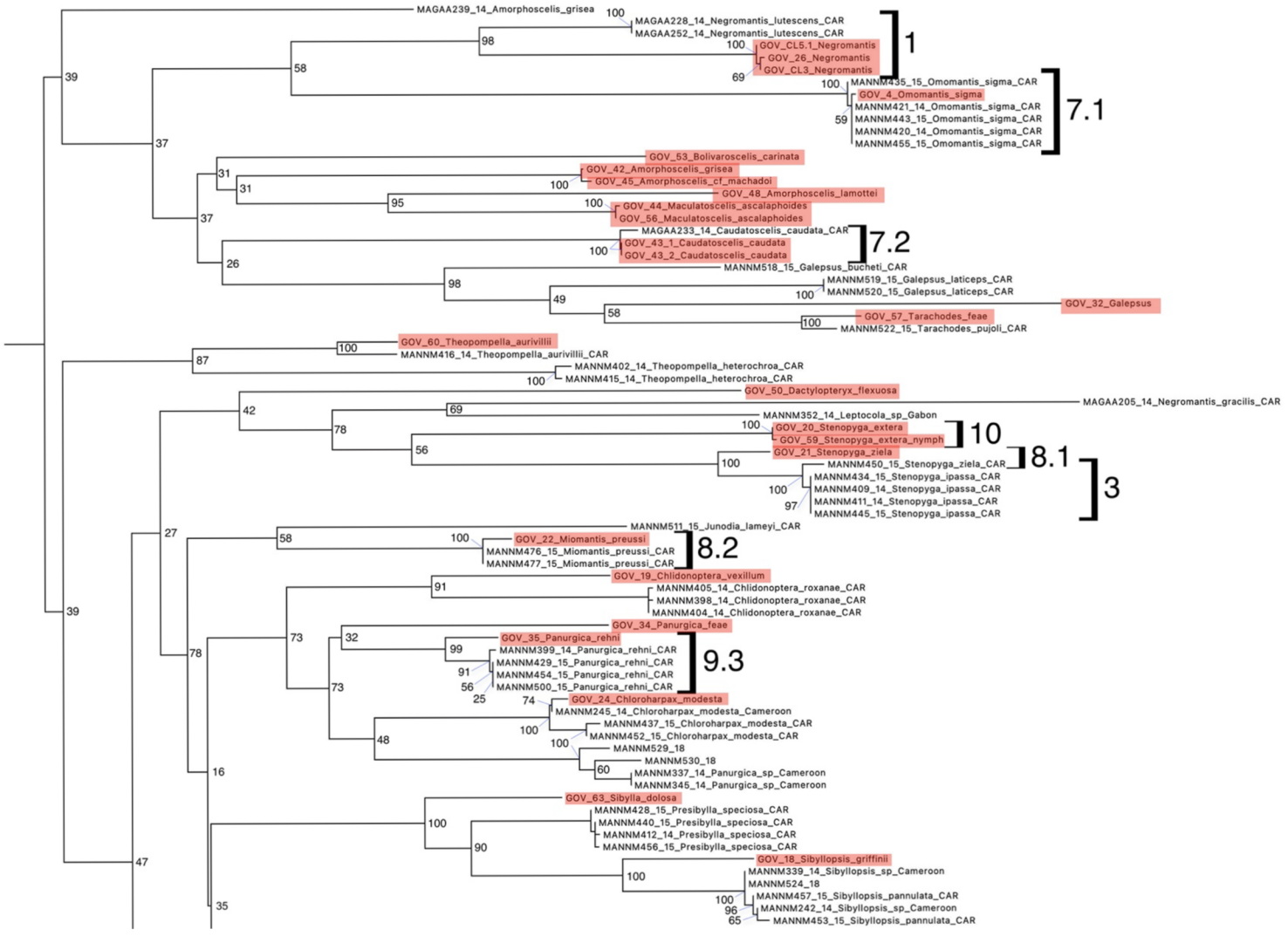

Figure 3.1. Maximum likelihood tree built using all available barcodes of Mantodea of Central African subregion.

