

# Journal of Integrated Field Science

## Vol.20



March. 2023

# Contents

## Preface

Yoshihisa SUYAMA Preface to the 20 <sup>th</sup> International Symposium on Integrated Field Science "Biodiversity and Phylogeography"	1
---	---

## Symposium mini review

Harue ABE, Hiroki MIURA and Rui KATAYAMA A Comprehensive Comparison of Flower Morphology in the Genus <i>Camellia</i> , with a Focus on the Section <i>Camellia</i>	2
--	---

<b>Program</b>	10
----------------	----

## Invited Presentations

### Invited Talk 1

Harue ABE, Saneyoshi UENO, Ayumi MATSUO, Shun K. HIROTA, Hiroki MIURA, Monghuai SU, Yunguang SHEN, Yoshihisa SUYAMA and Zhonglang WANG Evolution of the Genus <i>Camellia</i> Based on the Biological Interaction and the Historical Background	13
--	----

### Invited Talk 2

Gustavo Maruyama MORI Like a Mangrove out of Water: Dispersal Limitation and Adaptive Responses of Dominant Coastal Trees to Freshwater Limitation	14
---	----

### Invited Talk 3

Yuji ISAGI, Yoshihisa SUYAMA and Takashi MAKINO Tailor-made Biological Conservation of Endangered Plant Species with Genomic Information	15
---	----

### Invited Talk 4

Alison K.S. WEE Mangroves in a Changing World: Biogeography and Ecological Genomics of Southeast Asian Mangroves	16
---	----

## Poster Presentations

### Poster 1

Muxiye, Chinatsu YONEZAWA, Mizuhiko NISHIDA, Ryosuke TAJIMA, Ryohei YOKOYAMA, Koharu OKADA, Kouki TAKAMURA, Kaori AMAYA and Ken ICHIKAWA Effects of Cultivation Methods on Paddy Rice Growth Observed by UAV-mounted Multispectral Camera	17
--	----

### Poster 2

Shoki MURAKAMI, Takuro ITO, Tatsuya UEMACHI, Shinji FUJII, Ayumi MATSUO, Yoshihisa SUYAMA and Masayuki MAKI Phylogeography of Intraspecific Differentiation of <i>Hydrangea serrata</i> (Hydrangeaceae), a Widespread Shrub Species in the Japanese Archipelago	18
--	----

### Poster 3

Ryohei YOKOYAMA, Chinatsu YONEZAWA, Mizuhiko NISHIDA, Ryosuke TAJIMA, Muxiye, Koharu OKADA, Kouki TAKAMURA, Kaori AMAYA and Ken ICHIKAWA Comparison of Vegetation Indices and Spectral Reflectance Observed by Two Types of UAV-mounted Multispectral Camera	19
---	----

**Poster 4**

- Erick W. WEISSENBERG, João Vicente COFFANI NUNES, Isis SEBASTIÃO,  
 Patrícia Gleydes MORGANTE and Gustavo Maruyama MORI  
 Morphological and Genetic Data Do Not Support the Intraspecific Taxonomic Classification of  
*Pimenta pseudocaryophyllus* ..... 20

**Poster 5**

- Hiroya TAGUCHI, Daiki TAKAHASHI, Takuro ITO, Shuichiro TAGANE, Ryota SUGAWARA,  
 Emiko OGURI, Harue ABE and Yoshihisa SUYAMA  
 Phylogeography of *Juniperus* Species (Cupressaceae) with a Disjunct Distribution in the Island  
 Areas of Japan ..... 21

**Poster 6**

- Yuki KAWASAKI, Shunsuke MATSUOKA, Hirotoishi SATO, Václav POUSKA, Jenni NORDÉN,  
 Olga ORMAN, Radek BAČE, Momchil PANAYOTOV, Nickolay TSVETANOV, Martin MIKOLÁŠ,  
 Lucie ZÍBAROVÁ, Angelos PAPADIMITRIOU, Elias POLEMIS, Kamil KRÁL, Miroslav SVOBODA  
 and Yu FUKASAWA  
 Decay Types and Fungal Communities of Norway Spruce Dead Wood in Europe ..... 22

**Poster 7**

- Mana MOTOMIYA, Daiki TAKAHASHI, Shuichiro TAGANE, Akiyo NAIKI, Kenta WATANABE,  
 Takuro ITO and Yoshihisa SUYAMA  
 Population Genetic Structure of a Bamboo Taxon, *Pleioblastus* Sect. *Pleioblastus*, in the Ryukyu Islands  
 Formed by Geohistory and Human Activity ..... 23

**Poster 8**

- Kaho ISHII and Yu FUKASAWA  
 Effects of the Resource Distance on the Decisions of Mycelial Behavior ..... 24

**Poster 9**

- Kodai HAMATSU, Hiroya TAGUCHI, Daiki TAKAHASHI and Yoshihisa SUYAMA  
 Development of Plant Environmental DNA Analysis Method for Forest Soil ..... 25

**Poster 10**

- Satsuki KIMURA, Yu FUKASAWA, Yuji KOMINAMI, Masahiro TAKAGI, Kimiyo MATSUKURA,  
 Masayuki USHIO, Makoto KOBAYASHI, Satoshi SUZUKI, Shuhei TAKEMOTO, Nobuaki TANAKA,  
 Mayuko JOMURA, Kohmei KADOWAKI, Haruo KINUURA and Satoshi YAMASHITA  
 Effects of Oak Wilt Disease on Fungal Community Composition and Wood Decomposition in  
 Dead *Quercus serrata* Trunks ..... 26

**Poster 11**

- Henri ALLEKOTTE, Taguchi HIROYA, Daiki TAKAHASHI and Yoshihisa SUYAMA  
 Phylogenetic Origin of *Cryptomeria japonica* on Kinkasan Island in Japan ..... 27

**Poster 12**

- Taishi HOSON, Takuro ITO, Shinji FUJII, Daiki TAKAHASHI, Ayumi MATSUO,  
 Yoshihisa SUYAMA and Masayuki MAKI  
 Molecular Phylogenetic Analyses of Geographical and Ecological Speciation of  
*Anaphalis margaritacea* ..... 28

- List of scientific papers in 2022 published by field science group in Graduate School of Agricultural Science,  
 Tohoku University ..... 29

**Guidelines for Authors**

## **Preface to the 20<sup>th</sup> International Symposium on Integrated Field Science “Biodiversity and Phylogeography”**

Yoshihisa SUYAMA

Graduate School of Agricultural Science, Tohoku University

Biodiversity is becoming more important in biology and agriculture and is a common issue for humankind. One of its research fields is phylogeography, which attempts to elucidate the historical process of the geographical distribution of modern individuals, populations, and species based on the analysis of genetic genealogy patterns. In this international symposium, four invited talks by up-and-coming researchers and 12 posters with short oral presentations by young students were held under the broad theme of “Biodiversity and Phylogeography.” The purpose of this symposium was not only to share the latest research information on the topic but also to provide the “diverse” participants with valuable presentation and discussion opportunities on the international stage, which can be utilized in the future.

I sincerely hope that this international symposium will contribute to the understanding and conservation of global biodiversity, the development of phylogeography, and the future of the participants.





Symposium mini review



## A Comprehensive Comparison of Flower Morphology in the Genus *Camellia*, with a Focus on the Section *Camellia*

Harue ABE<sup>1</sup>, Hiroki MIURA<sup>2</sup> and Rui KATAYAMA<sup>2</sup>

<sup>1</sup>Sado Island Center for Ecological Sustainability, Niigata University, Koda 94-2 Sado, Niigata 952-2206, Japan

<sup>2</sup>Formerly of Graduate School of Science and Technology, Niigata University, 8050, Ikarashi 2-Nocho, Nishi-ku, Niigata 950-2181

### Keywords

Bird-pollination, *Camellia japonica*,  
*Camellia rusticana*, Pollinator shifts,  
Yellow *camellias*

### Corresponding Author

Harue ABE,  
habe@agr.niigata-u.ac.jp

### Abstract

This study compared floral traits between the bird-pollinated sect. *Camellia* and other sections within the genus *Camellia* to investigate the relationship between floral traits and shifts in pollinators. In the cluster analysis of floral traits, bird-pollinated species in sect. *Camellia* (red camellias) and yellow camellias were found to form the same clade. These traits are possible adaptations for bird pollination. Yellow camellias are smaller in size than flowers in sect. *Camellia*. While sect. *Camellia* mainly relies on Japanese white-eyes, which suck nectar by hooking their feet on the petals for pollination, yellow camellias have adapted to hovering bird pollinators, which require a different set of characteristics. Interestingly, *C. rusticana*, which is the only insect-pollinated species within sect. *Camellia*, and sect. *Theopsis*, which includes insect-pollinated white flowers, were included in the same clade. Our results revealed a high level of uniformity in floral traits among species within sect. *Camellia*. A comparison of these findings with those of previous molecular phylogenetic studies revealed that the rapid diversification of sect. *Camellia* may not be attributed to a common ancestor. Instead, it may be attributed to different lineages influenced by environmental factors. To gain a more comprehensive understanding, it is essential to conduct a thorough quantitative analysis of the morphological traits within the *Camellia* genus. This analysis should also involve a reassessment of their relationship with molecular phylogeny, as molecular data can provide valuable insights into the evolutionary history and relationships among *Camellia* species.

### Introduction

The family Theaceae is known to comprise approximately 28 genera and 600 species that are mainly distributed in moist temperate regions worldwide (Iwatsuki, 2006). Among them, the genus *Camellia* is distributed in East and Southeast Asia and consists of approximately 125 species (Ming and Zhang, 1995). Sect. *Camellia*, which is the focus of this study, is characterized by large red flowers that bloom in winter. Various traits, such as shape, size, color, reward to pollinators (e.g., amount and quality of nectar), and timing of flowering, are important characteristics of these species that attract pollinators and are specialized according to the pollination syndrome (Faegri and van der Pijl, 1979). The bird pollination

syndrome involves the presence of large flowers, red or orange colors, and abundant and thin nectar. The characteristic red petals in sect. *Camellia* can be considered a bird pollination syndrome trait.

Early classifications of *Camellia* were primarily based on morphological differences in leaves, flowers, and fruits (e.g., Sealy, 1958; Chang, 1998; Ming, 1999; Ming, 2007). Recently, these classifications have been revised using molecular phylogenetic analyses (e.g., Rao *et al.*, 2018; Zhang *et al.*, 2019; Cheng *et al.*, 2022; Wu *et al.*, 2022; Yan *et al.*, 2021). According to these analyses, the ancestral sections in the subgenus *Camellia* are sect. *Furfuracea*, sect. *Thea*, sect. *Glaberrima*, and sect. *Longissima*; they are characterized by white petals and a floral fragrance, which are adaptations

to insect pollinators. The results of molecular phylogenetic studies suggest that the major clades of *Camellia* radiated in the late Miocene along with the formation of subtropical evergreen broad-leaved forests in East Asia (Shengyuan *et al.*, 2023; Zan *et al.*, 2023). The polymorphism of flower color and size within the genus *Camellia* is thus thought to be a result of adaptation to pollinators (pollinator shifts). Moreover, it is predicted that the ancestral sect. *Camellia* with insect pollination traits differentiated into sect. *Camellia* with bird pollination traits. However, the relationship between molecular phylogeny and floral traits is not always straightforward, as some ancestral *Camellia* sections, such as sect. *Corallina* and sect. *Brachyandra*, have yellow or pink petals and are pollinated by bees or sunbirds (Sun *et al.*, 2017). Therefore, the relationship between molecular phylogeny and floral traits is more complex than considered previously. While some studies have attempted to examine the relationship between morphology and molecular phylogeny (Zan *et al.*, 2023), more quantitative assessments and comparisons between floral traits and pollination strategies are required.

The complex relationship between molecular phylogeny and floral traits is exemplified in two species of sect. *Camellia* that are distributed in Japan. *C. japonica* and *C. rusticana*, which belong to sect. *Camellia*, have characteristic large red petals, suggesting that they are bird-pollinated species. Although *C. japonica* is a bird-pollinated species (e.g., Yumoto, 1988; Abe *et al.*, 2008; Abe *et al.*, 2011), a different pollination system involving insects has been reported in *C. rusticana* (Ishizawa, 1988). The floral traits of *C. rusticana*, except for flower color, are characteristic of insect pollination (e.g., Ishizawa, 2005; Abe and Miura *et al.*, 2020).

