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 - 31/12/2021
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Narrative Midterm report

Executive Summary

We have successfully completed the following: the BIFA online workshop in August with Advanced and Basic badges; and conducted fieldwork in southern Thailand in October 2020. All of the samples have been processed to extract the target taxonomic groups (moths, hymenopterans and beetles). Before the university became officially closed in 2020 due to COVID-19 pandemic in Thailand, the project participants took some of the samples (and laboratory equipment with permission), so that they were able to work from home to process specimens for family, subfamily, genus and species level identification. The university became partially open from early 2021 and some of the project members are now able to process samples in the laboratory.

As we started using the IPT provided by CAS, we discovered that their platform had some bugs and did not support sampling event data. The issues could not be fully solved and we therefore have uploaded our data (Lepidoptera, Coleoptera and Hymenoptera specimens identified to families and some specimens to subfamily) via BIFA IPT (https://cloud.gbif.org/bifa).

As we obtained larger than expected number of specimens per sample, we decided to process particular superfamilies or families (instead of all families of the target groups). Due to travel restrictions, monitoring and evaluation of the project have been done via regular online meetings. The online meetings, however, has not been as effective. We expect travel restrictions to be lifted by the middle or late 2021. However, if travel restrictions are NOT to be lifted, we will rely on local co-PIs and students in Thailand to process samples for meta-DNA barcoding and complete all of the required tasks. The budget allocated for travelling may not be fully spent during the funding period.

Progress against milestones

Has your project published at least one dataset through GBIF.org?: Yes

Dataset published:

Dataset	DOI
Insect (Hymenoptera) Biodiversity Across Forest Canopy and Understorey in SE-Asia BIFA5_026	https://doi.org/10.15468/bne2yc
Insect (Coleoptera) Biodiversity Across Forest Canopy and Understorey in SE-Asia BIFA5_026	https://doi.org/10.15468/92ca8u
Insect (Lepidoptera) Biodiversity Across Forest Canopy and Understorey in SE-Asia BIFA5_026	https://doi.org/10.15468/yge43c

Has at least one member of your project team received certification following the BIFA capacity enhancement workshop?: Yes

Name of the workshop participant: Akihiro Nakamura

Certification obtained: Advanced Badge

Report on Activities

Activity progress summary

BIFA Capacity Enhancement Workshop: The PI (Nakamura) and the project assistant (Waitayachart), attended the online workshop and successfully completed with the advanced (Nakamura) and basic badges (Waitayachart). We have also been granted to access IPT via the CAS node to publish our data (but, as mentioned earlier, they did not provide sampling even data format and we could not resolve the issues with them, so we decided to upload our data via 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 288 samples (light traps: 2 locations x 2 seasons x 2 vertical strata x 9 plots = 72 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). Waitayachart and the participants involved in this project have successfully extracted specimens of the target taxonomic groups (beetles, moths and hymenopterans) from all samples collected from Mo Singto and Klong Naka in 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) are stored in the freezer for meta-DNA barcoding.

Arthropod sampling in Klong Naka (September): We have successfully completed the second field survey at Klong Naka during wet season. The survey was originally planed in July; 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 Thai local assistants and students. The fieldwork was completed successfully with all traps retrieved without a failure.

Higher taxonomic identification: Higher taxonomic-level identification has been started as soon as the target specimens were extracted. **Moths**: We collected 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 to superfamily and then family. For species/morphospecies level identification, we are using only target families and superfamilies, namely Noctuoidea, Pyraloidea and Geometroidea. Our target taxonomic scopes and taxonomic groups have been slightly modified from those listed in our proposal (Geometridae, Noctuidae, Arctiini) as the number of specimens from individual taxonomic groups were different from what we initially expected. **Beetles**: Beetle sorting and identification have been taking longer than we initially anticipated due to high family-level diversity of beetles and difficulties in accessing taxonomic help (due to travel restrictions in Thailand). We therefore decided to sort and identify all beetles to families or subfamilies from a subset of samples: samples collected from Mo Singto dry season and Klong Naka dry season by SLAM traps (236 specimens from 72 samples). For the remaining samples, we are extracting only target families that are ecologically relevant (different feeding guilds) and manageable to complete before the end of BIFA project and the student's PhD program. Target beetle families include Chrysomelidae (herbivores), Curculionidae (herbivores), Staphylinidae (primarily predators), Cleridae (predators) and Anthicidae (predators). **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 hymenopteran component withdrew from this project in 2020, the project assistant (Waitayachart) took over this role and is working on the remaining samples and sort them to families and morphospecies with assistance from the local taxonomists (Dr Alexey Reshchikov). As of April 2021, we have completed family-level identification of hymenopterans from Mo Singto dry and wet seasons and Klong Naka dry season (1451 specimens from 54 samples).