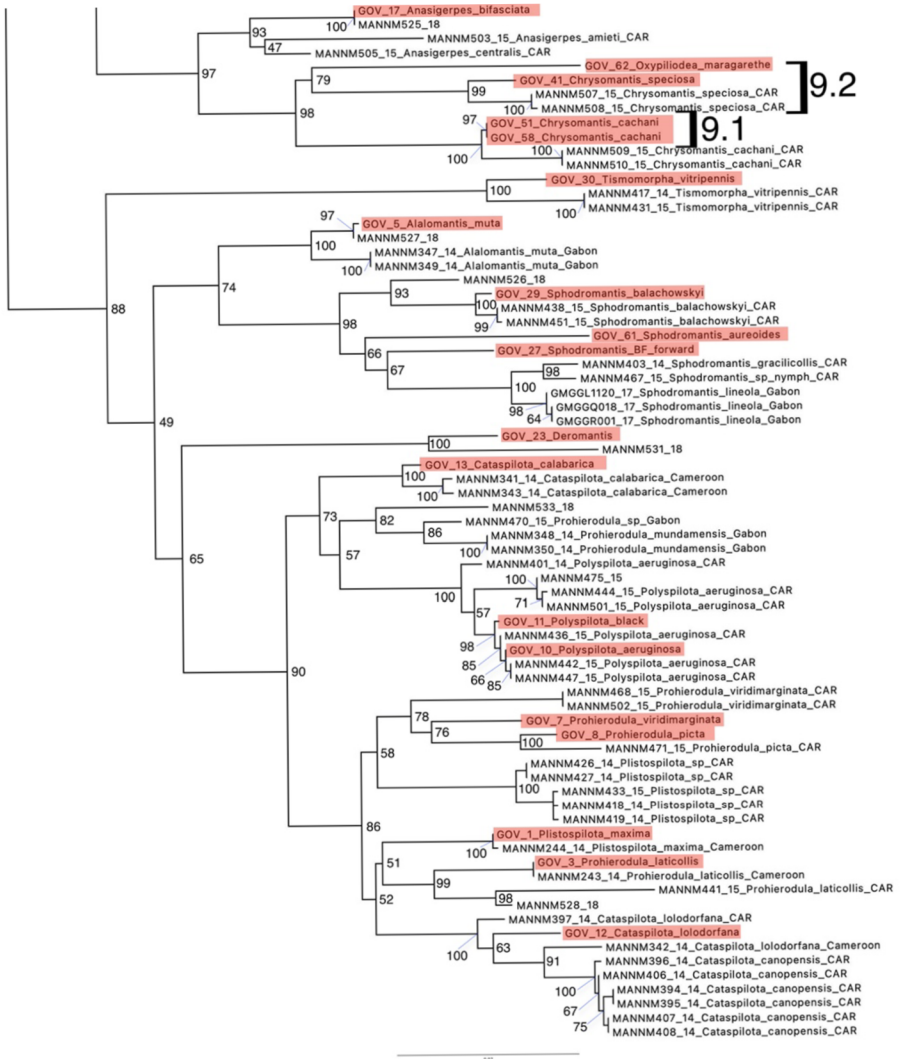

Figure 3.2. Maximum likelihood tree built using all available barcodes of Mantodea of Central African subregion.