Therefore, in this study, we comprehensively compared floral traits, with a focus on sect. *Camellia* which exhibits bird pollination traits. We also compared white-flowered species with insect pollination traits and yellow-flowered species with bird pollination traits. Our study assessed the systematic position of sect. *Camellia* and its relationship with pollinator shifts based on floral traits and their relationship with existing molecular phylogenies.

## Materials and Method

A total of 27 *Camellia* species, primarily belonging to sect. *Camellia*, were used in this study. Of these, 25 species were collected from the greenhouse of Inokuchi Tsubaki Kan in Nanto City, Toyama Prefecture. In addition, data from two species, *C. japonica* and *C. rusticana*, which grow naturally in Niigata Prefecture and were used in the study of Abe and Miura *et al.* (2020), were included in our study (Table 1). The breakdown was as follows: 15 species from sect. *Camellia*, two species from sect. *Paracamellia*, one species from sect. *Oleifera*, one species from the sect. *longipedicellata*, four species from sect. *Theopsis*, and four yellow species from sect. *Chrysanth*. Of these, 15 species had red flowers (sect. *Camellia*), eight had white flowers (sect. *Paracamellia*, sect. *Oleifera*, sect. *Longipedicellata*, and sect. *Theopsis*), and four had yellow flowers (sect. *Chrysanth*) (Table 1). To assess the differences in flower morphology of *Camellia* species, quantitative measurements of the flower diameter, corolla length, petal length, maximum stamen length, and stamen attachment rate (length of stamen attachment/maximum stamen

length) were performed (Fig. 1). Corolla and petal lengths were excluded from the measurement items because of large differences between flowers. Measurements were performed by disassembling the flowers into as many parts as possible. For the measurements, three flowers were collected from each species at the greenhouse of Inokuchi Tsubaki Kan from January to March 2018. For *C. japonica* and *C. rusticana*, data for one flower out of 52 and 59 individuals, respectively, were used from the study of Abe and Miura *et al.* (2020). One-way ANOVA was performed for each measurement item related to flower diameter, stamen length, and stamen attachment rate, and significant differences in the mean values among groups were calculated using Tukey's method. Furthermore, the obtained measurement values were standardized, and cluster analysis was performed using the squared Euclidean distance and Ward's method. R version 3.2.3 (R Core Team 2015) was used for statistical analysis.

## Results

Although no significant trend was noted in the measured values among species (Table 1), some trends were observed depending on flower color (Figs. 2–3). The flower diameter tended to be larger in sect. *Camellia* and smaller in sect. *Chrysanth*, indicating a high uniformity within the sections. However, in species with white flowers, the flower diameter of sect. *Paracamellia* and sect. *Oleifera* was larger, while that of sect. *Theopsis* and sect. *Longipedicellata* was smaller ( $P < 0.05$ , Tukey's test; Fig. 2, Table 1). In particular, *C. vietnamensis* belonging to sect. *Oleifera* and *C. yuhsienensis* belonging to sect. *Paracamellia* had a significantly larger flower diameter. Regarding stamen length, sect. *Camellia* and sect. *Chrysanth* tended to have longer stamens. In contrast, all species with white flowers tended to have shorter stamens. Furthermore, in sect. *Camellia*, only *C. rusticana* had a significantly shorter stamen length ( $P < 0.05$ , Tukey's test; Fig. 2, Table 1). No trends were observed among sections in terms of the anther filament cohesion rate, while variation was noted among species (Fig. 2, Table 1).

In the cluster analysis, the five sections and 27 species analyzed in this study were divided into two large clades (Fig. 3). Clade 1 consisted of *C. grijsii* in sect. *Paracamellia*, sect. *longipedicellata* and sect. *Theopsis*, as well as *C. rusticana* belonging to sect. *Camellia*. Clade 2 consisted of sect. *Camellia*, sect. *Chrysanth*, sect. *Oleifera*, and *C. yuhsienensis* belonging to sect. *Paracamellia*. The sections within clade 2 were further divided into two subclades. Sect. *Camellia* and sect. *Chrysanth* were found to be similar in terms of flower morphology.

## Discussion

### Diversification of floral traits

As shown in the results, the floral traits of the bird-pollinated species, namely sect. *Camellia* (red camellias) and yellow camellias, were found to belong to the same clade. Between red- and yellow-flowered species, although the flower size tended to be larger in sect. *Camellia*, the stamens were longer with a higher degree of cohesion between filaments and a structure that made it easy to accumulate nectar. A comparison of flower size and stamen length indicated that

**Table 1.** Comparative results of floral morphology of the genus *Camellia*

Section	Petal color	Species	No. of samples	length of flower diameter (mm)			stamen length (mm)			Rate of filament coalescence (%)			Location and Data ref.
				Mean	±SD	SD	Mean	±SD	SD	Mean	±SD	SD	
Chrysanthra	Yellow	C. longzhouensis	3	40.90	1.21	cdh	39.60	1.25	ab	51.17	0.04	bgh	Inokuchi Tsubaki Kan
		C. chrysanthra var. phaeopubisperma	3	48.80	5.63	bcdh	39.00	3.58	ab	57.61	0.07	ag	
		C. quephongensis	3	38.93	3.33	cdh	32.97	0.86	acd	44.63	0.06	fghi	
		C. cucphuongensis	3	36.67	3.66	dh	33.13	2.97	acd	39.26	0.00	gj	
Theopsis	White	C. lutchuensis	3	27.53	5.53	gh	14.20	1.22	gh	45.73	0.04	efghi	
		C. transnokoensis	3	41.03	1.76	cdh	20.70	0.75	eh	40.63	0.02	gj	
		C. trichoclada	3	23.00	1.14	h	11.53	1.12	h	24.93	0.10	jk	
		C. fraterna	3	32.87	1.35	fh	19.87	0.32	eh	56.53	0.02	agh	
Longipedicellata		C. longicarpa	3	33.73	2.31	efh	23.87	0.96	defg	63.00	0.04	abcdf	
Oleifera		C. vietnamensis	3	96.90	3.83	a	18.77	0.49	fh	17.00	0.02	k	
Paracamellia		C. yuhsienensis	3	96.73	3.50	a	13.53	0.61	gh	60.50	0.05	abcdf	
		C. grijsii	3	61.93	9.10	bcdf	11.87	0.78	h	38.11	0.06	gj	
Camellia	Red	C. brevigyina	3	64.60	8.49	bcd	29.70	1.92	abef	64.65	0.03	abcde	
		C. lungshenensis	3	61.27	7.83	bcdf	32.93	2.45	acd	72.19	0.03	a	
		C. bailinshanica	3	62.40	1.74	bcdf	34.07	1.91	acd	70.48	0.01	ab	
		C. brevicolumns	3	66.30	7.48	bcd	36.50	2.65	ac	72.43	0.05	a	
		C. kweichowensis	3	60.10	0.36	bcdf	31.07	1.29	abe	50.06	0.02	cgh	
		C. villosa	3	61.43	6.70	bcdf	34.43	0.38	acd	46.95	0.00	dghi	
		C. polyodonta	3	63.23	7.78	bcde	26.23	1.27	cef	40.51	0.02	gj	
		C. saluenensis	3	59.87	12.32	bcdf	30.60	2.52	abe	67.38	0.05	abc	
		C. lapidea	3	53.43	5.45	bcdfg	33.17	3.76	acd	36.91	0.09	hj	
		C. semiserrata	3	54.33	9.76	bcdfg	40.60	5.21	a	53.91	0.03	agh	
		C. pitardii var. pitardii	3	68.17	3.32	ac	33.73	1.96	acd	66.43	0.09	abcd	
		C. apolyodonta	3	62.77	6.66	bcdf	26.07	1.70	cef	39.37	0.02	gj	
		C. chekiangoleosa	3	78.60	8.69	ab	28.33	2.24	bcef	37.91	0.04	gj	
		C. japonica	52	52.25	12.66	cdf	34.59	4.58	ab	62.50	0.07	abc	Abe and Miura et al. (2019)
		C. rusticana	59	60.48	10.98	bc	15.97	2.71	gh	33.86	0.07	ij	

±SD indicates standard deviations. One-way ANOVA was performed for each measurement item, and significant differences (SD) in the mean values among groups were calculated using Tukey's method ( $P < 0.05$ ). Non-capital letters indicate statistical (in)significance in a concise way: if treatment groups share the same non-capital letter, then the differences between the groups are not statistically significant.

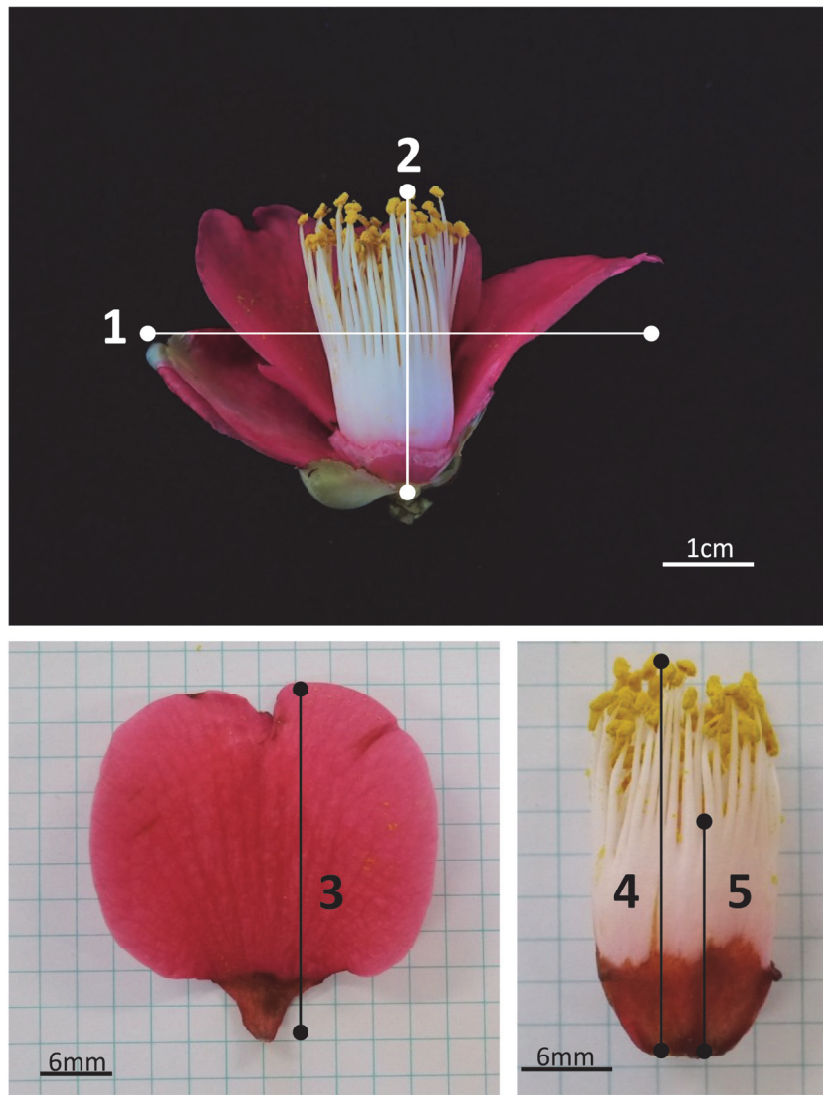
sect. *Camellia* had a larger and more homogeneous flower size. These traits can be predicted to be adaptations to bird pollination, as hypothesized. The stamen length may also be an adaptation to pollination by larger birds rather than insects. In addition, *C. rusticana* belonging to sect. *Camellia* and species belonging to sect. *Theopsis* with white flowers, known as insect-pollinated species, were included in the same clade. Assessment of the characteristics of yellow camellias revealed that the flower size was smaller than that of sect. *Camellia* (red camellias) but larger than that of white camellias. Moreover, the stamen was as long as that in sect. *Camellia*. According to Sun *et al.* (2017), *C. petelotii*, which belongs to sect. *Chrysanthra* (yellow camellias) with yellow petals, is pollinated by small birds called sunbirds (Nectariniidae). Although sunbirds are slightly smaller than the Japanese white-eye (the main pollinator of *C. japonica*), they hover to suck nectar instead of perching on branches or petals. While sect. *Camellia* (red camellias) is mainly pollinated by the Japanese white-eye (*Zosterops japonicus*) and brown-eared bulbul (*Hypsipetes amaurotis*) that perch on branches or petals to suck nectar, yellow camellias are pollinated by hovering birds and do not

require a large flower size. However, the stamen has likely lengthened to facilitate pollination by birds. Regarding the homogeneity of sect. *Camellia*, it is suggested to have diverged relatively quickly from the ancestral lineage of white-flowered species. This will be discussed in the following section.