Species-level identification: Due to COVID travel restrictions and university closure, it is difficult to get taxonomic assistance to identify our specimens to species. Nevertheless, we are doing our best to identify specimens to at least morphospecies, so that taxonomists can later give them scientific names. The student in charge of beetle (Punthuwat) has successfully identified a total of 421 specimens to species or morphospecies (291 from Mo Singto and 130 from Klong Naka so far). The student working on moths (Taveesri) has been working on species/morphospecies level identification of the target moth groups. The species-level data will be available for analysis and publication by the middle of this year.

DNA barcoding and meta-DNA barcoding: This has not been started due to university closure. Waitayachart and the students are currently working from home with some specimens taken from the university before the university became closed. One of the students who works on moths obtained a special permit to enter the university and he has been able to work on samples in the laboratory (but not everyday). Due to the extended closure and travel restrictions in Thailand, the progress of the higher taxonomic and species-level identification has been delayed, consequently we were unable to commence DNA barcoding as scheduled. We will commence DNA barcoding as soon as the university becomes accessible.

Data entry: Waitayachart has collated the higher taxon data and attempted to upload and publish the data via the CAS IPT. Nakamura has checked the data before publication. The data, however, could not be uploaded properly as the CAS IPT is having persisting bug issues and does not support sampling event data (they were using version 2.0 until we raised this issue). As these issues could not be resolved fully, we decided to upload the data via BIFA IPT. The data will be updated as we process more samples. Species-level data has not been finalized and will be published in due course.

First and Second evaluations: Nakamura has not been able to travel to Thailand due to the COVID situations in China and Thailand. One of the project students, Punthwat, is affiliated to Nakamura's institute in China but she has been stranded in Thailand since early 2020. She is currently working on the beetle specimens collected from Mo Singto and Klong Naka. All of the planned travelling plans, therefore, have been cancelled. We are communicating via online tools to evaluate the progress of the project on a regular basis.

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: 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) will be 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 (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").

Report on Deliverables

Deliverables progress summary

We have successfully extracted the target specimens (moths, hymenopterans and beetles) from all of our raw samples, and the participants who are responsible for each target groups have identified a large number of specimens to superfamily, family and subfamily. As we collected a large number of samples (see the attached Excel file with the list of samples we collected from the two locations using three different sampling techniques), we have identified priority set of specimens and sorted these samples instead of all of them to get the best results for ecological studies.

For publication via IPT, we have decided to combine higher taxonomic data and species-level data of the same target group, as publishing them separately will duplicate the data. The published datasets include only family-level

Moths (Lepidoptera): We have extracted and identified a total of 13725 moth specimens to superfamily or family. These specimens were collected from the two locations (Mo Singto and Klong Naka) and collected by light traps set at the forest canopy and understorey from a total of 9 sampling points in wet and dry seasons. We collected extremely large number of specimens, and we therefore decided to focus on particular superfamilies and families, namely Noctuoidea, Pyraloidea and Geometroidea for the subsequent identification work (instead of sorting and identifying ALL of the moths we have collected).