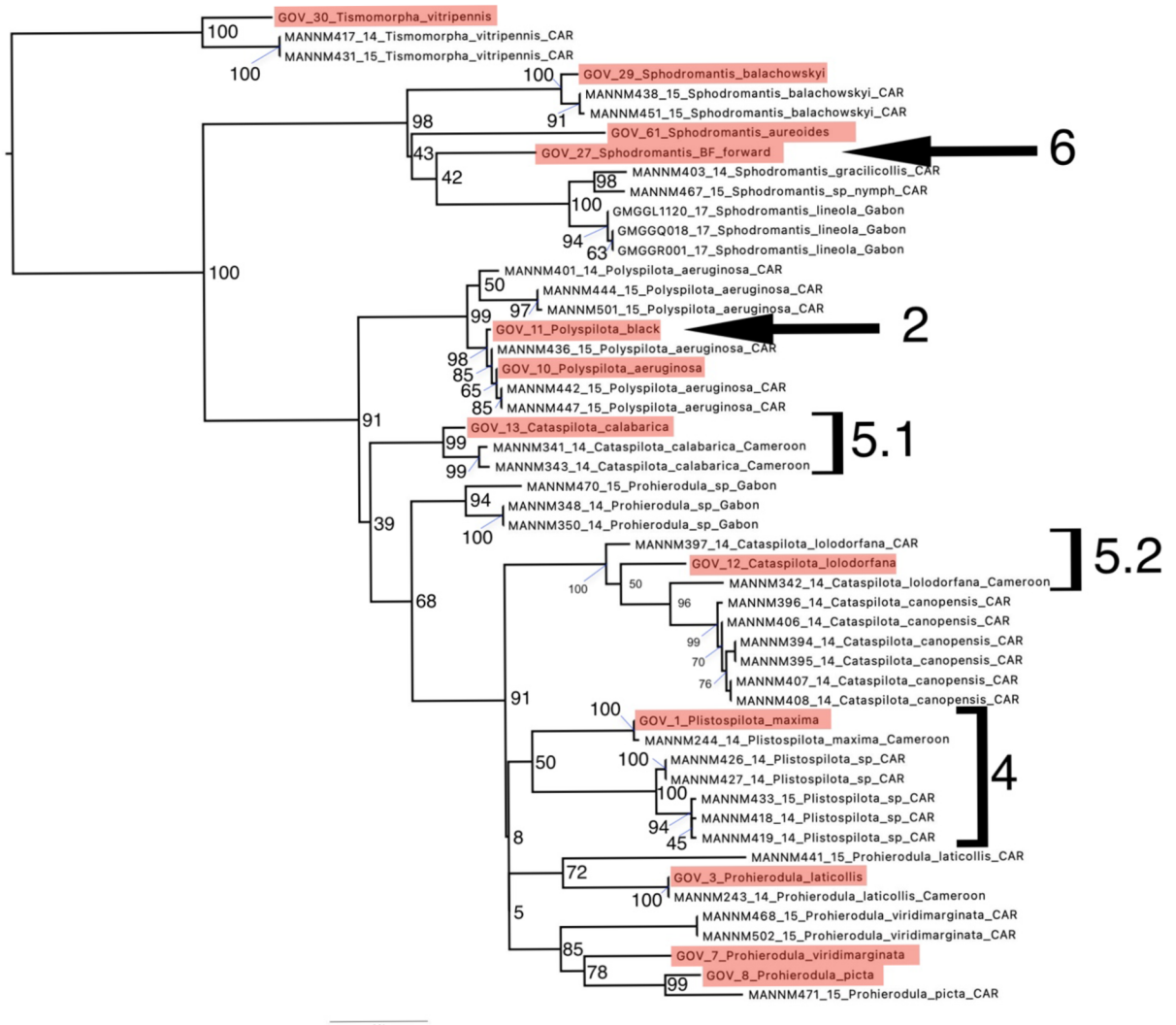

Figure 4. Maximum likelihood tree built with available barcodes from subfamily Tenoderinae.

5. Discussion

The data obtained during this work provide new insights into our knowledge of the diversity of praying mantids in Mbalmayo region and by extension in Cameroon.

Ten species, *A. lamottei*, *C. caudata*, *C. cachani*, *C. speciosa*, *O. sigma*, *P. rehni*, *P. viridimarginata*, *S. balachowskyi*, *S. ziela*, and *T. feae*, are reported for the first time for the country. Previously being recorded from neighboring countries, such as Angola, Congo, CAR, these taxa effectively fill the blind spots of their distribution in Africa and extend current list of praying mantis species of Cameroon. This indicates the importance of continuous efforts of assessment of the biodiversity of Congo Basin rainforests.

Another species found by us, *Sphodromantis aureoides* was described from south of Cameroon based on museum specimens dating from 1970. Judging by the absence of this species in consecutive collection efforts, Roy (2010) hypothesizes it might have been a victim of competition with *S. lineola* and possible hybridization with it, as in case of *S. biocellata* (Werner, 1906) (Roy & Cherlonneix 2009). While high abundance of *S. lineola* can be confirmed for the area of study, specimens undoubtably belonging to *S. aureoides* were collected. Understanding of this species biology and habitat preferences, as well as suggested rarity, is incomplete, however hard evidence of existence of *S. aureoides* population in a pristine forest points out at the importance of conservation of relatively undisturbed areas of the region.

Several collected specimens of Mantodea were not identified to species level. Three males of genus *Negromantis* were found to be morphologically closely related to *N. modesta* Giglio-Tos, 1915 but they differed from the original description of the species in number of posteroventral spines on the forefemora. Barcodes obtained from these specimens did not match with any entry in GenBank or BOLD, while distancing from *N. lutescens* from CAR for 19-20% (Fig. 3.1: 1). Considerable differences in barcodes should be evaluated by examining type material for the genus.

Similarly, a female of *Polyspilota aeruginosa* was found to possess blackened posternum, not typical for this species. Given that *P. aeruginosa* is a taxon with extreme intraspecific variation, it might be an individual character. Molecular analysis supports

this hypothesis, as the DNA barcode returned 100% similarity with voucher species for *P. aeruginosa* and the maximum likelihood tree for the tribe Polyspilotini nests this specimen close to some of sequences from CAR (Figure 4: 2). Moreover, the pairwise distance between typical looking sample and one with blackened posternum both collected in Ebogo II is less than 0.5%. On the other hand, our data is based on sequences from just COI gene, which can lead to clustering together morphologically distinct taxa. For example, Moulin et al. (2017) describe the sample of *S. ziela* grouped together with *S. ipassa* (Figure 3: 3) despite different habitus and structure of male genitalia. Studying nuclear DNA might help resolve such challenging situations.

Genus *Plistospilota* from the tribe Polispilotini is of complicated taxonomy. Original descriptions are mostly too brief, which makes morphological species identification difficult. At the same time, barcoding seems to clearly separate and group samples into distinct clusters (Figure 4: 4). Molecular analysis can complement traditional taxonomical means for revisioning this taxon. While examining the phylogenetic tree branch for another genus of the group, *Cataspilota*, it was readily noticeable, that sampled from Ebogo II branch out from conspecific entities from CAR (Figure 4: 5.1 and 5.2). The pairwise distances ranged from 4-7% in *C. lolodorfana*. Although it might be biased by sample size, the distance approaches species-level difference, and could possibly be a cryptic species, however, it is necessary to investigate nuclear genome.