### Relationship between molecular phylogeny and floral morphology

In this section, we discuss that the homogeneity of floral traits in sect. *Camellia* is caused by rapid evolution resulting from pollinator shifts for birds, based on the results of previous molecular phylogenetic analyses. Moreover, we discuss whether the ancestral insect-pollinated *C. rusticana* is phylogenetically ancestral or a new species.

As per previous studies on the molecular phylogeny of the genus *Camellia*, the diversification of sect. *Camellia* occurred in the following order in ancient times: the origin of the genus *Camellia* dates back to 39.5 million years ago, with rapid diversification of the sections having occurred around 20–30 million years ago (Zhao *et al.*, 2022). Other studies have reported that diversification occurred around



**Fig. 1: Measurement of flower morphology**

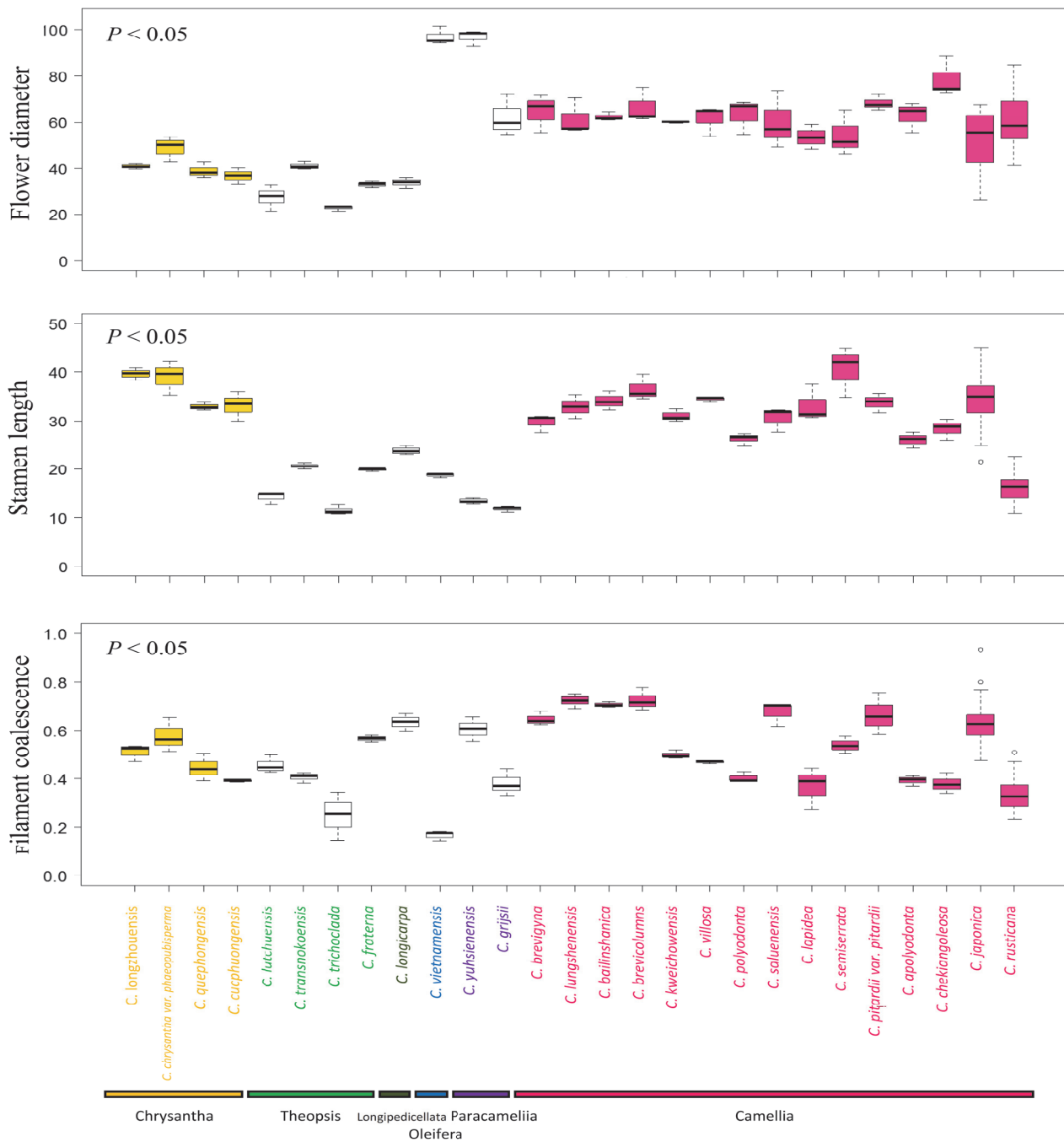
(1) length of flower diameter, (2) height from petal base to corolla, (3) petal length, (4) stamen length, and (5)/(4) Rate of filament coalescence  
(2) and (3) were not used for analysis due to significant variations within individuals. The photographs are *Camellia japonica*.

25 million years ago (Cheng *et al.*, 2022); radiation of major clades occurred during the late Miocene around 23–19 million years ago, followed by the occurrence of a species burst between 10 and 5 million years ago (Zan *et al.*, 2023); diversification occurred around 13 million years ago (Zhang *et al.*, 2022); diversification occurred during the middle to late Miocene (around 13.70–12.42 million years ago) in the genus *Camellia* (Shengyuan *et al.*, 2023); diversification of sections occurred around 12 million years ago (Zhang *et al.*, 2014); and diversification of sect. *Camellia* and sect. *Oleifera* and related sections in this study peaked around 6–7 million years ago in the late Miocene after section diversification began around 10.54 million years ago (Wu *et al.*, 2022). Although the origin and diversification of the sections occurred from 6 to 30 million years ago and in the Miocene epoch, respectively, they generally fall within the Miocene epoch.

When summarizing previous studies on the molecular phylogeny of sect. *Camellia* and its closely related sections, the divergence of sect. *Paracamellia* is estimated to have occurred 19 million years ago (Zhao *et al.*, 2022) and that of

*C. oleifera* belonging to sect. *Oleifera* is estimated to have occurred 5.88 million years ago (Wu *et al.*, 2022). Moreover, in the study of Shengyuan *et al.* (2023), assessments using a molecular phylogenetic tree based on nuclear genes suggested that sect. *Oleifera* should be merged with sect. *Paracamellia* and that sect. *Paracamellia* branched off after *C. japonica*. These previous studies revealed that sect. *Camellia* did not undergo rapid speciation at a particular time compared to other sections. Instead, it underwent speciation during the late Miocene, similar to other species. Therefore, the floral uniformity of sect. *Camellia* is considered to be a convergent trait specialized for bird pollination. Personal communication with Abe has confirmed that not only *C. japonica* but also other species within the sect. *Camellia* are primarily visited by white-eyes and bulbuls. In this study, it was shown that despite being closely related to sect. *Camellia* in terms of molecular phylogeny, sect. *Paracamellia* was classified into a separate clade morphologically and is likely to be grouped with insect-pollinated species (Fig. 3) Thus, it can be concluded that species with insect pollination traits are not necessarily





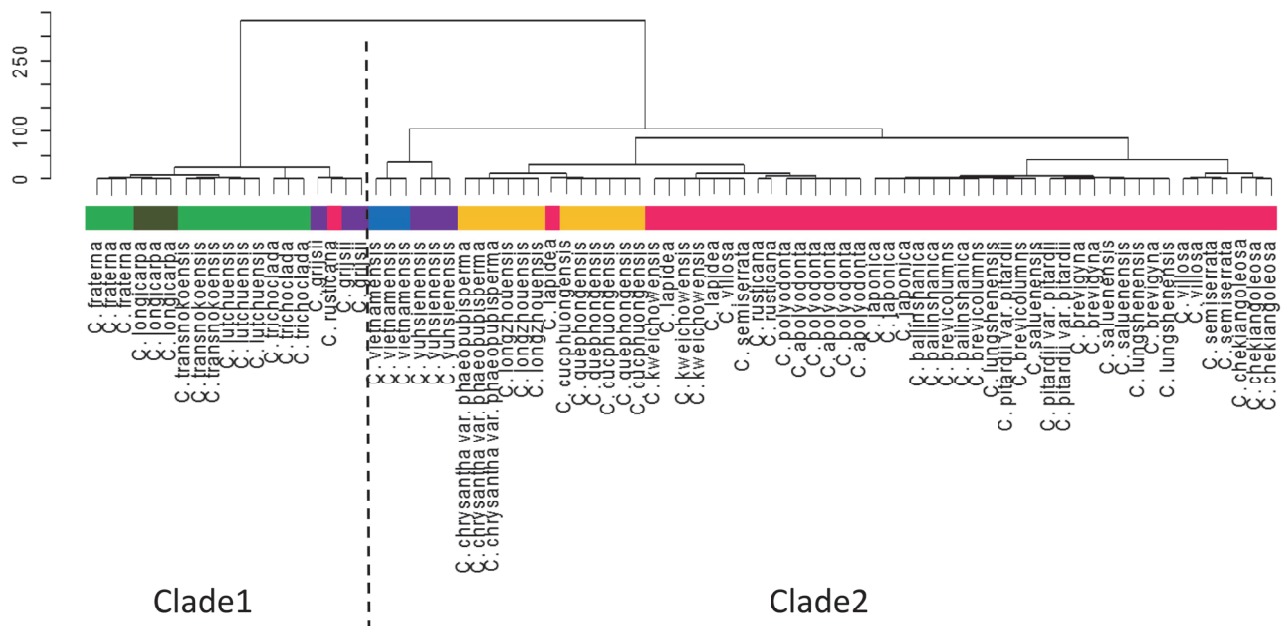
**Fig. 2: Comparisons of flower diameter, stamen length and floral filament coalescence rates in the genus *Camellia***

The thick line inside the box represents the median. The bottom of the box corresponds to the first quartile, while the top of the box represents the third quartile. The whiskers extend to the farthest values within a distance of 1.5 times the interquartile range from the lower or upper quartile. Any data points outside this range are depicted as individual points on the graph and are considered potential outliers. The color of the box indicates floral color, and the color of the species name is categorized by section. The color scheme for each section is as follows: red for sect. *Camellia*, purple for sect. *Paracamellia*, blue for sect. *Oleifera*, green for sect. *Longipedicellata* and sect. *Theopsis*, and yellow for sect. *Chrysantha*.

ancestral in terms of molecular phylogeny. *C. chrysantha*, which belongs to sect. *Chrysantha* with yellow petals and is a bird-pollinated species, is classified in the subgenus *Thea* and is considered to be in a more ancestral position than the subgenus *Camellia*, which includes sect. *Camellia*, because of having diverged from the subgenus *Camellia* in the early to middle Miocene (Wu *et al.*, 2022; Zhao *et al.*, 2022). Similar to the subgenus *Camellia*, the diversification of yellow camellias with bird pollination traits occurred during the Miocene period; therefore, the pollination syndrome is considered to

have evolved independently rather than following the order of molecular phylogenetic evolution.

Despite its belonging to sect. *Camellia*, little molecular phylogenetic research has been conducted on *C. rusticana*, which is morphologically classified as a member of sect. *Theopsis* within the subgenus *Metacamellia* in this study. However, Vijayan *et al.* (2009) used nrITS sequences of 112 *Camellia* species and found that *C. chekiangoleosa* occupies a more ancestral position compared to *C. japonica* and *C. rusticana*, and is separated into two clades: the *C. rusticana*



**Fig. 3: Result of cluster analysis on flower morphology in the genus *Camellia***

Flower diameter, stamen length, and rate of filament coalescence were measured for each of three individuals, and the obtained measurements were standardized for cluster analysis using the Euclidean square distance and Ward's method. The color scheme for each section is as follows: red for sect. *Camellia*, purple for sect. *Paracamellia*, blue for sect. *Oleifera*, green for sect. *Longipedicellata* and sect. *Theopsis*, and yellow for sect. *Chrysanthia*.

clade (including *C. azalea* and *C. edithae*) and the *C. japonica* clade (including *C. fluviatilis* and *C. brevistyla*). According to molecular phylogenetic research examining *C. chekiangoleosa* and *C. japonica*, Zhao *et al.* (2022) suggested that *C. japonica* and *C. chekiangoleosa* are sister species, while Cheng *et al.* (2022) suggested that *C. azalea* belonging to sect. *Camellia* similar to *C. chekiangoleosa* forms a sister group and that *C. japonica* diverged from that clade 15 million years ago. In the study of Shengyuan *et al.* (2023), phylogenetic trees based on nuclear genes demonstrated that sect. *Oleifera* should be merged into sect. *Paracamellia* and that *C. japonica* is phylogenetically related to *C. chekiangoleosa*, which is ancestral (albeit with short branches). Yan *et al.* (2021) reported similar results. Based on chloroplast genome sequences, Wu *et al.* (2022) reported that *C. chekiangoleosa* diverged from *C. sasanqua* in sect. *Paracamellia*, following which *C. chekiangoleosa* split into two sister species: *C. japonica* and *C. oleifera*. Moreover, Rao *et al.* (2018) suggested that *C. chekiangoleosa* is ancestral and that the *C. japonica* clade (including *C. fluviatilis* and *C. brevistyla*) diverged from it. Based on these findings, it is highly likely that *C. chekiangoleosa* is ancestral among the three species and that it is related to *C. japonica*. *C. chekiangoleosa* has a lower stamen cohesion rate (Table 1) and can be considered more ancestral than *C. japonica*. However, *C. rusticana*, which has more insect pollination traits, was derived later than *C. chekiangoleosa*.

