

大学院教育支援機構（DoGS）海外渡航助成金 報告書

Outcome report

計画名 Plan	欧州植物標本庫に収蔵されたさく葉標本を活用した次世代系統解析
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研究科・専攻・学年 Graduate school/Division/Year level	大学院理学研究科・生物科学専攻 博士後期課程・1年
渡航国 Country	Netherlands and UK
渡航日程 Travel schedule	2024年1月7日～2024年1月29日

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渡航計画の概要 Outline of the travel plan

The objective of my research trip is to visit the Kew Botanical Gardens and Naturalis Biodiversity Center herbaria to accomplish species identification, photographic documentation of morphological characteristics, and procure DNA samples of all target species of my doctoral thesis:

1- DNA Samples collection

My study group, *Hibiscus* section *Azanzae* which is diversified along Southeast Asia. Several species have been described as new species solely based on a handful of herbarium specimens without ever being collected in the wild. The application of next-generation sequencing (NGS) gives us the chance for accessing the genetic information conserved in these herbarium specimens. I aim to construct a comprehensive phylogeny of the genus and unravel its natural history.

2- Morphology documentation and species identification

Molecular analysis results must be accomplished by a careful morphological examination. Until now, the morphology of this section has been described by previous authors and used for its taxonomy, however, the presence of considerable morphological variation within the section can be occasionated by factors such as environmental conditions, genetic diversity or and hybridization. Then, it is still unclear which morphological characters have taxonomic importance.

3- Learning

Herbarium specimens handling is important for their conservation, especially when "destructive sampling" as DNA extraction is done. Hence, a special training is necessary prior samples collection.

The travel period took place between January 7th to 29th. During the first 2 weeks, I stayed at Naturalis Biodiversity Center herbarium, in Leiden (Netherlands). Afterwards, I moved to Kew Botanical Gardens herbarium, in London (UK).

成果 Outcome

During this research trip, I improved my knowledge on the research species, and advanced my samples collection. Therefore, three main goals of my travel were accomplished:

1- Samples collection

DNA samples from leaves were obtained for 28 taxa which, in addition to the samples obtained before this trip, cover the 88% of *Hibiscus* section *Azanzae* species.

2- Morphology documentation

On this trip I have taken 4292 photos (Fig. 1) of 35 *Azanzae* related taxa (only *H. bowersiae* left because the only specimen is in US herbarium), plus many yet-to-be-identified specimens which seems to be related with the group.



Figure 1: Examples of herbarium specimens photos (A) *H. dalbertsii* from Naturalis Biodiversity Center herbarium, and (B) *H. sterculiifolius* from Kew Botanical Gardens herbarium.

3- Learning

Working actively in two different herbaria has allowed me to learn very different specimens organization system and management techniques between both European herbaria and the Japanese herbarium. I could learn the best techniques for a minimum damage of herbarium specimens when “destructive sampling” is necessary. Also, I had the chance of having fruitful discussions with researchers and herbarium curators from both institutions allowing me to create an important contact network essential for my future career.

今後の展望 Prospects for the future

Short-term

The immediate next goal is to extract ancient DNA from the samples gathered in this trip, and process the DNA following Hyb-seq workflow (gene library preparation, hybridization capture, next-generation sequencing, and bioinformatic analysis).

Medium-term

After DNA sequences bioinformatic analysis, I will obtain the first comprehensive phylogeny of section Azanzae and unravel the natural history of the group. I expect to publish the findings in peer-reviewed journals and international congress as IBC (International Botany Congress) Madrid 2024.

Long-term

The phylogenetic framework garnered from the herbarium collection presents me with a valuable opportunity to establish a connection between the ecological aspects of *Hibiscus*. In addition to my phylogenetic analyses, my thesis encompasses an exploration of the reproductive ecology of *Hibiscus* species in East Asia. By utilizing the phylogeny, I aim to delve into the evolutionary processes behind the changes observed in pollination and seed dispersal modes among *Hibiscus* species.