Monitoring the whole forest: monitoring invertebrate biodiversity across forest canopy and understorey to assess impacts of anthropogenic disturbances in South-East Asia

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Programme:BIFA
Project ID: BIFA5_026
Project lead organization: Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences
Project implementation period:1/7/2020 - 31/12/2022
Report approved: 10/5/2023

Narrative Final report

Executive Summary

This project was based on a bilateral collaboration between Xishuangbanna Tropical Botanical Garden, China, and Mahidol University, Thailand, to understand the spatial and temporal dynamics of insects in the canopy and understory of tropical rainforests in Thailand. Unfortunately, due to the COVID-19 pandemic and strict border control imposed by the Chinese government until the end of 2022, many of our activities (such as international travel and specimen transport) have been either delayed or canceled, hugely impacting the progress of this project. Despite such difficulties, we have completed the following: the BIFA online workshop; fieldwork in southern Thailand; specimen sorting and identification; meta-barcoding samples (although we failed to obtain data from many degraded samples); uploaded the biodiversity data on GBIF; and additional activities such as online conferences to advertise the importance of ecological research and data sharing across the broader communities.

As the project members could not travel to conduct project evaluation meetings and specimen checks, we relied on online tools such as Zoom and Slack to evaluate the project progress and Google Drive to share the images of specimens to verify specimen identification. Although online tools were beneficial, we found that, without proper training, this can be highly challenging (i.e., specimen images were often taken inappropriately for taxonomic identification). In addition, actual specimens are often desired for taxonomic identification.

Chinese and Thai collaborators utilized online resources to communicate regularly and achieved most of our objectives. We continue working together and plan to apply for more research funding to carry out additional fieldwork in the future.

Progress against milestones

Has your project completed all planned activities?: No

Rationale: During the COVID-19 pandemic and subsequent strict border control by China, international traveling was impossible until the end of 2022. Consequently, we could not implement three (out of four) project evaluation and monitoring meetings in Thailand (travel expenses were part of the initially approved budget). In December 2022, we managed to bring back one of the project members (Laskamee Punthuwat) to China so that we were able to finalize the travel and field work reimbursements. The PI (Akihiro Nakamura) self-funded to travel to Thailand in December 2022 (listed as the first evaluation and monitoring in the amended budget) to meet his local collaborators and other project members in Thailand to check the overall progress and to confirm the completion of specimen sorting and identification. DNA barcoding was not carried out due to the increased costs of meta-barcoding, and we exhausted the budget allocated for DNA barcoding (please see below for more details).

Has your project produced all deliverables?: No

Rationale: The co-funding fully funded meta-barcoding, and we initially planned to send the samples to China to conduct DNA sequencing of all non-target arthropods (because the cost of meta-barcoding was less than half of that in Thailand). We shipped the specimens from Thailand in 2021; however, the shipment was delayed and eventually returned to Thailand due to the strict quarantine measures during the COVID-19 pandemic. During the transit, the samples were not stored properly (we requested the samples to be stored at -20 degrees, but the samples were instead stored in a conventional fridge). Consequently, the samples became heavily degraded. We eventually processed samples in Thailand, but we failed to extract DNA or obtained very short basepairs. We, therefore, decided not to publish the data (but see the attached meta-barcoding data). Due to the much-increased costs of meta-DNA barcoding, the remaining co-funding budget did not allow us to sequence DNA from individual specimens.

Report on Activities

Activity implementation summary

BIFA Capacity Enhancement Workshop: The PI (Nakamura) and the project assistant (Waitayachart) attended the online workshop in August 2020 and completed it with the advanced (Nakamura) and basic badges (Waitayachart). After completing this workshop, we were granted access to the IPT via the CAS node to publish our data. However, the CAS node did not provide an online platform for sampling event data. We could not resolve the issues with them, so we eventually decided to upload our data via the BIFA IPT.