In summary, based on the results of our research on floral traits, the uniformity of traits in sect. *Camellia* is considered to have undergone rapid diversification in recent years. However, according to previous studies on molecular phylogeny, other sections also showed species diversification in the late Neogene period, similar to sect. *Camellia*. Thus, the results of molecular phylogenetic analyses have provided no clear indication regarding the uniformity of floral traits in sect.

*Camellia*.

### How did the evolution of floral traits occur?

In this study, no correlation was noted between floral characteristics and molecular phylogeny. Rao *et al.* (2018) evaluated the environmental factors and evolutionary dynamics (speciation times and diversification rates) that form the diversity patterns of 145 species in the family Theaceae, consisting of the genus *Camellia*, based on chloroplast and nuclear ITS regions. They reported that the overall species diversity was significantly correlated with environmental variables, particularly soil pH. At the section level, the species diversity was correlated with the phylogenetic structure. Despite being in different sections, many species that are geographically (and environmentally) close to each other can form a clade together based on molecular phylogeny, indicating that environmental factors and patterns of species diversification are likely related. For example, studies focusing on species related to *C. japonica* revealed that *C. oleifera* in sect. *Oleifera*, which has a wide distribution in mainland China and widely cultivated, forms the same clade as *C. japonica* with a bootstrap value of 50 (while other species have a high independence of almost 100) (Zhang *et al.*, 2019; Wu *et al.*, 2022). According to the results of Rao *et al.* (2018), *C. chekiangoleosa* differentiated first, becoming an ancestral lineage. This was followed by the emergence of two clades: one consisting of *C. azalea* and *C. edithae* and the other consisting of *C. japonica*, *C. fluviatilis*, and *C. brevistyla*. The clade consisting of *C. japonica* is consistent with the findings of Vijayan *et al.* (2009). *C. fluviatilis* and *C. brevistyla* have regions where their distribution overlaps with that of *C. japonica*. Additionally, it clarifies that *C. fluviatilis* and *C. brevistyla* belong to sect. *Paracamellia*, while *C. japonica* belongs to a different section. According to the findings of Cheng *et al.* (2022), the clade that includes

*C. japonica* has a subclade consisting of *C. sasanqua* from sect. *Oleifera*, which is distributed in Japan and diverged from *C. japonica* around 13–14 million years ago. This is followed by a shorter branch of *C. fluviatilis*, as well as the subsequent differentiation of *C. cordifolia* (distributed in Taiwan, Guangdong, and Jiangxi) from sect. *Camelliopsis* and *C. oleifera* from sect. *Oleifera*. Thus, the derivatives after *C. japonica* do not belong to sect. *Camellia*. There are other examples within the *C. japonica* clade that do not fall under sect. *Camellia*. Shengyuan *et al.* (2023) also demonstrated that sect. *Paracamellia* branched off later than *C. japonica*. Furthermore, it is difficult to clearly distinguish between sect. *Oleifera* and sect. *Paracamellia* (Wu *et al.*, 2022; Shengyuan *et al.*, 2023), as mentioned above. Based on molecular phylogenetic results, Yan *et al.* (2021) reported that the closest sister species to *C. japonica* is *C. lutchuensis*, classified under sect. *Theopsis*; it exclusively grows in the Ryukyu Islands and exhibits significant morphological differences. As mentioned above, in cases where species from different sections form the same clade as *C. japonica* or are derived from it, the species are often geographically close or overlapping. When species not only belong to a different section from *C. japonica* but also exhibit completely different morphologies, the influence of overlapping distribution and hybridization under wild conditions can be considered. Moreover, for species like *C. oleifera*, which have been widely cultivated for oil production or used as ornamental varieties, human influences should be considered along with geographical factors. Thus, when considering the correlation between environmental factors and molecular phylogeny, careful consideration of the influence of hybridization is necessary.

We considered speciation by a pollination shift to birds as an environmental factor in sect. *Camellia*. The genus *Camellia* is widely distributed across the temperate forests of mainland Asia, ranging from northern regions, such as Honshu in Japan, to southern regions, such as Southeast Asia. The center of diversity for this genus lies in southern China, which is also considered the core of the Sino-Japanese Floristic Region (SJFR). During the early to middle Miocene, East Asia experienced an increase in temperature and precipitation. The warm and humid climate, along with the intensified summer monsoon system in Asia (Sun and Wang, 2005), facilitated the widespread distribution of the genus *Camellia* (which consists of warm-temperate evergreen broad-leaved trees) throughout the SJFR (Yang *et al.*, 2016). These geological and climatic events likely played a significant role in influencing the speciation and diversification of the genus *Camellia*. The genus *Camellia* is known for its characteristic of flowering primarily during the winter season. Within this genus, sect. *Camellia* consists of species that are geographically distributed to the north. The diversification of sect. *Camellia* occurred during the Miocene, which was the warmest period from the Neogene to the present, characterized by generally warm climates and gradual cooling thereafter. During this cooling trend, species in the northern regions that were geographically distributed adapted from insect pollination, which is limited by the low presence of insects during winter, to bird pollination, which is facilitated by endothermic animals capable of winter activity. This advantageous trait, possibly resulting from the spread of beneficial mutations within the population, could

have led to the evolution of sect. *Camellia*.

In summary, species belonging to the genus *Camellia* with bird pollination traits are not believed to have rapidly diversified from a common ancestor. Instead, they may have originated from different lineages because of environmental conditions, such as climate. As this is currently a matter of speculation, it is necessary to comprehensively and quantitatively organize the morphological traits of species in the genus *Camellia* and reevaluate their relationship with molecular phylogeny.

## Acknowledgment

The authors thank the staff of Inokuchi Tsubaki Kan for their cooperation during sample collection.

This work was supported by the JSPS KAKENHI (grant number JP15K07473).

## References

- Abe, H. and Hasegawa, M. (2008) Impact of volcanic activity on a plant-pollinator module in an island ecosystem: the example of the association of *Camellia japonica* and *Zosterops japonica*. *Ecol. Res.*, **23**: 141–150.
- Abe, H., Miura, H. and Motonaga, Y. (2020) Quantitative classification of *Camellia japonica* and *Camellia rusticana* (Theaceae) based on leaf and flower morphology. *Plant Divers.*, **43**(3): 216–224.
- Abe, H., Ueno, S., Tsumura, Y. and Hasegawa, M. (2011) Expanded home range of pollinator birds facilitates greater pollen flow of *Camellia japonica* in a forest heavily damaged by volcanic activity. In *Single-Pollen Genotyping*, edited by Isagi, Y. and Suyama, Y. Springer, Tokyo, pp. 47–62.
- Chang, H.T. (1998) Theaceae (1) Theioideae 1. *Camellia*. In *Flora Reipublicae Popularis Sinicae*, **49**, Sci. Press, Beijing, pp. 3–195.
- Cheng, L., Li, M., Han, Q., Qiao, Z., Hao, Y., Balbuena, T.S. and Zhao, Y. (2022) Phylogenomics resolves the phylogeny of Theaceae by using low-copy and multi-copy nuclear gene makers and uncovers a fast radiation event contributing to tea plants diversity. *Biology*, **11**: 1007. DOI: 10.3390/biology11071007
- Faegri, K. and van der Pijl, L. (1979) *The Principles of Pollination Ecology*. Pergamon Press, Oxford.
- Huang, H., Tong, Y., Zhang, Q.J. and Gao, L.Z. (2013) Genome size variation among and within *Camellia* species by using flow cytometric analysis. *PLoS ONE*, **8**(5): e64981.
- Ishizawa, S. (1988) Life history of *Stewartia pseudocamellia*. In *Newton Spec. Issue: World Plants, 1*, Kyodo Printing Co., Ltd. pp. 28–55. (in Japanese)
- Ishizawa, S. (2005) Tree form, external morphology and fruiting of *Stewartia pseudocamellia* (Part 2: trees that bloom in spring). *Planta*, **99**: 22–32. (in Japanese)
- Iwatsuki, K., Boufford, D. E. and Ohba, H. (eds.) (2006) *Flora of Japan*, vol. *IIa*, Kodansha, Tokyo.
- Ming, T. and Zhang, W. (1995) The evolution and distribution of genus *Camellia*. *Acta Bot. Yunnanica*, **18**(1): 1–13.
- Ming, T. and Bartholomew, B. (2007) Theaceae. In *Flora of China*, edited by Wu, Z. and Raven, P. Sci. Press, Beijing, pp. 366–478.
- Ming, T.L. (1999) A systematic synopsis of the genus *Camellia*. *Acta Bot. Yunnanica*, **21**: 149–159.
- R Core Team. (2015) R: A language and environment for statistical computing. R Found. Stat. Comput., Vienna, Austria. <https://www.R-project.org/>
- Rao, M., Steinbauer, M.J., Xiang, X., Zhang, M., Mi, X., Zhang, J., Ma, K. and Svenning, J.C. (2018) Environmental and evolutionary drivers of diversity patterns in the tea family (Theaceae s.s.) across China. *Ecol. Evol.*, **8**(2): 11298–11311. DOI: 10.1002/ece3.3819
- Sealy, J.R. (1958) *A revision of the genus Camellia*. Royal Hort. Soc., London.
- Shengyuan, Q., Chen, K., Zhang, W., Xiang, X., Zuo, Z., Guo, C., Zhao, Y., Li, L.-F., Wang, Y., Song, Z., Yang, J., Yang, X., Zhang, J., Jin, W., Wen, Q., *et al.* (2023) Phylogenomic insights into

- the reticulate evolution of *Camellia* sect. *Paracamellia* Sealy (Theaceae). *J. Syst. Evol.*, **61**(3): 237-251. DOI: 10.1111/jse.12948
- Sun, S.G., Huang, Z.H., Chen, Z.B. and Huang, S.Q. (2017) Nectar properties and the role of sunbirds as pollinators of the golden-flowered tea (*Camellia petelotii*). *Am. J. Bot.*, **104**(3): 468-476.
- Sun, X. and Wang, P. (2005) How old is the Asian monsoon system?—Palaeobotanical records from China. *Palaeogeogr. Palaeoclimatol. Palaeoecol.*, **222**(3-4): 181-222.
- Vijayan, K., Zhang, W.-J. and Tsou, C.-H. (2009) Molecular taxonomy of *Camellia* (Theaceae) inferred from nrITS sequences. *Am. J. Bot.*, **96**(7): 1348-1360.
- Wu, Q., Tong, W., Zhao, H., Ge, R., Li, R., Huang, J., Li, F., Wang, Y., Mallano, A.I., Deng, W., Wang, W., Wan, X., Zhang, Z. and Xia, E. (2022) Comparative transcriptomic analysis unveils the deep phylogeny and secondary metabolite evolution of 116 *Camellia* plants. *Plant J.*, **111**(2): 406-421. DOI: 10.1111/tpj.15799
- Yan, Y., Davis, C.C., Dimitrov, D., Wang, Z., Rahbek, C. and Borregaard, M.K. (2021) Phytogeographic history of the tea family inferred through high-resolution phylogeny and fossils. *Syst. Biol.*, **70**(6): 1256-1271. DOI: 10.1093/sysbio/syab042
- Yang, L.Q., Hu, H.Y., Xie, C., Lai, S.P., Yang, M., He, X.J. and Zhou, S.D. (2016) Molecular phylogeny, biogeography, and ecological niche modelling of *Cardiocrinum* (Liliaceae): insights into the evolutionary history of endemic genera distributed across the Sino-Japanese floristic region. *Ann. Bot.*, **119**: 59-72.
- Yumoto, T. (1988) Pollination systems in the cool temperate mixed coniferous and broad-leaved forest zone of Yakushima Island. *Ecol. Res.*, **3**(2): 117-129.
- Zan, T., He, Y.T., Zhang, M., Yonezawa, T., Ma, H., Zhao, Q.M., Kuo, W.Y., Zhang, W.J. and Huang, C.H. (2023) Phylogenomic analyses of *Camellia* support reticulate evolution among major clades. *Mol. Phylogenet. Evol.*, **182**: 107744.
- Zhang, F., Li, W., Gao, C.W., Zhang, D. and Gao, L.Z. (2019) Deciphering tea tree chloroplast and mitochondrial genomes of *Camellia sinensis* var. *assamica*. *Sci. Rep.*, **9**(1): 209. DOI: 10.1038/s41597-019-0201-8
- Zhang, Q., Zhao, L., Folk, R.A., Zhao, J.L., Zamora, N.A., Yang, S.X., Soltis, D.E., Soltis, P.S., Gao, L.M., Peng, H. and Yu, X.Q. (2022) Phylotranscriptomics of Theaceae: generic-level relationships, reticulation, and whole-genome duplication. *Ann. Bot.*, **129**: 457-471. DOI: 10.1093/aob/mcac007
- Zhang, W., Kan, S.L., Zhao, H., Li, Z.Y. and Wang, X.Q. (2014) Molecular phylogeny of tribe Theae (Theaceae s.s.) and its implications for generic delimitation. *PLOS ONE*, **9**(5): e98133. DOI: 10.1371/journal.pone.0098133
- Zhao, D.W., Hodkinson, T.R. and Parnell, J.A.N. (2022) Phylogenetics of global *Camellia* (Theaceae) based on three nuclear regions and its implications for systematics and evolutionary history. *J. Syst. Evol.*, DOI: 10.1111/jse.12837