Hymenopterans: We have extracted and identified a total of 1451 hymenopteran specimens to family. These specimens were collected from one of the two locations (Mo Singto) and collected by yellow pan FIT traps set at the forest canopy and understorey from a total of 9 sampling points in wet and dry seasons. As the participant who was in charge of this taxonomic group has left the university, we have assigned our research assistant (Waitayachart) to continue to work on the remaining work. We are also getting taxonomic assistance from Dr Alexey Reshchikov who resides in Thailand for species-level identificattion.

Beetles: We have sorted and identified a total of 421 beetles (291 from Mo Singto and 130 from Klong Naka so far) to families, subfamilies, genus and species. As the species level identification is taking longer than expected due to difficulties in taxonomy and accessing the local taxonomists, we have decided to focus on particular families of beetles that are ecologically relevant.

Progress towards deliverables

Title: Arthropod sample event data (non-target groups) from Mo

Singto and Klong Naka

Type: Dataset

Status update: We will carry out meta-DNA barcoding using the residual samples (i.e., samples after extracting the target specimens). Target specimens have been extracted from all of the samples (see List of the samples with completed tasks). Due to COVID pandemic and subsequent closure of the university, we are however unable to carry out meta-DNA barcoding until travel restrictions are lifted and the university opens. It is uncertain when we will be able to organize samples and send them to the company for meta-DNA barcoding but we are hoping to carry this out within a few months.
Dataset scope: Specimens of the non-target groups will be meta-brcoded. MOUTs, genus or species. We expect a large number of MOUTs and species assignments from each sample and the number of records are very difficult to predict.}
Expected number of records: 20000
Data holder: Akihiro Nakamura and Ekgachai Jeratthitikul
Data host institution: Chinese Academy of Sciences
Sampling method: SLAM traps, light traps, and flight interception traps with yellow pans. A total of 216 samples (2 locations x 2 strata x 2 seasons x 9 sampling points x 3 sampling methods) to be processed.
% complete: 0
DOI:
Expected date of publication: 2021-07-01

Title: Lepidoptera (moths) sample event data (higher taxonomic identification)

Type: Dataset

Status update: We have extracted and identified a total of 13814 moth specimens to family. These specimens were collected by light traps set at the forest canopy and understorey of a total of 9 sampling points at each location in wet and dry seasons. We collected extremely large number of specimens with the total number of moths exceeding the expected number of specimens (9300 entries) listed in the proposal.
Dataset scope: The data is highly useful for ecological studies and macro-scale studies to understand the distribution patterns of Lepidoptera. }
Expected number of records: 13814
Data holder: Ronnarot Taveesri, Akihiro Nakamura, Ekgachai Jeratthitikul and Alyssa Stewart
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 location) from two locations in two seasons.
% complete: 100
DOI: https://cloud.gbif.org/bifa/resource?r=insect_biodiversity_across_forest_canopy_and_understorey_in_se-asia_lepidoptera_sampling_event_data_bifa5_026&v=1.0
Expected date of publication:

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

Type: Dataset

Status update: We are currently processing the specimens that have been identified to family. Over 1000 specimens have been sorted to species.
Dataset scope: The total number of records will be smaller than the total number of family-level records as we will only sort some families (viz. Geometridae, Noctuidae, Arctiini) to described species.}
Expected number of records: 2000
Data holder: Ronnarot Taveesri, Akihiro Nakamura, Ekgachai Jeratthitikul and Alyssa Stewart
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 location).
% complete: 50
DOI:
Expected date of publication: 2021-07-31

Title: Hymenoptera sample event data (higher taxonomic identification)

Type: Dataset

Status update: We have extracted and identified a total of 1451 hymenopteran specimens to family. These specimens were collected from Mo Singto in dry and wet seasons and Klong Naka in dry season using yellow pan FIT traps set at the forest canopy