Sample sorting to pick the target insects: From the total of four field surveys (2 locations x 2 seasons), we have obtained a total of 432 samples (light traps: 2 locations x 2 seasons x 2 vertical strata x 9 plots x 3 nights = 216 samples; Yellow pan FIT: 2 locations x 2 seasons x 2 vertical strata x 9 plots = 72 samples; SLAM traps: 2 locations x 2 seasons x 2 vertical strata x 9 plots x 2 trap components = 144 samples). By the middle of 2021, Waitayachart and other participants involved in this project have successfully extracted all specimens of the target taxonomic groups (beetles, moths, and hymenopterans) from all samples collected from Mo Singto and Klong Naka in the wet and dry seasons (**100% complete**). Dry samples (light-trapped moth specimens) were always kept in the freezer, and wet samples in 99% ethanol until the target specimens were dry-mounted for further taxonomic identification. Legs of target specimens were taken and stored in 99% ethanol for DNA barcoding. The remaining samples (i.e., residual samples) were stored in the freezer for meta-DNA barcoding (but as mentioned above, the samples were heavily degraded during the transit, and meta-barcoding was conducted only for a small subset of samples).

Arthropod sampling in Klong Naka (September): We have successfully completed the second field survey at Klong Naka during the wet season. The survey was originally planned for July 2020; however, due to the COVID-19 situation in Thailand and prolonged rainfall in July, we decided to delay our survey till September. As Nakamura was unable to travel to Thailand, the fieldwork was carried out by the local Thai assistants and students. The fieldwork was completed successfully, with all traps retrieved without failure.

Higher taxonomic identification: Higher taxonomic-level identification started after the target specimens were extracted. **Moths**: We collected a larger number of specimens than we initially anticipated (we estimated to be 9300, but we collected 13814 specimens from 72 samples). Despite this, we have identified all of the moth specimens into superfamily and then family. For species/morphospecies level identification, we used only target families and superfamilies, namely Noctudae and Nolidae. Our target taxonomic scopes and taxonomic groups were modified from those listed in our proposal (Geometridae, Noctuidae, Arctiini) as the number of specimens from individual taxonomic groups was different from what we initially expected. **Beetles**: Beetle sorting and identification took longer than we initially anticipated due to the high family-level diversity of beetles and difficulties in accessing taxonomic help (due to travel restrictions in Thailand during the COVID-19 pandemic). Despite this, one of the participants who is currently working on her PhD project (Laksamee Punthwat) completed species/morphospecies-level identification of all beetles collected from SLAM traps. These beetles were also categorized into major feeding guilds (e.g., herbivores, saprophages, xylophages) for ecological studies. There are some beetle specimens not identified to the family or genus due to taxonomic difficulties, but they consist of a very small number (69 specimens in total). **Hymenopterans**: All hymenopterans collected from yellow pan FIT traps in Mo Singto have been sorted and identified to families by one of the students involved in this project. As the student who was involved in the hymenopteran component withdrew from this project in 2020, the project assistant (Waitayachart) took over this role and worked on the remaining samples, and sorted them into families and morphospecies. The problem arose as hymenopterans were sorted by two persons independently when teamworking (cross-checking specimen identification by the two members) was difficult due to the COVID-19 pandemic. In addition, the local taxonomist (Dr Alexey Reshchikov) could not travel to check the specimen identification. This resulted in erroneous and inconsistent identification was inconsistent. This was realized during data analyses in 2020, and the amendments were completed in November 2021.

Species-level identification: Due to the COVID-related travel restrictions and university closure, it was difficult to obtain taxonomic assistance to identify our specimens to species. Therefore, we first identified all specimens to at least morphospecies so that taxonomists could later give them scientific names. The student in charge of beetles (Punthuwat) has successfully identified a total of 1622 specimens to species or morphospecies, and species-level identification of some specimens have been confirmed by local taxonomists using online platforms. The student working on moths (Taveesri) identified all of the target moth families (Noctudae and Nolidae) into species or morphospecies. Due to COVID-19 travel restrictions to access local taxonomists, species-level identification was long-delayed, and beetle species identification was completed in November 2022 and moth species identification in February 2023. Due to the problems associated with family and morphospecies-level identifications, most of the hymenopteran specimens were only identified to family and then morphospecies.

DNA barcoding: DNA barcoding of the specimens from the target groups was initially planned but canceled due to the lack of co-funding. This resulted from the increased cost of meta-DNA barcoding in Thailand instead of China due to strict quarantine requirements during the COVID-19 pandemic. The cost of meta-barcoding in Thailand was twice as expensive as that in China, and we had to reallocate the budget to complete metabarcoding. Although we could not conduct DNA barcoding of individual specimens, many species have been identified using morphological characteristics with help from local taxonomists (using online platforms). As the samples for DNA barcoding have been kept at Mahidol University, we expect to process these samples in the future when some budget has been allocated. Alternatively, we could bring these samples to China as the processing fees are much less.