Proceedings of  
the 20th International Symposium on Integrated Field Science  
“Biodiversity and Phylogeography”



November 23, 2022

Graduate School of Agricultural Science, Tohoku University,  
Sendai, Japan



The 20th International Symposium on Integrated Field Science  
"Biodiversity and Phylogeography"

**Registration**

10:10–

**Opening remarks**

10:30–10:40 Organizer: **Yoshihisa Suyama** (Tohoku University, Japan)

**Invited Presentations**

- 10:40–11:10 **Harue Abe** (Niigata University, Japan)  
Evolution of the genus *Camellia* based on the biological interaction and the historical background
- 11:10–11:40 **Gustavo Maruyama Mori** (São Paulo State University (UNESP), Brazil)  
Like a mangrove out of water: dispersal limitation and adaptive responses of dominant coastal trees to freshwater limitation
- 11:40–12:00 Q & A
- 12:00–13:00 Lunch
- 13:00–13:30 **Yuji Isagi** (Kyoto University, Japan)  
Tailor-made biological conservation of endangered plant species with genomic information
- 13:30–14:00 **Alison Kim Shan Wee** (University of Nottingham Malaysia Campus, Malaysia)  
Mangroves in a changing world: biogeography and ecological genomics of Southeast Asian mangroves
- 14:00–14:10 Q & A
- 14:10–14:20 Tea Break

**Poster Preview**

14:20–14:35

**Poster Presentations**

14:35–15:50

**Closing Remarks**

15:50–16:00 **Yoshihisa Suyama** (Tohoku University, Japan)

The 20th International Symposium on Integrated Field Science  
“Biodiversity and Phylogeography”

Date: November 23, 2022

Venue: Graduate School of Agricultural Science, Tohoku University, Sendai, Japan

Organizer: Yoshihisa Suyama (Field Science Center, Graduate School of Agricultural Science,  
Tohoku University, Sendai, Japan)

---

Proceedings of  
the 20th International Symposium on Integrated Field Science  
“Biodiversity and Phylogeography”

November 23, 2022  
Graduate School of Agricultural Science,  
Tohoku University,  
Sendai, Japan

---

## Evolution of the Genus *Camellia* Based on the Biological Interaction and the Historical Background

Harue ABE<sup>1</sup>, Saneyoshi UENO<sup>2</sup>, Ayumi MATSUO<sup>3</sup>, Shun K. HIROTA<sup>4</sup>, Hiroki MIURA<sup>5</sup>, Monghuai SU<sup>6</sup>,  
Yunguang SHEN<sup>7</sup>, Yoshihisa SUYAMA<sup>8</sup> and Zhonglang WANG<sup>7</sup>

<sup>1</sup>Niigata Univ.

<sup>2</sup>Affrc

<sup>3</sup>GENODAS

<sup>4</sup>Osaka Metropolitan Univ.

<sup>5</sup> Aquarium Asamishi

<sup>6</sup>Chinese Culture Univ.

<sup>7</sup>Kunming Botanical Garden

<sup>8</sup>Tohoku Univ.

The genus *Camellia* (Theaceae) is particularly prevalent in East and Southeast Asia (82-280 species). According to the Flora of China, there are 13 species in the sect. *Camellia*, of which 12 are found in China (11 being endemic), and only two species, *C. japonica* and *C. rusticana*, are found in Japanese islands. Since these two species are distributed at the northern limit of the genus *Camellia*, it is thought to have come from the continent and have speciated in Japan. Comparing the morphology, most species of *Camellia* have separated flower filaments, but the sect. *Camellia* species except for *C. rusticana* and *C. chekiangoleosa* have connected filaments, which indicates the bird-pollinated flower characteristics to keep a large amount of nectar. *C. japonica* blooms in the winter when insects are absent and must depend on bird pollination whereas other *Camellias* depend on both pollination, insects and birds. Therefore *C. japonica* might be the most adaptable species for bird pollination. On the other hand, *C. rusticana* has ancestral traits with not-connected filaments in the sect. *Camellia*. We hypothesized that the pollinator shift from insects to birds may have caused speciation from the ancestral genus *Camellia* to the sect. *Camellia*. Later, *C. rusticana* might get back to insect pollination to fit the snowy environment in Japan. Hence, this study aims to examine the speciation of Japanese *Camellias* based on pollinator shift by comparing the floral morphologies and the genetic differentiation of the genus *Camellia*. Next, we examined the demographic history of *C. japonica*, which is widely distributed in the Japanese archipelago, the Korean peninsula, and the coastal areas of mainland China and Taiwan. Through the above examinations, we discuss the evolution of the genus *Camellia* in Japan based on biological interaction and the historical background.

We compared their morphologies of leaf hypodermis, flower form, petal color, filament color, and filament color in the twenty populations and estimate quantitatively the differentiation. In the results, PCA analysis clearly distinguished between these species, and both petal and filament colors were also statistically different between these species. The floral traits of *C. japonica* such as filament connection rates, nectar, and sugar contents are one of the most adapted characteristics for bird pollination. The eight cpSSR and the genome-wide SNPs by MIG-Seq revealed largely congruent results indicating that the genetic structures are divided into 3; southern and northern *C. japonica*, and *C. rusticana*. The relationship between the three species including the related species in China was further inferred from the phylogeny generated by RAxML using SNP data. It was found that *C. chekiangoleosa* is the ancestral species and that *C. rusticana* and *C. japonica* are more related. However, demographic analysis, discussed below, reveals that the divergence date between *C. rusticana* and *C. japonica* is also older. The intraspecific genetic structure of *C. japonica* was investigated using ADMIXTURE 1.3.0, and the populations were divided into (1) mainly northern and (2) mainly southern populations in the Japanese archipelago, (3) Chinese and Korean populations, and (4) Okinawa and Taiwanese populations. Demographic analysis using DIYABC was carried out on the four populations in which hybrid individuals were excluded by ADMIXTURE predicted that the northern Japanese populations firstly differentiated from the southern Japanese populations, and then the Okinawa and Taiwan populations differentiated. Later, the Chinese and Korean populations returned to the mainland (the continent) from the southern Japanese populations. This result is consistent with the results of ENM. The optimum distribution of *C. rusticana* during the last glacial period was almost the same as that of the present distribution on the Sea of Japan, suggesting that *C. rusticana* is a relict species in Japan since before the glacial period. The northern population is the ancestral group as a relict in Honshu Japan. The results of this study could provide not only the evolutionary history of the species but also the population priorities that should serve as the focus for future management and conservation of these species.



**Photo.** White-eye feeding on camellia nectar

## Like a Mangrove out of Water: Dispersal Limitation and Adaptive Responses of Dominant Coastal Trees to Freshwater Limitation

Gustavo Maruyama MORI

Department of Biological and Environmental Sciences, Institute of Biosciences,  
São Paulo State University (UNESP), São Vicente, SP, Brazil

As climate changes, freshwater unavailability due to reducing precipitation, lower air humidity, and rising temperatures may increase mass tree mortality not only in arid regions, but also in tropical and subtropical environments like mangroves forests. These tree communities inhabit the habitats between land and sea and are composed by few broadly distributed plants whose populations face high environmental heterogeneity, from arid to rainy/wet sites, and from subtropical to equatorial regions. Thus, mangroves provide suitable models to unveil the mechanisms underlying trees adaptation to freshwater limitation. First, this presentation will be focused on how geography and oceanography shape the dispersal of mangroves along the Brazilian coast. As intraspecific gene flow is limited in this region, local adaptation is expected to take place as one observes contrasting environments, at different geographic scales. Then, I will explore recent findings on the adaptive responses of two black mangroves species (*Avicennia*) across the Brazilian coast to drought tolerance or response to hydric stress. Evidence of natural selection has also been observed at much smaller geographic scale. There are signs of natural selection in *A. germinans* in response to abrupt limitation in access to soil freshwater, after a road was constructed in the mid-70s. To conclude, there will be a brief discussion on how these findings may support mangrove trees conservation and its associated challenges.





## Tailor-made Biological Conservation of Endangered Plant Species with Genomic Information

Yuji ISAGI<sup>1</sup>, Yoshihisa SUYAMA<sup>2</sup> and Takashi MAKINO<sup>3</sup>

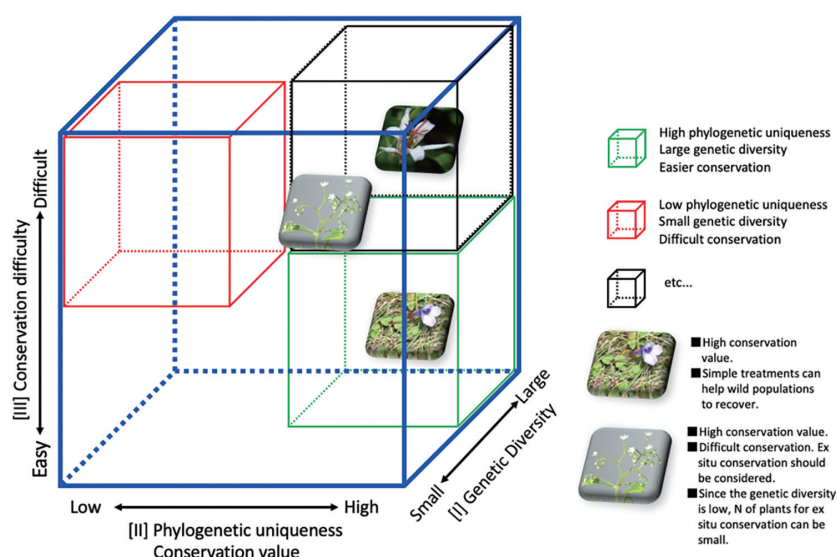
<sup>1</sup>Graduate School of Agriculture, Kyoto University

<sup>2</sup>Graduate School of Agriculture, Tohoku University

<sup>3</sup>Graduate School of Life Sciences, Tohoku University

The multifaceted importance of biodiversity is increasingly recognized, but the situation in various ecosystems is crucial and many endangered species are recognized. Based on the “Conservation of Species Act”, the Japanese government has designated the species with the highest conservation priority as Domestic Rare Wild Fauna and Flora and is trying to conserve them, and the number of the designated species is scheduled to be as many as 700 in the near future. However, limited resources available for the conservation of biodiversity require the development of rational and effective methods for the conservation of many endangered species. How can we appropriately preserve such a large number of endangered species with limited conservation resources? Until now, the conservation status of endangered species has been assessed primarily by the number of individuals surviving, but it is difficult to prioritize species for conservation based only on their population size. We explored ways to appropriately conserve a large number of endangered species with three criteria: (I) genetic diversity of remnant populations, the most common value for assessing the status of endangered species, (II) conservation value based on the phylogenetic uniqueness of the taxon, and (III) conservation difficulty estimated from the status of the genome. We evaluated the uniqueness of populations based on genetic diversity and phylogenetic perspectives through contracted genome sequencing on individuals growing in Japan and overseas of rare species. Furthermore, by comprehensively analyzing the expressed genes by RNA-seq, we found genetic indicators characteristic of endangered species in terms of genetic diversity, deleterious mutation accumulation, and duplicated gene rate, thus estimating the vulnerability of species and local populations and their ability to adapt to the environment.