During morphological identification of a specimen of genus *Galepsus*, it was found to have unique genitalia structure. While the structure of vertex fits the diagnosis of nominative subgenus, none of the described species possess the same genitalia. Based on the fact of having 4 anteroventral spines on the forefemora, this specimen is closely related to *G. (Galepsus) tenius* Stål, 1877 but has distinct copulatory organ. Blasting the DNA barcode did not return a result, although the database of tribe Tarachodini is far from complete. Available sequences of *G. (Galepsus) laticeps* Werner, 1907 and *G. (Syngalepsus) bucheti* Moulin, 2018 differ significantly from this sample, with distance being 32.8% and 33% respectively. This specimen is likely of species new to science, research on nuclear DNA as well as sequencing more representatives of the taxon is required.

Morphological identification of species of genus *Sphodromantis* is based on pronotum shape, denticulation of the forelegs and male genitalia. Several collected specimens resembled quite closely a described species, *S. lineola*. They have same body shape, spination of the forelegs and very similar structure of genitalia in males. At the same time, these specimens differed in larger body size and most noticeably, pigmented spots on forefemora. Such combination of morphological characters was not matched with any described species. DNA barcode of the sample has the closest match with a sequence from *S. lineola*, with 93.03% similarity, while on phylogenetic tree the unidentified species formed a close, but distinct branch with same species (Figure 4: 6). It might be suggested that femoral spots are an early developing character resulted from predator pressure. These spots are used in threat display (Fig. 5) against main enemies of praying mantises – birds and primates, both visual hunters. Larger body size might also facilitate in repelling the offenders.

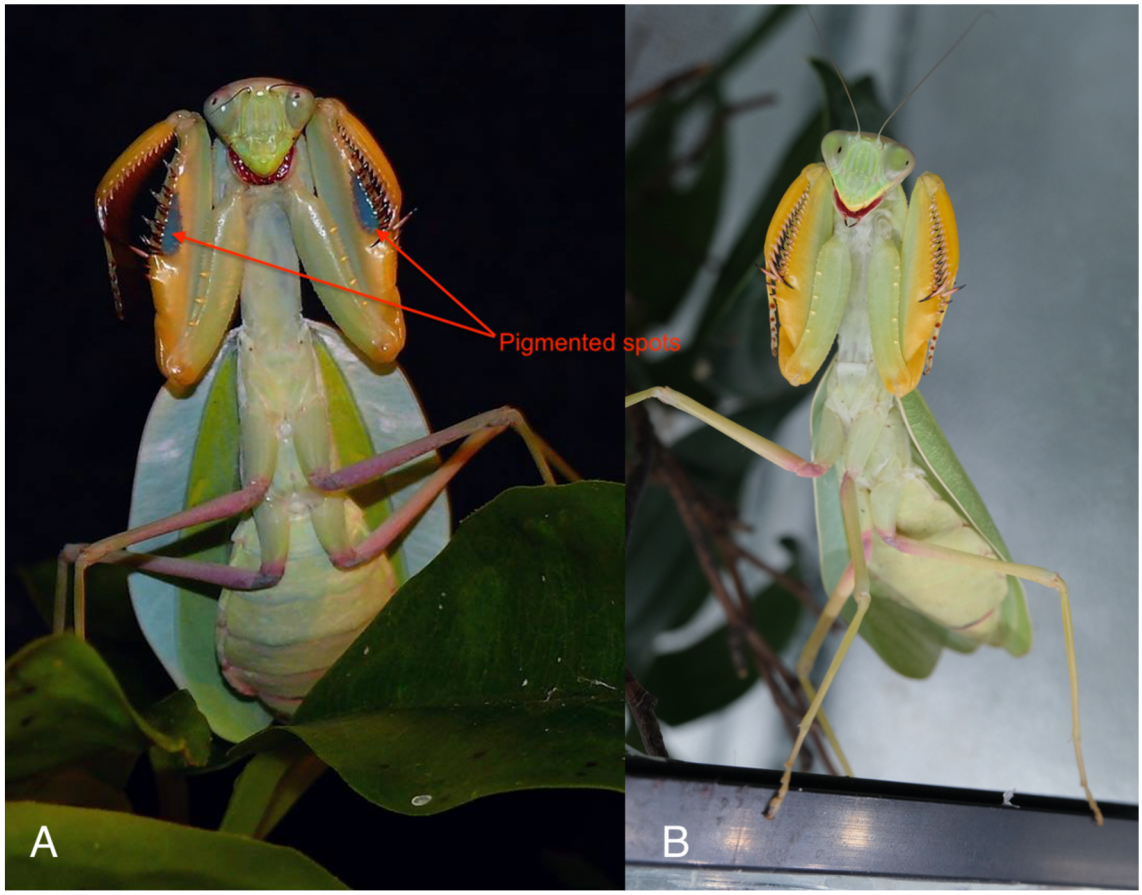

Figure 5. Comparison of coloration of inner side of forefemora of *Sphodromantis* sp. (A) and *Sphodromantis lineola* (B)

Phylogenetic tree for all available barcodes of Mantodea from Central African subregion allowed for direct comparison of conspecific samples from different localities. Noticeably, such taxa as *Omomantis sigma* and *Caudatoscelis caudata* had their samples from Ebogo II and CAR clustered together on the branch with almost null length (Figure 3.1: 7.1). This situation might be explained by external morphology of the species. Both sexes of these species are macropterous and capable of flight (Fig. 6). The higher mobility of individuals advocates better admixture and lower population structure, so it is possible, that these two taxa have same population spanning from CAR to Cameroon.