Meta-DNA barcoding: Meta-barcoding was long delayed due to the university closure during the COVID-19 pandemic. Meta-barcoding was fully funded by the co-funding, and we initially planned to send the samples to China to conduct DNA sequencing of all non-target arthropods. We shipped the specimens from Thailand in 2021; however, the shipment was delayed and eventually returned to Thailand due to the strict quarantine measures during the COVID-19 pandemic. During the transit, the samples were not stored properly (we requested the samples to be stored at -20 degrees, but the samples were instead stored in a conventional fridge). Consequently, the samples became heavily degraded. We eventually decided to process samples in Thailand, but we failed to extract DNA from many samples. we successfully extracted DNA, and amplified COI gene from seven samples, but after sequencing, the obtained sequences were of low quality and unable to assemble to get long basepairs. We, therefore, decided not to publish the data (but please find attached data below).

Data entry: We initially attempted to upload our biodiversity data via the CAS (Chinese Academy of Sciences) IPT. Nakamura checked the data before publication. The data, however, could not be uploaded properly as the CAS IPT was having persisting bug issues. As these issues could not be resolved fully, we uploaded the data via BIFA IPT. Before the interim report, we uploaded the three sets of data (moths, beetles, and hymenopterans). These datasets have been updated as we fixed identification errors and obtained species/morphospecies level information.

First, Second, and Third evaluation and monitoring: This BIFA project was approved and implemented as an international project between Chinese and Thai research institutes. This required the PI (Nakamura) to regularly travel to Thailand to conduct the fieldwork, help sort and identify specimens, monitor the progress and project implementation, and check the biodiversity data to be uploaded with his Thai collaborators. Nevertheless, Nakamura could not travel to Thailand during the COVID-19 pandemic which covered most of the project duration. One of the project students, Punthwat, is affiliated with Nakamura's institute in China, but she was stranded in Thailand from early 2020 to December 2022 until China fully opened to international traveling. All of the planned travelings, therefore, were canceled, and we communicated via online platforms to evaluate the progress of the project on a regular basis. The PI (Akihiro Nakamura) self-funded to travel to Thailand in December 2022 (listed as the first evaluation and monitoring in the amended budget) to meet his local collaborators and other project members in Thailand to check the overall progress and to confirm the completion of specimen sorting and identification.

Midterm report preparation: The due date for the submission of the midterm report was on the 31st of January 2021; however, due to delays in sorting specimens and data uploading to GBIF, our midterm report was submitted late and approved on the 9th of September 2021.

Final report preparation and final meeting: The due date for the submission of the final report was on the 31st of August 2021; however, due to delays in the overall project progress primarily caused by the COVID-19 pandemic, we were unable to meet the deadline for the final report, and subsequently extended the deadline. The PI (Nakamura) self-funded his travel to go and meet his Thai collaborators in Bangkok in December 2022 so that Nakamura was able to discuss the problems associated with specimen identification and data entry and to check the overall progress with other members of this BIFA project.

Ronnarot Taveesri presented his oral talk at the 4th Environment and Natural Resources International Conference in Bangkok (online): One of the project members, Ronnarot Taveesri, gave an oral presentation at the 4th Environment and Natural Resources International Conference in Thailand (online) on the 16th of December 2021. His talk was based on the results we obtained from this project. He presented how seasonal changes influenced the vertical stratification of moth diversity in the two rainforests we surveyed.

Nakamura hosted the One Day Canopy Conference Online: The PI, Akihiro Nakamura, presented his recent research project on species interactions of ants in the forest canopy at the One Day Canopy Conference online where over 100 participants from more than 20 countries joined. This conference was hosted by Nakamura. Nakamura acknowledged the BIFA as one of the funding agencies for his project.

Other seminar presentations: Nakamura was invited to give seminars at various universities (e.g., Dali University, Sun Yat Sen University) during the course of this project. He presented his recent research progress related to forest canopy biodiversity and addressed the importance of data sharing using online platforms such as GBIF.

Completed activities

Activity name: BIFA Capacity Enhancement Workshop

Description: Nakamura and Waitayachart attended the workshop and successfully completed the assessment with Advanced (Nakamura) and Basic (Waitayachart) Badges.
Start Date - End Date: 6/7/2020 - 31/8/2020
Verification Sources: Please find attached copies of the digital badges (biodiversity-data-mobilisation-advanced-badge Nakamura.png biodiversity-data-mobilisation-basic-badge Waitayachart.png)

Activity name: Sample sorting to pick the target insects

Description: Specimens of the target groups (moths, beetles and hymenopterans) taken from the raw samples and counted.
Start Date - End Date: 1/7/2020 - 28/2/2021
Verification Sources: Please find attached Excel spread sheet ("List of the samples with completed tasks") that summarizes the list of samples with completed taxonomic tasks.