As a result of detailed genome-level analysis of endangered plant species growing in the Ogasawara and Ryukyu islands, which are designated World Natural Heritage sites, we found significant differences between species in phylogenetic uniqueness, amount of deleterious mutation, and ability to adapt to a variety of environments. By combining these evaluation axes I, II and III described above based on the different types of genomic information, we categorized the conservation status of endangered species and developed a tailor-made conservation strategy by which conservation resources can be allocated more effectively and rationally according to the species' unique conservation status (**Figure**).



**Figure.** Categorization of critically endangered species based on [I] genetic diversity, [II] phylogenetic uniqueness and [III] conservation difficulty

## **Mangroves in a Changing World: Biogeography and Ecological Genomics of Southeast Asian Mangroves**

Alison K.S. WEE

School of Environmental and Geographical Sciences, University of Nottingham Malaysia Campus, Jalan Broga,  
Semenyih, 43500 Selangor, Malaysia

Mangroves are one of the most threatened ecosystems in the world. Understanding the drivers and limitations of gene flow, phylogeography, genetic adaptation and tools for natural resource management is crucial to effectively address the threats, conserve the long-term evolutionary potential, and ensure the sustainable management of mangroves. The first part of this talk summarizes key research findings on the biogeography of major mangrove tree species in Southeast Asia and the greater Indo-West Pacific region. In essence, propagule dispersal capabilities, land barriers and ocean currents are drivers of gene flow and underscores the importance of long-distance dispersal in connecting fragmented mangrove populations. The second part of the presentation describes our work on abiotic stress response in mangroves, especially at the species range limits. Current understanding of the molecular mechanism underlying stress adaptation points toward diverging strategies in stress response, even among closely related species. These studies will be important in estimating the adaptive potential of mangroves under climate change. The third part of this talk focuses on recent proof-of-concept studies on the application of environmental DNA (eDNA) as a biomonitoring tool in mangroves. Findings showed that fish communities change across the salinity gradient, and that biological invasion is a threat to the mangrove ecosystem. Collectively, these studies highlight the genetic uniqueness in Southeast Asian mangroves, the urgency of their conservation and how recent technological advances can contribute to this cause.



## Effects of Cultivation Methods on Paddy Rice Growth Observed by UAV-mounted Multispectral Camera

Muxiye<sup>1</sup>, Chinatsu YONEZAWA<sup>1\*</sup>, Mizuhiko NISHIDA<sup>1</sup>, Ryosuke TAJIMA<sup>1</sup>, Ryohei YOKOYAMA<sup>2</sup>, Koharu OKADA<sup>2</sup>, Kouki TAKAMURA<sup>3</sup>, Kaori AMAYA<sup>3</sup> and Ken ICHIKAWA<sup>3</sup>

<sup>1</sup>Graduate School of Agricultural Science, Tohoku University

<sup>2</sup>Faculty of Agricultural, Tohoku University

<sup>3</sup>Fukken Gijyutsu Consultants Co., Ltd.

Remote sensing technology is effective for monitoring paddy rice growth and yield estimation. Vegetation indices (VIs) obtained from remote sensing data are related to rice grain protein content, which is an indicator of rice taste and has been used to estimate the best harvesting time. It is observed that the red-edge band spectrum is sensitive to chlorophyll and nitrogen content, the reflectance from the plants changes rapidly in this spectral region, and the VI obtained using the red-edge band is less saturated than that obtained using the red band. In this study, considering that different cultivation methods affect rice growth, we compared the VI based on the red-edge band with two other VIs based on red and green bands to observe the differences in the growth of paddy rice in conventional and organic farming paddy plots. We captured images using an unmanned aerial vehicle (UAV) mounted multispectral camera, on August 5, August 22, and September 13, 2022, in a paddy field located at the Kawatabi Field Science Center of Tohoku University in Osaki City, Miyagi Prefecture, Japan. The drone DJI Inspire 2 was equipped with a RedEdge-MX Dual camera, which can observe in 10 bands. As a result, the mean values of all three VIs showed a decreasing tendency with increasing growth period. Growth difference between conventional and organic cultivation methods were more pronounced for the VI obtained using the red-edge band compared with the VIs obtained using green and red bands. The difference between the two cultivation methods was apparent before the heading date, and it became difficult to discern thereafter. The values of the VIs in conventional farming were larger than those in organic farming.



## Phylogeography of Intraspecific Differentiation of *Hydrangea serrata* (Hydrangeaceae), a Widespread Shrub Species in the Japanese Archipelago

Shoki MURAKAMI<sup>1,2</sup>, Takuro ITO<sup>2</sup>, Tatsuya UEMACHI<sup>3</sup>, Shinji FUJII<sup>4</sup>, Ayumi MATSUO<sup>5</sup>,  
Yoshihisa SUYAMA<sup>5</sup> and Masayuki MAKI<sup>1,2</sup>

<sup>1</sup>Graduate School of Life Sciences, Tohoku University

<sup>2</sup>Botanical Gardens, Tohoku University

<sup>3</sup>School of Environmental Science, The University of Shiga Prefecture

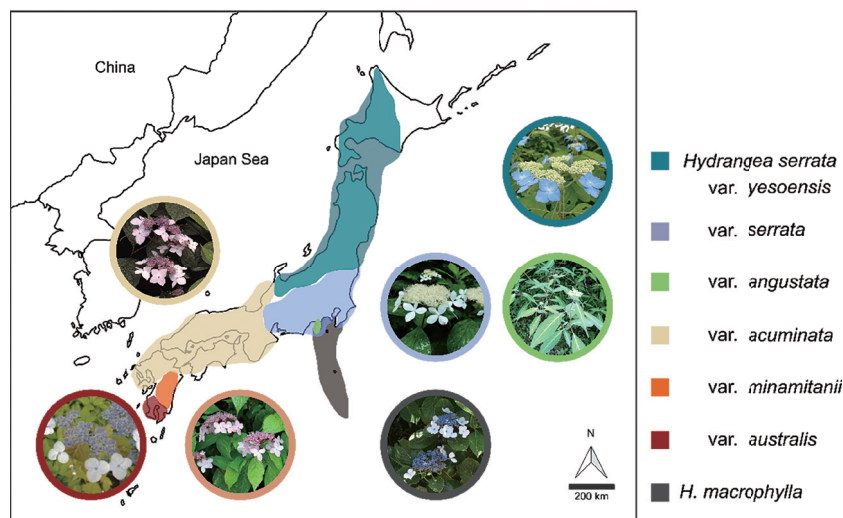
<sup>4</sup>Department of Environmental Science, University of Human Environments

<sup>5</sup>Graduate School of Agricultural Science, Tohoku University

*Hydrangea serrata* (Thunb.) Ser. is a deciduous shrub species, distributed throughout Japan and in a part of East Asia. This species comprises of six varieties, var. *serrata*, var. *acuminata* (Siebold et Zucc.) H. Ohba et S. Akiyama, var. *yessoensis* (Koidz.) H. Ohba, var. *minamitanii* H. Ohba, var. *australis* T. Yamaz., and var. *angustata* (Franch. et Sav.) H. Ohba (Ohba and Akiyama, 2016); since their distributions are allopatric in Japan and composes sect. *Macrophyllae* together with *H. macrophylla* (De Smet et al., 2015), *H. serrata* will be a useful material to understand allopatric speciation in the plants distributed widely in the Japanese Archipelago. Although several phylogenetic studies of *H. serrata* have been previously conducted, the phylogenetic relationships among these varieties remain unclear because of limited information by genetic markers used and incomplete taxon samplings (Uemachi et al., 2014; Hirota et al., 2022). Therefore, more comprehensive phylogenetic analyses are required to elucidate the phylogenetic relationships and the history of diversification within sect. *Macrophyllae*, particularly at infraspecific level of *H. serrata*.

In this study, we reconstructed an infraspecific phylogeny of *H. serrata* and estimated divergence time of sect. *Macrophyllae*, including *H. serrata*, from the sister species, based on genome-wide SNPs. Additionally, we reconstructed the ancestral geographic areas to investigate phylogeographic history of *H. serrata*.

The phylogenetic trees reconstructed in this study showed the monophyly of most varieties of *H. serrata*. The divergence time between sect. *Macrophyllae* species and the outgroups was estimated to be in the Pleistocene period. The ancestral biogeographic history of *H. serrata* suggested some evidence of biogeographic isolations at various scales in the Japanese Archipelago.



**Figure.** Distributions of varieties of *Hydrangea serrata* and *H. macrophylla* in the Japanese Archipelago

## Comparison of Vegetation Indices and Spectral Reflectance Observed by Two Types of UAV-mounted Multispectral Camera

Ryohei YOKOYAMA<sup>1</sup>, Chinatsu YONEZAWA<sup>2</sup>, Mizuhiko NISHIDA<sup>2</sup>, Ryosuke TAJIMA<sup>2</sup>, Muxiye<sup>2</sup>,  
Koharu OKADA<sup>1</sup>, Kouki TAKAMURA<sup>3</sup>, Kaori AMAYA<sup>3</sup> and Ken ICHIKAWA<sup>3</sup>

<sup>1</sup>Faculty of Agricultural, Tohoku University, Japan

<sup>2</sup>Graduate School of Agricultural Science, Tohoku University, Japan

<sup>3</sup>Fukken Gijyutsu Consultants, Japan

Remote sensing in agriculture using multispectral cameras has increased in availability due to their advantages, such as high flexibility, ease of operation, and high spatial resolution. Several multispectral cameras with UAVs have been developed and utilized. The observed value can be converted to spectral reflectance and vegetation indices are calculated. However, the accuracy of the observed reflectance should be confirmed for vegetation monitoring. In this study, we compared images obtained by the two types of multispectral cameras mounted on UAVs, RedEdge MX-dual with Inspire-2 and P4 Multispectral (P4M) for paddy rice fields in the Kawatabi Field Science Center. We obtained spectral reflectance and calculated vegetation indices such as Normalized Difference Vegetation Index (NDVI), Green Normalized Difference Vegetation Index (GNDVI), and Red Edge Normalized Difference Vegetation Index (RENDVI). On August 5th, 2022, and September 13th, 2022, we observed target area almost simultaneously by two cameras. Because of the battery duration, the region was separated into two portions and monitored individually. Radiometric calibration was performed for the orthomosaic images by RedEdge MX-dual using a reflectance panel. P4M has a sunlight sensor, and it is possible to obtain vegetation indices without calibration, however, spectral reflectance is uncertain. Therefore, radiometric calibration was performed for the observation on September 13. For the comparison of RedEdge MX-dual and P4M, the average of vegetation indices and spectral reflectance were computed on each of the agricultural parcels for paddy rice. The results show that the spectral reflectance and RENDVI obtained by P4M without calibration were inconsistent with those of RedEdge MX-dual. The differences were clearly visible, especially in the spectral reflectance. NDVI and GNDVI obtained by P4M without calibration on September 13 corresponded to those obtained by the RedEdge MX-dual, however, RENDVI was smaller than that of the RedEdge MX-dual. After the calibration, RENDVI and spectral reflectance, except for blue and red edge, acquired by the first flight of P4M on September 13 almost corresponded to those obtained by RedEdge MX-dual. Blue was larger than that by RedEdge MX-dual and red edge was smaller than that by RedEdge MX-dual. RENDVI and spectral reflectance were discordant with those of the RedEdge MX-dual on the second flight on September 13. Blue, green, and RENDVI were larger than these by RedEdge MX-dual. Red, red edge, and near infrared were smaller than these by RedEdge MX-dual. These results show that the UAV multispectral remote sensing technology is instructive for precision agriculture; however, calibration and evaluation are necessary to obtain accurate observation results.