and understory of a total of 9 sampling points in wet and dry seasons. As the participant who was in charge of this taxonomic group has left the university, we have assigned our research assistant (Waitayachart) to continue to work on the remaining specimens. We are also getting taxonomic assistance from Dr Alexey Reshchikov who resides in Thailand for species-level identification.
Dataset scope: Higher-level taxonomic identification of hymenopteran specimens collected from the forest canopy and understorey of Mo Singto and Klong Naka.}
Expected number of records: 3000
Data holder: Achariyaporn Janmaneeporn, Pattharawadee Waitayachart, Akihiro Nakamura, Ekgachai Jeratthitikul and Alyssa Stewart
Data host institution: Chinese Academy of Sciences
Sampling method: SLAM traps (10 days), light traps (3 nights) and flight interception traps with yellow pan (10 days) in the forest canopy and understorey of the sampling points (9 sampling points at each location)
% complete: 48
DOI: https://cloud.gbif.org/bifa/resource?r=insect_biodiversity_across_forest_canopy_and_understorey_in_se-asia_hymenoptera_sampling_event_data_bifa5_026&v=1.0
Expected date of publication: 2021-03-31

Title: Hymenoptera sample event data (species-level identification)

Type: Dataset

Status update: A total of six samples have been sorted and identified to morphospecies to date. As the person originally assigned to work on hymenopterans has left this project, my assistant (Waitayachart) will complete the remaining tasks with local taxonomist, Dr Alexey Reschikov.
Dataset scope: We take conservative estimations that we will be able to identify about a third of these specimens to described species based on morphological characteristics and DNA sequences with the aid of local taxonomists.}
Expected number of records: 1000
Data holder: Achariyaporn Janmaneeporn, Pattharawadee Waitayachart, Akihiro Nakamura, Ekgachai Jeratthitikul and Alyssa Stewart
Data host institution: Chinese Academy of Sciences
Sampling method: Flight interception traps with yellow pan (10 days) in the forest canopy and understorey of the sampling points (9 sampling points at each location).
% complete: 10
DOI:
Expected date of publication: 2021-07-31

Title: Coleoptera sample event data (higher taxonomic identification)

Type: Dataset

Status update: We have so far identified a total of 236 beetles to family (and they are all identified to species also) The data has been uploaded and published via BIFA IPT. Due to slow progress speed and time limitation, we have decided to focus on particular families of beetles (instead of ALL beetles to family) for higher and species level taxonomic identification. See also attached pictures of beetles identified to family ("Beetle pic identified to family")
Dataset scope: We estimated a total of over 2000 beetles from Mo Singto location and we expect to have approximately two times as many specimens (4000) in Klong Naka, southern Thailand.}
Expected number of records: 6000
Data holder: Laksamee Punthuwat, Akihiro Nakamura, Ekgachai Jeratthitikul and Alyssa Stewart
Data host institution: Chinese Academy of Sciences
Sampling method: SLAM traps (10 days) in the forest canopy and understorey of the sampling points (9 sampling points at each location).
% complete: 4
DOI: https://cloud.gbif.org/bifa/resource?r=insect_biodiversity_across_forest_canopy_and_understorey_in_se-asia_coleoptera_sampling_event_data_bifa5_026&v=1.1
Expected date of publication: 2021-06-30

Title: Coleoptera sample event data (species-level identification)

Type: Dataset

Status update: Although progress has been slower than initially anticipated, Punthwat has identified many of the specimens to genus and described species. Please also see attached Excel file with raw data containing beetles identified to species or morphospecies ("Coleoptera (beetles) species level identification raw data SLAM traps Mo Singto Dry season" and "Coleoptera (beetles) species level identification raw data SLAM traps Klong Naka Dry season").

Dataset scope: Specimens belonging to Chrysomelidae, Curculionidae, Staphylinidae, Cleridae and Anthicidae to be identified to described species based on morphological characteristics and DNA sequences with the aid of the local taxonomists.}
Expected number of records: 1000
Data holder: Laksamee Punthuwat, Akihiro Nakamura, Ekgachai Jeratthitikul and Alyssa Stewart
Data host institution: Chinese Academy of Sciences
Sampling method: SLAM traps (10 days), light traps (3 nights) and flight interception traps with yellow pan (10 days) in the forest canopy and understorey of the sampling points (9 sampling points at each location).
% complete: 42
DOI:
Expected date of publication: 2021-06-30