Activity name: Arthropod sampling in Klong Naka (September)

Description: Second arthropod sampling in Klong Naka Wildlife Sanctuary in September (during the dry season)
Start Date - End Date: 12/9/2020 - 17/10/2020
Verification Sources: Please refer to the pictures of our activities attached ("Pictures of KN field work Thailand").

Activity name: Higher taxonomic and morphospecies identification

Description: Identifying specimens to higher taxa such as family and genus, and then giving morphospecies numbers for ecological studies.
Start Date - End Date: 1/10/2020 - 30/11/2021
Verification Sources: We have updated the existing biodiversity data with family-level taxonomic information using IPT hosted by BIFA.

Activity name: Species level identification

Description: Specimens of the target groups will be further identified to species with the aid of the local taxonomists in Thailand.
Start Date - End Date: 1/12/2020 - 28/2/2023
Verification Sources: We have updated the existing biodiversity data with species-level information using IPT hosted by BIFA.

Activity name: Meta-DNA barcoding

Description: For non-target specimens collected from this project, we will use Illumina's MiSeq system to meta-barcode COI sequences of all target and non-target individuals (instead of 'conventional' DNA barcoding which was applied only to the target group specimens). Taxonomic assignment will be done using BLAST systems based on BOLD and GBIF sequence data.
Start Date - End Date: 1/10/2021 - 28/2/2023
Verification Sources: We will upload the COI sequences with sample information to GBIF and BOLD.

Activity name: Data entry

Description: Biodiversity data (taxonomic and DNA information of the specimens) will be continuously updated right after some specimen sorting has been completed in August 2020.
Start Date - End Date: 1/7/2020 - 15/3/2023
Verification Sources: After completion of the BIFA workshop, we started uploading the biodiversity data using IPT system hosted by BIFA. We uploaded the three sets of data (moths, beetles and hymenopterans) and subset of samples with COI sequences generated from meta-DNA barcoding.

Activity name: First (and last) evaluation and monitoring

Description: All project participants will get together at Mahidol University in Thailand to check the progress and discuss issues arising during the data entry. The final report was drafted and discussed in the meeting.
Start Date - End Date: 26/12/2022 - 29/12/2022
Verification Sources: The PI, Nakamura, self-funded this trip to have meetings with Thai colleagues.

Activity name: Midterm report preparation

Description: PI and co-PIs collaborators will prepare the interim report and to check the progress on sorting and identification. NB Nakamura and Punthuwat will not travel to Thailand. They will instead work in China to remotely collaborate with Thai colleagues.
Start Date - End Date: 1/8/2021 - 9/9/2021
Verification Sources: Finalize the interim report which will be written by both PI and co-PIs.

Activity name: Final report preparation and final meeting

Description: All participants will get together at Mahidol University in Thailand to prepare the interim report and to check the progress on data entry.
Start Date - End Date: 26/12/2022 - 31/3/2023
Verification Sources: Finalise the final report which will be written by both PI and co-PIs.

Activity name: Project presentation at the 4th Environment and Natural Resources International Conference in Bangkok (online)

Description: One of the project members, Ronnarot Taveesri, gave an oral presentation at the 4th Environment and Natural Resources International Conference in Thailand (online) on the 16th of December 2021. His talk was based on the results we obtained from this project and he presented how seasonal changes influenced the vertical stratification of moth diversity in the two rainforests we surveyed.
Start Date - End Date: 16/9/2021 - 16/9/2021
Verification Sources: Please find attached pdf copy of the presentation. The conference website is as follows: https://en.mahidol.ac.th/enric/?fbclid=IwAR2VYgPqwvC_NMSgbFLOKgyFH7aVTF8wmW1JD2c4yA_o_Nh_3n2F4Rv_J8Q

Activity name: Nakamura hosted the One Day Canopy Conference Online

Description: The PI, Akihiro Nakamura, presented his recent research project that looked at species interactions of ants in the forest canopy at the One Day Canopy Conference online where over 100 participants from more than 20 countries joined. This conference was hosted by Nakamura. Nakamura acknowledged the BIFA as one of the funding agencies of his project.
Start Date - End Date: 18/10/2021 - 18/10/2021
Verification Sources: Please find attached a pdf copy of Nakamura's presentation and the conference information can be found from here:
http://english.xtbg.cas.cn/at/cs/202110/t20211013_284693.html