## Morphological and Genetic Data Do Not Support the Intraspecific Taxonomic Classification of *Pimenta pseudocaryophyllus*

Erick W. WEISSENBERG<sup>1</sup>, João Vicente COFFANI NUNES<sup>2</sup>, Isis SEBASTIÃO<sup>2</sup>,  
Patrícia Gleydes MORGANTE<sup>2</sup> and Gustavo Maruyama MORI<sup>1</sup>

<sup>1</sup>Department of Biological and Environmental Sciences, Institute of Biosciences, São Paulo State University (UNESP)

<sup>2</sup>Faculdade de Ciências Agrárias do Vale do Ribeira - Câmpus de Registro, São Paulo State University (UNESP)

*Pimenta pseudocaryophyllus* Landrum (Myrtaceae) is an important plant for traditional communities in southwestern Brazil, used both medicinally and for cultural. Due to the predatory exploitation, it may be at risk of vulnerability requiring. However, little is known about this species, including whether the name *P. pseudocaryophyllus* corresponds to a species or a species complex. This plant is widely distributed in South America, occupying different biomes but the distribution records are concentrated in the Atlantic Forest and the Cerrado. It presents three taxonomic varieties defined based on vegetative morphology, especially on the shape of the leaves. *P. pseudocaryophyllus* var. *hoehnei* (DC.) Landrum is in the coastal region of southern to southeastern Brazil, mainly in herbaceous, shrubby, and arboreal coastal sandy habitats (*restingas*); *P. pseudocaryophyllus* var. *pseudocaryophyllus* (Gomes) Landrum, is distributed in southeastern Brazil mainly in the highlands of ombrophilous dense forests, and *P. pseudocaryophyllus* var. *fulvescens* (Burret) Landrum that occurs in the Cerrado, with rare exceptions in the Bolivian Chaco. However, in the field and in collections records, a great variation in the shape of the leaves is observed. This study sought to analyze whether there is a congruence between genetics and morphological aspects of representatives of these taxonomic varieties. We sampled 153 *P. pseudocaryophyllus* individuals across four sites and genotyped them using a set of 11 polymorphic microsatellites. We quantified the genetic diversity of each sample and described their population genetic structure. Complementarily, we used a geometric morphometry of leaves from a subset of the total samples. We considered the leaf closest to the site's average and normalized them using General Procrustes Analysis and performed a Principal Component Analysis (PCA) to describe how taxonomic varieties are organized considering the leaves' shapes and sizes. The PCA of the morphology showed individuals comprised groups according to sampling site and variety. Conversely, the population genetic structure was not congruent with the observed morphological variation. Despite forming clearly separated clusters. We observed that varieties *pseudocaryophyllus* and *fulvescens* grouped together, whereas *hoehnei* was clearly differentiated. This preliminary study suggests that, because of the absence of correspondence between leaf morphology and genetics, leaf shape is likely not a reliable character for the intraspecific taxonomy.

## Phylogeography of *Juniperus* Species (Cupressaceae) with a Disjunct Distribution in the Island Areas of Japan

Hiroya TAGUCHI<sup>1</sup>, Daiki TAKAHASHI<sup>1</sup>, Takuro ITO<sup>2</sup>, Shuichiro TAGANE<sup>3</sup>, Ryota SUGAWARA<sup>4,5</sup>, Emiko OGURI<sup>5</sup>, Harue ABE<sup>6</sup> and Yoshihisa SUYAMA<sup>1</sup>

<sup>1</sup>Grad. Sch. Agr. Sci., Tohoku Univ.

<sup>2</sup>Bot. Gardens., Tohoku Univ.

<sup>3</sup>Kagoshima Univ. Museum

<sup>4</sup>Tokyo Metropolitan Univ.

<sup>5</sup>Tokyo Gakugei Univ.

<sup>6</sup>Sado Isl. Ctr. Ecol. Sustainabil., Niigata Univ.

A coastal conifer, *Juniperus taxifolia* var. *lutchuensis* (Cupressaceae) is distributed in the Ryukyu Islands, Izu Islands, and a part of the Izu peninsula. This species is treated as a variety of *J. taxifolia* var. *taxifolia* which is endemic to the Bonin (Ogasawara) Islands. Since these three Island groups are separated by more than 1,000 km away, it is interesting where this species originated and how it expanded its distribution. On the other hand, *J. conferta* is distributed in Hokkaido, Honshu, and Kyushu Islands. This species grows in a coastal environment like *J. taxifolia* var. *lutchuensis* and the two taxa are distinguished by the traits of their leaves. In areas where distributions of these two species overlap, morphologically intermediate individuals have been reported; however, their phylogenetic relationships are unclear.

In this study, we collected 267 samples of 7 *Juniperus* species including 27 populations of *J. taxifolia* and *J. conferta* from Japan and Taiwan Island in order to reveal the phylogeographic relationship among these three taxa. We extracted DNA from leaves by the CTAB method and obtained genome-wide SNPs by the MIG-seq analysis. Based on MIG-seq data, we conducted phylogenetic and population genetic analyses.

The result of the phylogenetic analysis indicated that *J. taxifolia* var. *lutchuensis* didn't form a monophyletic clade with var. *taxifolia* but with *J. conferta*. Moreover, *J. taxifolia* var. *taxifolia* was monophyletic with *J. formosana* which is endemic to Taiwan Island and southeast of mainland China. The results of the population genetic analyses indicated that *J. taxifolia* var. *lutchuensis* from Izu Islands is genetically different from the Ryukyu Islands population and is closely related to *J. conferta* from Honshu Island. These results suggest that *J. taxifolia* var. *taxifolia* originated from Taiwan or mainland China and that *J. taxifolia* var. *lutchuensis* has the same origin as *J. conferta* with some genetic differentiation by expanding its distribution along the coast.



**Photo.** *Juniperus taxifolia* var. *lutchuensis* in Amami Oshima Island



## Decay Types and Fungal Communities of Norway Spruce Dead Wood in Europe

Yuki KAWASAKI<sup>1</sup>, Shunsuke MATSUOKA<sup>2</sup>, Hirotoshi SATO<sup>2</sup>, Václav POUSKA<sup>3</sup>, Jenni NORDÉN<sup>4</sup>, Olga ORMAN<sup>5</sup>, Radek BAČE<sup>3</sup>, Momchil PANAYOTOV<sup>6</sup>, Nickolay TSVETANOV<sup>6</sup>, Martin MIKOLÁŠ<sup>3</sup>, Lucie ZÍBAROVÁ<sup>7</sup>, Angelos PAPADIMITRIOU<sup>8</sup>, Elias POLEMIS<sup>9</sup>, Kamil KRÁL<sup>10</sup>, Miroslav SVOBODA<sup>3</sup> and Yu FUKASAWA<sup>1</sup>

<sup>1</sup>Graduate School of Agricultural Science, Tohoku University, Japan

<sup>2</sup>Kyoto University, Japan

<sup>3</sup>Czech University of Life Sciences Prague, Czech Republic

<sup>4</sup>Norwegian Institute for Nature Research, Norway

<sup>5</sup>University of Agriculture Krakow, Poland

<sup>6</sup>University of Forestry, Bulgaria

<sup>7</sup>Personal, Czech Republic

<sup>8</sup>Personal

<sup>9</sup>Agricultural University of Athens, Greece

<sup>10</sup>The Silva Tarouca Research Institute for Landscape and Ornamental Gardening, Czech Republic

Fungi are the major decomposers of dead wood in forest ecosystems. Differences in fungal community structure affect the lignin decomposition of dead wood through differences in ligninolytic enzyme profiles of the fungal species in the community. Such differences in decomposition patterns are expected to affect carbon stocks in forests. Therefore, it is important to understand the driving factors and functions of wood-inhabiting fungi (WIF) communities in dead wood, and how they may respond to environmental changes. In this study, we investigated the relationship between fungal community composition and environmental variables in dead wood of Norway spruce (*Picea abies*) across the latitudinal gradient in Europe.

We sampled 374 dead Norway spruce logs from forests in six sites in five European countries along the latitudinal gradient. DNA metabarcoding was used to examine the fungal community structure of each log, and the functions of the fungal species that compose the community were estimated by the FUNGuild database. In this study, we also quantitatively evaluated the decay type of dead woods by using the Dilute Alkali Solubility (DAS) method, which is a method for quantifying and evaluating the chemical changes associated with the decomposition and alteration of lignocellulose in dead woods. The value of DAS (%) tends to be higher in the brown rot decay type, in which lignin remains with little modification.

DNA metabarcoding identified 1408 OTUs, of which 18 OTUs were brown rot fungi. The structure of the fungal community varies across a climatic gradient, DAS (%), an index of brown rot, was significantly correlated with mean annual temperature. The frequency of occurrence of brown rot fungi was positively correlated with DAS and annual mean temperature. These results suggested that the frequency of brown rot may increase with temperature as some species of brown rot fungi, which are sensitive to the site environment, become more dominant in a warmer temperature.



Photo. Norway spruce forest

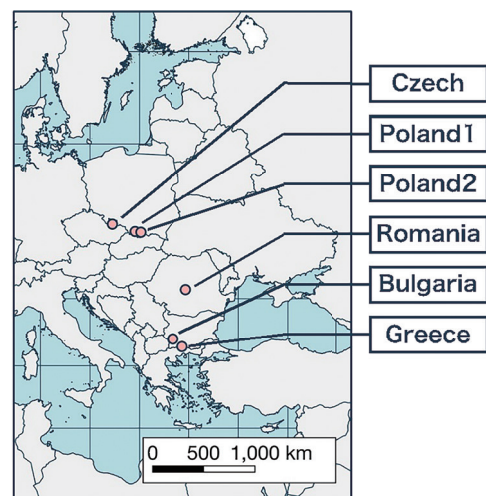


Figure. Study sites in Europe (6 sites)

## Population Genetic Structure of a Bamboo Taxon, *Pleioblastus* Sect. *Pleioblastus*, in the Ryukyu Islands Formed by Geohistory and Human Activity

Mana MOTOMIYA<sup>1</sup>, Daiki TAKAHASHI<sup>1</sup>, Shuichiro TAGANE<sup>2</sup>, Akiyo NAIKI<sup>3</sup>, Kenta WATANABE<sup>4</sup>,  
Takuro ITO<sup>5</sup> and Yoshihisa SUYAMA<sup>1</sup>

<sup>1</sup>Tohoku Univ.

<sup>2</sup>Kagoshima Univ. Museum

<sup>3</sup>TBRC, Univ. Ryukyus, NIT

<sup>4</sup>Okinawa KOSEN, <sup>5</sup>Tohoku Univ. Bot. Gard.

In island ecosystems, past geohistorical events, such as the formation of land bridges and trenches, have strongly influenced the distribution of organisms that constitute the ecosystem. However, some plant species commonly used in human life may be influenced by significant anthropogenic effects on their distribution and population genetic structure. In this study, we focused on a bamboo taxon, *Pleioblastus* Sect. *Pleioblastus* (*P. hindsii* sensu Nakai, *P. linearis*, *P. gramineus* and *P. gozadakensis*), which have been used in human life in the Ryukyu Islands. A total of 187 ramets from 11 islands were collected for population genetic analysis using the MIG-seq methods. First, the clone identification analysis revealed that several identical genets were found tens of kilometers apart on the same island, and even from different islands separated by the ocean. Such long-distance dispersal could not be expected under natural conditions, suggesting that their distribution is due to human transplantation and propagation. On the other hand, the results of population genetic structure analysis excluding these widely distributed genets indicated that distinct local genetic clusters are formed in the islands as observed in other organisms. These results clearly demonstrate not only geological history, but also human activities have a strong impact on the distribution and formation of population genetic structure in human-related plant species.



**Left Photo.** A high-density population of *P. linearis* at Cape Miyako, Amami Oshima Island which is considered to be a natural distribution.

**Right Photo.** *P. linearis* growing on the roadside at Amami Oshima Island which is considered to be a planted population.

## Effects of the Resource Distance on the Decisions of Mycelial Behavior

Kaho ISHII<sup>1</sup> and Yu FUKASAWA<sup>2</sup>

<sup>1</sup>Faculty of Agriculture, Tohoku University, Japan

<sup>2</sup>Graduate School of Agricultural Science, Tohoku University, Japan

Cord-forming basidiomycetes develop large mycelial networks and play a major role in organic matter decomposition and nutrient cycling in forest ecosystems. Fungal mycelia alter their foraging and migrating behavior flexibly in response to the presence of outer resource and their nutritional status. Previous studies showed that, when a mycelium extending from a wood block (inoculum) finds a new piece of wood (bait), the mycelium makes a decision whether or not to move from the inoculum to the bait depending on the bait size and the timing of bait placement. For example, relatively larger baits tend to induce mycelial migration from inoculum wood to bait wood more frequently than smaller ones. This suggests that mycelia may decide to move out based on the size of the wood resources and their own nutritional status. However, the influence of other factors, such as distance from the inoculum to the bait, on the decision to move out is not clear. We hypothesized that, if the distance from the inoculum is longer, mycelia might move to the baits even with smaller size, because maintaining the hyphal connection between the inoculum and the bait at a longer distance might be energetically more expensive than that in a shorter distance. Therefore, this study examined the effects of distance from the inoculum to the bait and the size of the bait on the decision-making of mycelial migration.