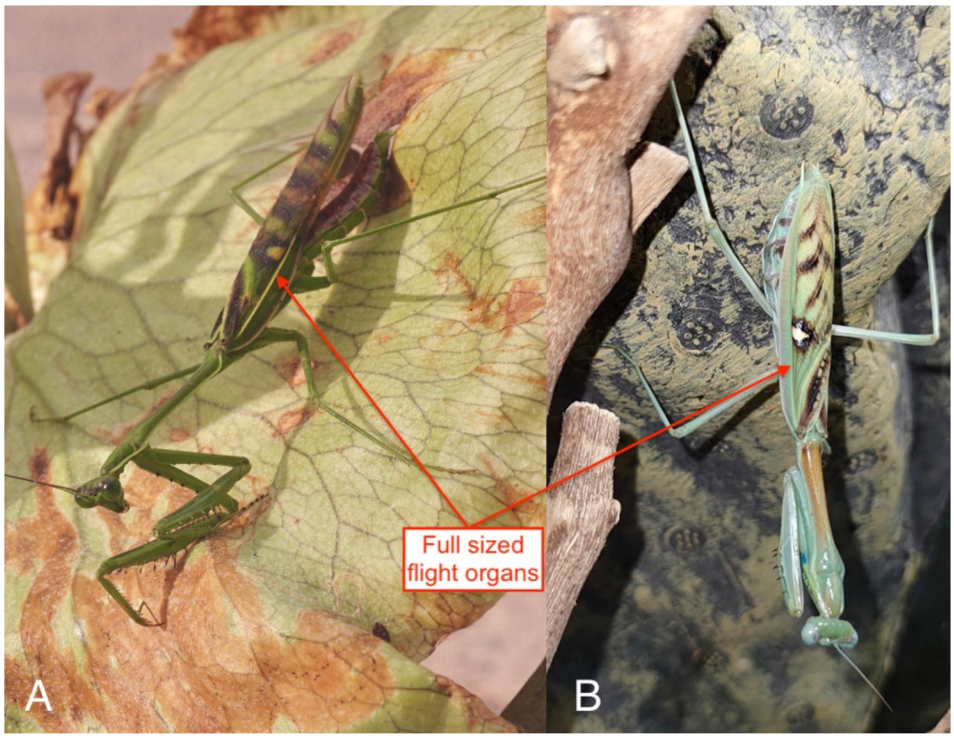

Figure 6. Adult male (A) and female (B) of genus *Omomantis*

In contrast, sequences of *Stenopyga ziela* and *Miomantis preussi* from Ebogo II branch out significantly from same species sequences from CAR (Figure 3.1: 8.1 and 8.2). In both species, only males are capable of flight, while females are micropterous and brachypterous (Fig. 7, on example of *S. ziela*), which limits their possible dispersal and consecutive admixture. Other species, for instance, *Chrysomantis cachani*, *C. speciosa* and *Panurgica rehni* create distant branches as well (Figure 3.2: 9.1 and 9.2, Figure 3.1: 9.3), however, it is harder to connect it with their morphology – either female of the

species is unknow (and, consequently, its habitus) or female possesses fully developed wings. In case of *Chrysomantis*, which mimics foliose lichens, it might be possible, that representatives of this genus have a strict attachment to a certain microhabitat, which may patchy distribution over the forest. Finding another suitable area takes relatively higher time and energy costs, therefore it is probably not prioritized.