Activity name: A seminar given by Nakamura at Sun Yat Sen University, China

Description: On the 27th of May 2022, Nakamura gave a seminar about his recent research at Sun Yat Sen University. The audience was the students and staff from the university and I acknowledged BIFA and the co-funder as the funding agencies.
Start Date - End Date: 27/5/2022 - 27/5/2022
Verification Sources: Please find a copy of the invitation letter and Nakamura's presentation (pdf)

Report on Deliverables

Production of Deliverables - Summary

We initially proposed to generate a total of six datasets, as we initially planned to identify all specimens of beetles, moths, and hymenopterans to family and only subsets of specimens (certain families) to species and morphospecies. We, however, decided to sort and identify all of the beetle and hymenopteran specimens to species or morphospecies because the total number of specimens were much smaller than we first anticipated. As a result, the family and species-level datasets were merged for these two target groups. Moths, on the other hand, were treated as planned and the family and species-level datasets were published separately. For meta-barcoding, we failed to extract DNA from many samples. We successfully extracted DNA, and amplified COI gene from only seven samples, but after sequencing, the obtained sequences were of low quality and unable to assemble to get long basepairs. We, therefore, decided not to publish the data (but please find attached data below).

Production of deliverables

Title: Lepidoptera (moths) sample event data (family-level taxonomic identification)

Type: Dataset

Status update: A total of 13814 specimens of moths were collected from Mo Singto with 5604 moth specimens from Klong Naka with 8210 specimens. All specimens were sorted and identified to family.
Dataset scope: Moths collected from the forest canopy and understory of the two rainforests in southern Thailand.}
Expected number of records: 1110
Data holder: Ronnarot Taveesri, Ekgachai Jeratthitikul, Alyssa Stewart and Akihiro Nakamura
Data host institution: Chinese Academy of Sciences
Sampling method: Three nights of light trappling in the forest canopy and understorey of the sampling points (9 sampling points at each Mo Singto and Klong Naka rainforests).
% complete: 100
DOI: https://www.gbif.org/dataset/7ea1fc18-5e4c-44a6-a5cd-35a746b13dbb
Expected date of publication:

Title: Coleoptera sample event data (family, subfamily, genus and species or morphospecies identification)

Type: Dataset

Status update: A total of 1622 beetle (Coleoptera) specimens (1057 from Mo Singto and 565 from Klong Naka rainforests) were collected and identified to species or morphospecies.
Dataset scope: Beetles collected from the forest canopy and understory of the two rainforests in southern Thailand}
Expected number of records: 1073
Data holder: Laksamee Punthuwat, Ekgachai Jeratthitikul, Alyssa Stewart, and Akihiro Nakamura
Data host institution: Chinese Academy of Sciences
Sampling method: SLAM traps (10 days) in the forest canopy and understory of the sampling points (A total of nine sampling points at each Klong Naka and Mo Singto rainforest site).
% complete: 100
DOI: https://www.gbif.org/dataset/7ba1318c-04ed-4521-8369-63731e2867f7
Expected date of publication:

Title: Lepidoptera (moths) sample event data (species or morphospecies-level taxonomic identification)

Type: Dataset

Status update: We have sorted and identified a total of 1067 moth (Nolidae and Noctuidae) specimens from Mo Singto and Klong Naka. Where possible, these specimens were identified into family, subfamily, genus, and species (or morphospecies)
Dataset scope: Moths (Nolidae and Noctuidae only) collected from the forest canopy and understory of the two rainforests in southern Thailand.}
Expected number of records: 591
Data holder: Laksamee Punthuwat, Ekgachai Jeratthitikul, Alyssa Stewart, and Akihiro Nakamura
Data host institution: Chinese Academy of Sciences
Sampling method: Light traps (3 nights) in the forest canopy and understorey at each sampling point (9 sampling points at each location) over two seasons in Mo Singto and Klong Naka rainforests.
% complete: 100
DOI: https://www.gbif.org/dataset/30a14970-3f5c-4f39-bb8f-1ecb7a698fd0
Expected date of publication:

Title: Hymenoptera sample event data (family, subfamily, genus and species or morphospecies identification)