Communications and visibility

Our project has been published via BIFA IPT, and the PI (Nakamura) publicized the project using SNS (Facebook) and through various seminars that he presented. These seminars include: invited seminars at Yunnan University on the 17th September 2020 and at Dali University on the 7th January 2021, Ecological Society of Yunnan Conference held between 27th and 29th December 2020, and Xishuangbanna Tropical Botanical Garden Annual Conference held between 4th and 5th December 2020. Communication and publicizing activities, however, have been difficult due to the travel restrictions. Nakamura and other co-PIs have not been able to attend international conferences, as various national and international conferences and meetings have been cancelled. Despite this, we attended online conferences in 2021 (e.g., Ecological Society of Japan Annual Conference in March 2021) and utilize other online opportunities to publicize our project this year. Nakamura is also organizing the 8th International Canopy Conference from the 13 to 16th October 2021 where the preliminary results of our project will be presented. Nakamura and his co-PIs in Thailand will seek more opportunities to publicize our project through popular magazines and other media. Recently, Chinese National Geography contacted Nakamura about his canopy studies, and they are planning to come and interview him this year. Peer reviewed scientific papers based on this project will be published in due course.

Monitoring and evaluation

Monitoring and evaluation findings

We initially planned to have regular visits to Mahidol University, Thailand, by Nakamura and his student (Punthwat) to monitor the progress and evaluate our project on a regular basis. This, however, has been impossible due to travel restrictions in China and Thailand. We therefore opted to have regular online meetings with all of the project core members (Nakamura, Waitayachart, Jeratthitikul, Stewart and our students). Although communication has been quite effective, it is difficult for Nakamura to evaluate details of the project as he was unable to see actual specimens and laboratory conditions.

We have completed the online capacity enhancement workshop, successfully conducted the last fieldwork, and sorted and identified a large number of specimens to superfamily, family and subfamily. However, the participants have been struggling with the large number of specimens and Nakamura was unable to see their daily progress and unable to give timely academic and taxonomic advice. Also the students are clearly not focusing on their work when they are working from home.

It is critical that PIs and co-PIs discuss with individual students and research assistants separately via regular online meetings (instead of just having group meetings), so that we can find individual problems and solutions. We are hoping that travel restrictions and university closure to be lifted by the middle of 2021 so that students can have access to all of the samples and commence DNA barcoding.

As most activities are carried out in Thailand, we set the budget in Thai Baht in the proposal. This however caused a problem as we received the money in Chinese Yuan and most purchases are made in China and the salary has been paid in Yuan (and then exchanged as the money was transferred online).

Impact of COVID-19 pandemic on project implementation

Due to the COVID-19 pandemic and subsequent travel restrictions and university closure, progress of our project has been slow, and the PIs and co-PIs have not been able to effectively monitor and evaluate the project progress. Our work has been fragmented into individual PI, co-PIs, the project assistant and students, and students have been forced to work from home without the physical presence of supervisors. Nakamura has been unable to travel to Thailand to have meetings and check progress of the sample sorting, identification and data organization. DNA barcoding has not been commenced due to travel restrictions and university closures in Thailand. We have been doing our best to coordinate the project activities via online meetings but this cannot fully replace the required tasks. Nevertheless, we have made a good progress and meet most of the scheduled activities (namely attending the online workshop, completing 2nd insect survey at Klong Naka, and completing sample sorting to extract the target specimens). Higher taxonomic identification has been completed and morphospecies identification is well underway. The research assistants and students took some of the samples home with microscopes before the university became officially closed so that they are able to study and conduct lab work from home. But the progress has been slower than initially anticipated.

We now plan to cancel all of the international travels for 2021, but as soon as travel restriction is lifted, Nakamura plans to go visit Mahidol University to check the samples and commence DNA barcoding. Due to travel restrictions and university closures, taxonomic identification has been difficult as we have been unable to access all of the specimens stored in the university and we have been unable to transport the specimens to the taxonomists for species-level identification. All of these activities will become possible once international (for Nakamura to go to Thailand) and domestic (for the participants to access taxonomic assistance) travelling become possible.

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