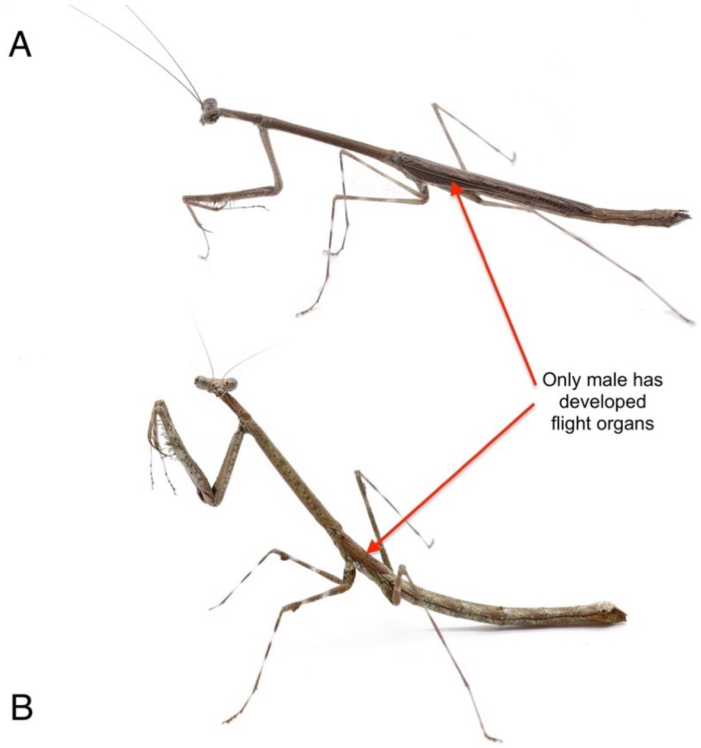

Figure 7. Adult male (A) and female (B) of *Stenopyga ziela*

One of the advantages of using DNA barcodes is identification of samples, otherwise impossible to determine due to life stage or sex. This is illustrated on obtained tree in *Stenopyga extera*. One of the samples we obtained the sequence from was immature female mantis, belonging to genus *Stenopyga*. However, identification to species-level based on morphological characters was not possible, as the diagnostic characters for the genus include wing coloration (not developed at nymphal stage) and structure of male genitalia (obviously absent in a female). While building phylogenetic tree, the barcode of immature *Stenopyga* clustered with a sequence from same locality of an adult male *Stenopyga extera* (Figure 3.1: 10), which was possible to identify based on morphological characters. The distance between two samples is <0.5%, which strongly suggests these two specimens are conspecific.

6. Conclusions

Morphological means of identification predominates in current taxonomy of praying mantises. Accurate combination of such diagnostic characters, as forelegs spination, pronotum structure and male genitalia complex, provides solid foundation for reliable identification. At the same time, given natural intraspecific variability, these characters can be subject to slight changes not always obvious in case of, for example, low number of samples. Minute deviations could be indicators of cryptic species and can be estimated by molecular analysis, with additional assessment of taxonomically stable taxa. In this thesis, it is demonstrated that mitochondrial COI gene-based DNA barcoding was comparable to morphological identification of species of praying mantises, with more than two thirds of sample size matching conspecific records in existing libraries. The unmatched barcodes were mainly of species not present in databases and of likely undescribed taxa. Barcoding proved to be a reliable method for identification of praying mantises even in more complicated scenarios, as with identification of immature stages of these insects. Accuracy of molecular identification could be further improved by enriching existing libraries with barcodes of more taxa.

Establishment of a library of DNA barcodes for mantises of Cameroon complements existing efforts from neighboring countries and allows for comparison with existing phylogeny of the order. Phylogenetic trees built using sequences of Mantodea of Central African subregion are adequately congruent with current taxonomical consensus. The trees, complemented by pairwise distances, demonstrate unresolved taxonomy of genera *Cataspilota*, *Negromantis*, *Plistospilota*. It should be taken into account that more in-depth investigations of the evolutionary relationships within the group should be based on more markers from nuclear genome.

Existing libraries from Gabon and CAR allowed us to directly compare it with sequences from Ebogo II. It demonstrated population continuity in such species as *Omomantis sigma* and *Caudatoscelis caudata*, while pointing out dissimilarity in *Stenopyga ziela* and *Miomantis preussi*. It can be connected to morphological characters in these species and subsequent strategies of dispersal, which remains poorly studied in Mantodea. Other comparisons revealed blank spots in biology and ecology of *Chrysomantis* and *Panurgica*, where most of the species are known only by males.

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Appendices

List of the Appendices:

Appendix 1: List of species based on morphological identification

Family **AMORPHOSCELIDAE** Stål, 1877

Genus *Amorphoscelis* Stål, 1871

Amorphoscelis grisea Bolivar, 1908

Type locality. Cameroon.

Material examined. 1♂: Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 5-15.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Congo, Democratic Republic of the Congo, Gabon, Guinea, Ivory Coast, Uganda.

Amorphoscelis lamottei Roy, 1963

Type locality. Guinea.

Material examined. 1♂: Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 10-11.VIII.2021, V. Govorov leg.

Distribution. CAR, Congo, Democratic Republic of the Congo, Gabon, Ghana, Guinea, Ivory Coast, Tanzania, Uganda.

Note. It is the first time this species has been reported for Cameroon.

Genus *Bolivaroscelis* Roy, 1973

Bolivaroscelis carinata (Bolivar, 1908)

Type locality. Cameroon.

Material examined. 1♀ nymph, Cameroon, Mbalmayo Region, Ebogo II village, timber works 3°23'27.9"N 11°28'16.0"E, 22.VIII.2021, V. Govorov leg.

Distribution. Cameroon.

Genus *Caudatoscelis* Roy, 1973

Caudatoscelis caudata Giglio-Tos, 1914

Type locality. Gabon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 2-10.VIII.2021, V. Govorov leg.

Distribution. CAR, Gabon.

Note. It is the first time this species has been reported for Cameroon.