Type: Dataset

Status update: A total of 1763 hymenopteran specimens were extracted from yellow pan flight

interception traps (FITs) and were sorted and identified into family, genus and species (or morphospecies). The specimens are currently curated by Alexey Reschikov and taxonomic information will be updated in due course.
Dataset scope: Hymenopterans collected from the forest canopy and understory of the two rainforests in southern Thailand.}
Expected number of records: 1258
Data holder: Laksamee Punthuwat, Ekgachai Jeratthitikul, Alyssa Stewart, and Akihiro Nakamura
Data host institution: Chinese Academy of Sciences
Sampling method: Flight interception traps with yellow pan (10 days) in the forest canopy and understorey at each sampling point (9 sampling points at each location). Hymenoperans were collected from Mo Singto and Klong Naka rainforests in southern Thailand in the wet and dry seasons.
% complete: 100
DOI: https://www.gbif.org/dataset/cd451e0f-789e-4416-94f4-e583e57f20ce
Expected date of publication:

Impact of COVID-19 pandemic on project implementation

Due to the COVID-19 pandemic and subsequent travel restrictions and university closure, the progress of our project was delayed substantially. Due to international and domestic travel restrictions, onsite collaborative work, such as specimen sorting and identification with local taxonomists, was impossible for over one year in Thailand. Nakamura could not travel to Thailand to have meetings and to check the progress of sample sorting, identification, and data organization. As a result, one of the data sets (hymenopterans) contained many identification errors due to limited accessibility to local taxonomists and two persons working individually without physically cross-checking the specimens. Meta-DNA barcoding was initially scheduled to be processed in China, but the quality of samples became degraded during the international transit and eventually returned to Thailand due to strict quarantine measures in China. This resulted in increased costs of meta-barcoding and failures of DNA extractions from many samples. As our research money from the co-funding was exhausted, we had to cancel DNA barcoding from individual specimens of the target groups (but the specimens are kept for future DNA barcoding when we obtain further financial assistance in China or Thailand). International travel restrictions prohibited Punthuwat (one of Nakamura’s students) from returning to China until the end of 2022. Three of the four evaluation and monitoring meetings were subsequently canceled (Nakamura self-funded his trip for the first and last meeting in Thailand in December 2022). Despite such difficulties, all project members worked hard, and we utilized online platforms to have meetings and to check the progress. We generated the four datasets (moth family, moth species, beetle, and hymenoptera), which have been uploaded to the GBIF.

Events

One Day Canopy Conference Online

Dates: 2021-10-18 - 2021-10-18
Organizing institution: Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences
Country: China
Number of participants: 110
Comments: Please also find attached the conference agenda.
Website or sources of verification:
https://www.xtbg.cas.cn/2018/tzgg/xs/202110/t20211011_6220483.html

Communications and visibility

We believe that making biodiversity data publicly available through the GBIF platform is essential for developing science and for open and clear communications among the scientific communities. We are currently working on one manuscript based on the data from this project, and upon publication, the links to the relevant GBIF data will be provided in the paper. We will continue to publish other sample-event ecological data via the GBIF so that everyone can access our data which are generated mainly by publicly funded projects (such as BIFA). When Nakamura and other members presented their research at a seminar or conference, we acknowledged the BIFA as one of our funding agencies and addressed the significance of data sharing among Chinese, Thai, and other international communities.

On our BIFA project webpage, we would like to inform about the 8th International Canopy Conference, which will be held in Xishuangbanna, China from the 15th to 19th of October 2023 (hosted by Nakamura). At this conference, we will showcase the results of our BIFA project. Other international participants will present relevant biodiversity projects. At the conference, I would like to acknowledge the BIFA as one of our funding agencies and disseminate information about the significance of GBIF for biodiversity data sharing. The conference website is under construction (but see https://canopy8th.casconf.cn/).

Monitoring and evaluation

Final Evaluation

This project was funded by the BIFA amid the COVID-19 global pandemic. As a result, our project schedule and budget had to be rearranged accordingly. The project implementation was hugely affected by the COVID-19 pandemic, as our project was based on bilateral collaborations between Chinese and Thai research institutes, and travel restrictions prohibited us from organizing project evaluation and monitoring meetings. Despite such difficulties, we regularly had online meetings and checked data quality and taxonomic identification. Nakamura and other members also gave online presentations at conferences and seminars to disseminate our project's outcomes and inform the public about the scientific significance of the GBIF and biodiversity data sharing with the international communities. We apologize for the substantial delays we caused. Nevertheless, we gave our best to deliver biodiversity data that can be used by the broader scientific communities.

Before the BIFA-funded project was implemented, Chinese PI (Nakamura) and Thai co-PI (Jeratthitikul) had been working together and established a solid collaborative foundation. As a result, communications between Chinese and Thai members were always effective even though we had to rely on online meeting platforms. The samples collected from the two rainforests were handled properly (except when the samples were shipped for meta-barcoding, but this was outside of our control) and we successfully generated the five datasets, as we promised in our proposal. Our weakness was the lack of taxonomic expertise for beetles and hymenopterans (Jeratthitikul is highly knowledgeable on Lepidoptera taxonomy). We initially planned to obtain assistance from local taxonomists, but due to the COVID-19 related travel restrictions, this was either not possible (for hymenopterans as the students graduated before the end of COVID-19 travel restrictions) or delayed substantially (for beetles). Our datasets published via the GBIF attracted significant attention from the international communities. We published our family-level datasets in 2021 (NB, the beetle and hymenopteran species-level data were added to the existing family-level data in March 2023), and all three datasets have been cited at least five times. We also received some email inquiries about the data as the occurrence of certain families in southern Thailand may be new to science.

This project was definitely the hardest one to implement in the career of PI and co-PI. But we are proud that we gave our best and successfully delivered the datasets via the GBIF and we continue to publish our data on the GBIF.

Best Practices and Lessons Learned

The COVID-19 pandemic imposed the most difficult challenges to implementing the international project. In 2020, we were rather optimistic that the travel restrictions will be lifted within a year. But China held one of the most stringent travel restrictions until the end of 2022. We believe that it is best to assume the worst-case scenarios whilst giving our best to implement our activities. We were a little too optimistic especially when we rearranged our schedule and budget in the midterm report.

Post Project Activity(ies)

We are currently working on one manuscript with Thai collaborators (Jeratthitikul and Taveesri) and Chinese counterparts (Nakamura and Punthuwat). The results of this manuscript is based on our datasets (beetles, moths, and hymenopterans), describing how spatiotemporal variabilities influence the vertical stratification of insects. We aim to publish in a high-profile international journal (such as Ecography or Insect Diversity and Conservation, both published by Wiley).

Nakamura will host the 8th International Canopy Conference in Xishuangbanna, China from the 15th to 19th of October 2023 where he and his project members will showcase the result of this BIFA project and share our experience with BIFA whilst addressing the significance of sharing biodiversity information with wider communities. This is critically important as Asian scientists often hesitate to share the data with others even though most of our projects are publicly funded.

Taxonomic information is continuously revised, and our datasets may still contain some errors (especially beetles and hymenopterans). We will continue to check and update our data as we analyze and prepare our scientific manuscripts. We have continued to contact Thai and Chinese taxonomists, and they are willing to offer continuing help to improve our data.

Sustainability plans

This BIFA project further solidified the collaborative relationships between the Chinese and Thai institutes, and Nakamura and Jeratthitikul continue striving for more collaborative international projects. This project also led one of Nakamura’s students (Thilina Nimalrathna) and his taxonomic collaborator (Alexey Reschkov) to collaborate and successfully obtain another BIFA grant (https://www.gbif.org/project/BIFA6_006/tending-to-the-neglected-diversity-of-beetles-and-darwin-wasps-in-southwest-chinas-lost-worldrld” (gbif.org)).

Thai and Chinese collaborators will continue to work together to generate scientific publications and to host the conferences (the 8th International Canopy Conference 2023 in Xishuangbanna, China). We now recognize that publishing ecological data is feasible (sample-event data) using the BIFA IPT platform. We wish to continue publishing the data as we currently hold many datasets generated from Australia, Thailand, and China. Nakamura will continue to seek funding to improve our understanding of the spatiotemporal pattern of insect biodiversity in the tropical forests of Southeast Asia.

With no more travel restrictions, Nakamura can readily travel to Thailand and other Southeast Asian countries. He will continue to collaborate with Thai co-PI and monitor and evaluate the future progress of our collaborative projects.

GBIF leads the Biodiversity Information Fund for Asia (BIFA), a programme funded by the Ministry of the Environment, Government of Japan. The programme provides supplementary support for activities addressing the needs of regional researchers and policymakers through mobilization and use of biodiversity data.

GBIF