Genus *Maculatoscelis* Roy, 1973

Maculatoscelis ascalaphoides (Bolivar, 1908)

Type locality. Cameroon.

Material examined. 2♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 30.VII-15.VIII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, CAR, Congo, Gabon, Ghana, Guinea, Tanzania.

Family **NANOMANTIDAE** Brunner de Wattenwyl, 1893

Genus *Negromantis* Giglio-Tos, 1915

Negromantis lutescens (Sjöstedt, 1900)

Type locality. Cameroon.

Material examined. 1♀ Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 2-10.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR.

Negromantis sp.

Material examined. 3♂: Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 1-18.VIII.2021, V. Govorov leg.

Note. Studying type specimens is required for an accurate identification.

Family **EREMIAPHILIDAE** Saussure, 1869

Genus *Tarachodes* Giglio-Tos, 1911

Tarachodes (Tarachodes) feae Giglio-Tos, 1911

Type locality. Congo.

Material examined. 1♂: Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 7-15.VIII.2021, V. Govorov leg.

Distribution. Congo, Gabon.

Note. It is the first time this species had been reported for Cameroon.

Genus *Galepsus* Stål, 1876

Galepsus (Galepsus) sp.

Material examined. 1♂: Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 18.VIII.2021, V. Govorov leg.

Note. Morphology of genitalia does not match any of the described species. More research is required.

Family **MIOMANTIDAE** Westwood, 1889

Genus *Miomantis* Saussure, 1870

Miomantis preussi Karsch, 1892

Type locality. Barombi (Cameroon).

Material examined. 1♀ Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Equatorial Guinea (Bioko Island), Gabon.

Family **HYMENOPODIDAE** Giglio-Tos, 1915

Genus *Sibylla* Stål, 1877

Sibylla (Sibylla) dolosa Roy, 1975

Type locality. CAR.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 1.VIII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, CAR, Democratic Republic of the Congo, Gabon, Gambia, Ghana, Guinea, Ivory Coast, Nigeria.

Sibylla (Sibyllopsis) griffinii Giglio-Tos, 1915

Type locality. Guinea.

Material examined. 1♂: Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 25.V-2.VI.2022, J. Šobotník leg.

Distribution. Benin, Cameroon, CAR, Democratic Republic of the Congo, Gabon, Ghana, Ivory Coast, Liberia, Nigeria, Sierra Leone, Togo.

Genus *Chlidonoptera* Karsch, 1892

Chlidonoptera vexillum Karsch, 1892

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Democratic Republic of the Congo, Tanzania.

Genus *Chloroharpax* Werner, 1908

Chloroharpax modesta (Gerstaecker, 1883)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 2-10.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Congo, Democratic Republic of the Congo, Gabon, Ghana, Guinea, Ivory Coast, Nigeria.

Genus *Panurgica* Karsch, 1896

Panurgica feae Griffini, 1907

Type locality. Bioko Island (Equatorial Guinea).

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 31.VII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, CAR, Equatorial Guinea, Gabon.

Panurgica rehni (La Greca, 1954)

Type locality. Democratic Republic of the Congo.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 11.VIII.2021, V. Govorov leg.

Distribution. CAR, Democratic Republic of the Congo, Gabon.

Note. It is the first time this species has been reported for Cameroon.

Genus *Chrysomantis* Giglio-Tos, 1915

Chrysomantis cachani (Roy, 1964)

Type locality. Ivory Coast.

Material examined. 2♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 14-5.VIII.2021, V. Govorov leg.

Distribution. CAR, Democratic Republic of Congo, Gabon, Ghana, Guinea, Ivory Coast.

Note. It is the first time this species has been reported for Cameroon.

Chrysomantis speciosa Giglio-Tos, 1915

Type locality. Ghana.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 31.VII.2021, V. Govorov leg.

Distribution. Angola, CAR, Democratic Republic of Congo, Gabon, Ghana, Ivory Coast.

Note. It is the first time this species has been reported for Cameroon.

Genus *Oxypiloidea* Schulthess, 1898

Oxypiloidea (Catasigerpes) margarathae (Werner, 1912)

Type locality. Ethiopia.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-22.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Chad, Democratic Republic of the Congo, Eritrea, Ethiopia, Gabon, Kenya, Niger, Nigeria, Sudan, Uganda.

Genus *Anasigerpes* Giglio-Tos, 1915

Anasigerpes bifasciata Giglio-Tos, 1915

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, CAR, Congo, Democratic Republic of the Congo, Equatorial Guinea, Gabon, Ghana, Guinea, Ivory Coast, Nigeria, Uganda.

Family **Dactylopterygidae** Giglio-Tos, 1915

Genus *Dactylopteryx* Karsch, 1892

Dactylopteryx flexuosa Karsch, 1892

Type locality. Gabon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, primary forest 3°23'01.6"N 11°27'50.7"E, 7.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Congo, Gabon, Ghana, Ivory Coast.

Genus *Theopompella* Giglio-Tos, 1917

Theopompella aurivillii (Sjöstedt, 1900)

Type locality. Cameroon.

Material examined. 1♂, Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 5.VIII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, CAR, Congo, Democratic Republic of the Congo, Equatorial Guinea, Gabon, Malawi.

Family **DEROPLATYIDAE** Westwood, 1889

Genus *Stenopyga (Stenopyga)* Karsch, 1892

Stenopyga (Stenopyga) extera Karsch, 1892

Type locality. Cameroon.

Material examined. 1♂, 1♀ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, Liberia.

Stenopyga (Stenopyga) ziela Roy, 1963

Type locality. Guinea.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 11-22.VIII.2021, V. Govorov leg.

Distribution. CAR, Democratic Republic of the Congo, Gabon, Ghana, Guinea, Ivory Coast.

Note. It is the first time this species has been reported for Cameroon.

Family **MANTIDAE** Latereille, 1802

Genus *Deromantis* Giglio-Tos, 1916

Deromantis limbalicollis (Karsch, 1892)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 25.V-2.VI.2021, J. Šobotník leg.

Distribution. Cameroon, CAR, Democratic Republic of the Congo, Gabon.

Genus *Omomantis* Saussure, 1899

Omomantis sigma Rehn, 1949

Type locality. Democratic Republic of the Congo.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 2-10.VIII.2021, V. Govorov leg.

Distribution. CAR, Democratic Republic of the Congo, Gabon.

Note. It is the first time this species has been reported for Cameroon.

Genus *Polyspilota* Burmeister, 1838

Polyspilota aeruginosa (Goeze, 1778)

Type locality. Unknown.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, Cape Verde, CAR, Comoros, Congo, Democratic Republic of the Congo, Ethiopia, Gabon, Ghana, Guinea, Kenya, Liberia, Madagascar, Namibia, South Africa, Tanzania, Uganda, Zanzibar, Zimbabwe.

Polyspilota sp.

Material examined. 1♀ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 11-22.VIII.2021, V. Govorov leg.

Note. This specimen is similar to *P. aeruginosa*, but has a blackened posternum. More research on tribe Polyspilotini is needed.

Genus *Plistospilota* Giglio-Tos, 1911

Plistospilota cf. *P. maxima* Giglio-Tos, 1917

Type locality. Unknown.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Democratic Republic of the Congo, Ivory Coast, Gabon.

Note. Genus needs to be revised, identification to species level is not reliable.

Genus *Prohierodula* Bolivar, 1908

Prohierodula laticollis (Karsch, 1892)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Democratic Republic of the Congo, Gabon.

Prohierodula picta (Gerstaecker, 1883)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Equatorial Guinea, Gabon.

Prohierodula viridimarginata La Greca, 1956

Type locality. Democratic Republic of Congo.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. CAR, Democratic Republic of the Congo, Gabon.

Note. It is the first time this species has been reported for Cameroon.

Genus *Cataspilota* Giglio-Tos, 1917

Cataspilota calabarica Westwood, 1889

Type locality. Nigeria.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Equatorial Guinea, Gabon, Liberia, Nigeria.

Cataspilota lolodorfana (Giglio-Tos, 1911)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 2-10.VIII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Congo, Democratic Republic of the Congo, Gabon, Nigeria.

Genus *Alalomantis* Giglio-Tos, 1917

Alalomantis muta (Wood-Mason, 1882)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Angola, Cameroon, CAR, Democratic Republic of the Congo, Gabon, Uganda.

Genus *Sphodromantis* Stål, 1871

Sphodromantis aureoides Roy, 2010

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Limbé, primary forest, 1-30.VIII.2019, Ntah Eliot Nji Bama leg.

Distribution. Cameroon.

Sphodromantis balachowskyi La Greca, 1967

Type locality. Democratic Republic of Congo.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 8.VIII.2021, V. Govorov leg.

Distribution. CAR, Democratic Republic of the Congo, Gabon.

Note. It is the first time this species has been reported for Cameroon.

Sphodromantis lineola pinguis La Greca, 1967

Type locality. Democratic Republic of the Congo.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 27.VII-1.VIII.2021, V. Govorov leg.

Distribution. Angola, CAR, Cameroon, Congo, Democratic Republic of the Congo, Gabon.

Sphodromantis sp.

Material examined. 1♂ Cameroon, Limbé, secondary forest, 1-30.VIII.2019, Ntah Eliot Nji Bama leg.

Note. Closely related morphologically to *S. lineola pinguis* but differs in relatively larger body size and a pigmented spot on the interior surface of forecoxa. More research is required.

Genus *Tismomorpha* Roy, 1973

Tismomorpha vitripennis (Bolivar, 1908)

Type locality. Cameroon.

Material examined. 1♂ Cameroon, Mbalmayo Region, Ebogo II village, light trap 3°23'38.4"N 11°28'15.6"E, 30.VII.2021, V. Govorov leg.

Distribution. Cameroon, CAR, Gabon.