A beech wood block (0.5 cm<sup>3</sup>), incubated with a basidiomycete *Phanerochaete velvina* for 1 month on 2% malt extract agar medium for colonization, was put onto a corner of a tray (24 cm × 24 cm) filled with soil ca. 5 mm depth (Fig. 1). When mycelium grew at least 15 cm from the inoculum, a bait wood block was placed 1 cm or 15 cm away from the inoculum and incubated at 20°C in the darkness for 50 days. We prepared two sizes of bait wood blocks (4 cm<sup>3</sup> and 8 cm<sup>3</sup>). After incubation, inoculum wood blocks were retrieved from the tray, surface cleaned, transferred to new soil trays, and incubated at 20°C in the darkness for 8 days to check the re-growth of mycelium and its direction. Trays were photographed every 3 days during the experiment. We measured hyphal coverage by ImageJ. Inoculums and baits were dried at 70°C and weighed before and after incubation to check their weight loss during incubation. The dry weight of 40 inoculums at the time of bait placement was estimated by creating a regression line from the dry weight and mycelial area of 73 inoculums removed at that time.

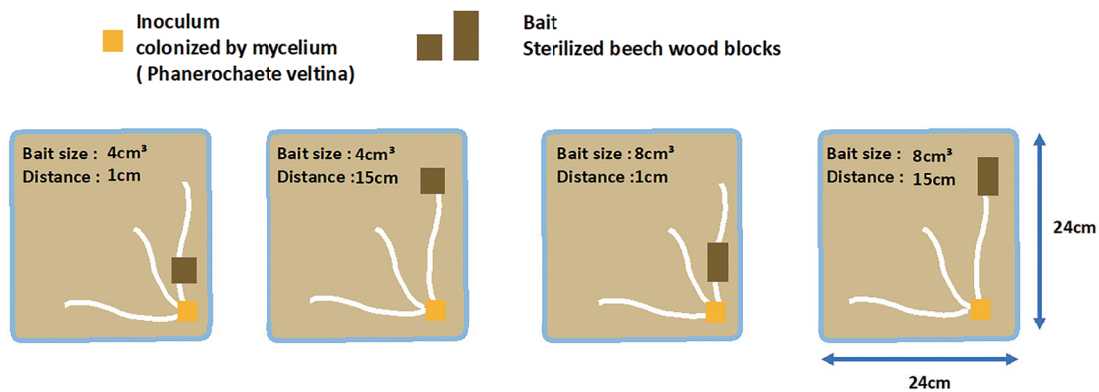


Figure. Experimental design of microcosm



## Development of Plant Environmental DNA Analysis Method for Forest Soil

Kodai HAMATSU, Hiroya TAGUCHI, Daiki TAKAHASHI and Yoshihisa SUYAMA

Tohoku university, Japan

Environmental DNA analysis is a useful method for identifying species that live in a place. In our laboratory, we are developing technology with the aim of applying this method to intraspecific diversity analysis. As a preliminary step of this study, we examined forest soil samples to confirm whether the plant DNA detected in the soil matches the composition of the surrounding plant species. Soil samples were collected from an artificial forest of *Cryptomeria japonica* and DNA was extracted using a commercially available soil DNA extraction kit. Multiple plant DNA barcode regions were amplified from the extracted DNA, and sequence data were obtained by next-generation DNA sequencing. In addition, plant samples growing in the vicinity of the sampling site were also collected, and sequence data were obtained by the same method after DNA extraction. As a result of analyzing the sequence data detected from the soil sample, the sequences were six species of woody plants including *C. japonica* and seven species of herbaceous plants growing in the vicinity. From these results, it was confirmed that plant environment DNA analysis of forest soil is possible, but it was also found that there is room for improvement in DNA extraction library construction methods. In the next step, we will conduct a similar analysis of forest soils with different vegetation to confirm the validity of the acquired data. And then we plan to develop it into an intraspecific level diversity analysis method after improving the basic technology by referring to the DNA extraction and library construction methods of ancient soil DNA conducted in previous studies.



**Photo 1.** Soil and plant samples were collected in an artificial forest of *Cryptomeria japonica*



**Photo 2.** Soil samples were collected from *ca.* 5 cm depth



## Effects of Oak Wilt Disease on Fungal Community Composition and Wood Decomposition in Dead *Quercus serrata* Trunks

Satsuki KIMURA<sup>1</sup>, Yu FUKASAWA<sup>1</sup>, Yuji KOMINAMI<sup>2</sup>, Masahiro TAKAGI<sup>3</sup>, Kimiyo MATSUKURA<sup>4</sup>, Masayuki USHIO<sup>5</sup>, Makoto KOBAYASHI<sup>6</sup>, Satoshi SUZUKI<sup>7</sup>, Shuhei TAKEMOTO<sup>7</sup>, Nobuaki TANAKA<sup>7</sup>, Mayuko JOMURA<sup>4</sup>, Kohmei KADOWAKI<sup>8</sup>, Haruo KINUURA<sup>2</sup> and Satoshi YAMASHITA<sup>2</sup>

<sup>1</sup>Tohoku University

<sup>2</sup>Forestry and Forest Products Research Institute

<sup>3</sup>University of Miyazaki

<sup>4</sup>Nihon University

<sup>5</sup>The Hong Kong University of Science and Technology

<sup>6</sup>Hokkaido University

<sup>7</sup>The University of Tokyo

<sup>8</sup>Kyoto University

In Japan, mass attacks of an ambrosia beetle *Platypus quercivorus*, vectoring a pathogenic fungus *Raffaelea quercivora*, cause oak wilt outbreaks in recent decades. Since *P. quercivorus* inoculates symbiotic fungi into wood tissue, it can alter the fungal community composition within the dead wood. A change in the fungal community composition may alter the decomposition function of the community, as well as the physical and chemical properties of the dead wood. The difference in properties of the dead wood may impact surrounding biological communities. Therefore, understanding the effects of oak wilt disease on a dead wood fungal community is important for predicting wood decomposition and forest biodiversity after the dieback. In this study, we used DNA metabarcoding to compare the fungal communities between *Q. serrata* trunks killed by oak wilt and healthy trunks that felled artificially at three sites across latitude in Japan. A total of 1200 samples from 5-time points during the 2016 autumn – 2018 spring were subjected to amplicon sequencing of the fungal internal transcribed spacer 1 region and 1128 fungal operational taxonomic units (OTUs) were detected. Fungal community composition differed significantly between *Q. serrata* trunks killed by oak wilt and healthy-cut trunks (Fig. 1), and diversity indices showed that trunks killed by oak wilt were significantly lower than that of healthy-cut trunks (Fig 2). The Fungal Trait database was used to estimate the function of each OTU and revealed a dominance of wood-decomposing fungi, mainly white rot fungi, which have the ability to decompose wood. The generalized linear mixed model (GLMM) showed that the OTU richness and DNA copy number of white rot fungi were significantly affected by the sampling period, mean air temperature, precipitation, and oak wilt infestation, and that the OTU richness and DNA copy number of white rot fungi increased with oak wilt. During the ca. 1.5-year experiment, wood density decreased by an average of 9.2%. Structural equation modeling (SEM) showed that oak wilt and environmental variables significantly affected the fungal community, but the fungal community didn't significantly affect wood decomposition (Fig 3). Rather, trunk moisture and mean air temperature strongly affected decomposition. This study focused on the initial decomposition of the trunks during ca. 1.5 years after the start of the experiment. It is important to conduct further research over a longer time period to evaluate the effects of oak wilt and associated fungal communities on trunk decomposition.

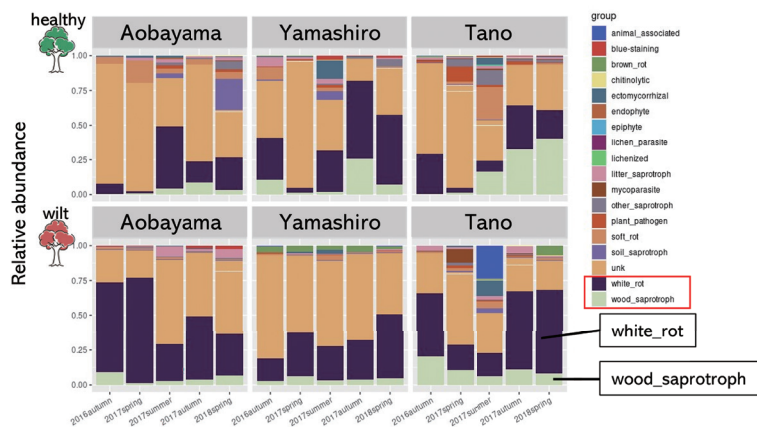


Figure 1. Relative abundance of fungi (functional group)

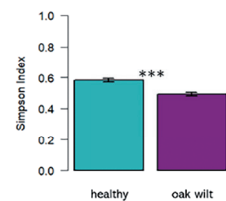


Figure 2. Diversity index

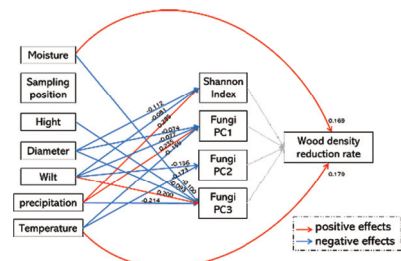


Figure 3. SEM

## Phylogenetic Origin of *Cryptomeria japonica* on Kinkasan Island in Japan

Henri ALLEKOTTE, Taguchi HIROYA, Daiki TAKAHASHI and Yoshihisa SUYAMA

Tohoku University, Japan

**Sugi ( 杉 )** – *Cryptomeria japonica* is widely planted throughout Japan accounting for about 44 % of the total area of planted forests but its natural populations with its original local lineage are limited. Natural forests and local tree lineages are important for regional biodiversity and future breeding resources. Kinkasan in Miyagi prefecture is known as an island where the natural forest has been protected; therefore, we thought that it is a candidate for an unknown natural population of the species. Therefore, we wanted to figure out if the population on the island has a surviving local lineage of this region or not.

We collected 24 samples from the island including individuals from natural habitats as well as planted populations. We also used reference samples (83 samples from 17 natural populations in Japan and 28 samples from local populations near Kinkasan) to compare the genetic structure. Genome-wide SNP data was collected with the MIG-seq approach and genetic analysis was conducted by using Stacks (ver. 2.60), RAxML (ver.8.2.12), and ADMIXTURE (ver. 1.3.0).

The results showed that the eight trees from the natural habitats were supposed to be originated from a local lineage related to the local populations near Kinkasan. Their values of genetic diversity and inbreeding coefficient are almost the same levels as other natural populations. In addition, the lineage of the Pacific Ocean side was found in planted populations and partial mixing of the Sea of Japan side lineage was also observed in some individuals which may indicate genetic disturbance in the natural genetic structure.

The trees with local lineage discovered in this study are important for the conservation of the local genetic resources and diversity. It is important to consider the conservation of local genetic diversity in upcoming afforestation and restoration projects.



**Photos 1 and 2.** Over hundred years old trees of *Cryptomeria japonica* on Kinkasan island

## Molecular Phylogenetic Analyses of Geographical and Ecological Speciation of *Anaphalis margaritacea*

Taishi HOSON<sup>1</sup>, Takuro ITO<sup>2</sup>, Shinji FUJII<sup>3</sup>, Daiki TAKAHASHI<sup>4</sup>, Ayumi MATSUO<sup>4</sup>,  
Yoshihisa SUYAMA<sup>4</sup> and Masayuki MAKI<sup>1,2</sup>

<sup>1</sup>Graduate School of Life Sciences, Tohoku University

<sup>2</sup>Botanical Gardens, Tohoku University

<sup>3</sup>Department of Environmental Science, University of Human Environments

<sup>4</sup>Graduate School of Agricultural Science, Tohoku University

*Anaphalis margaritacea* (Asteraceae) is a perennial species distributed widely from Asia to North America. In Japan, *A. margaritacea* consists of three varieties; var. *margaritacea* distributed mainly in the mountain areas in eastern Japan, var. *angustifolia* distributed in mountain areas in western Japan, var. *yedoensis* distributed in riverbanks covered with pebbles throughout Japan. These varieties are considered to have been derived via different speciation patterns such as geographical and ecological speciations. They seem to need taxonomic reexamination based on the molecular analysis because morphological intermediates between these varieties have been sometimes reported. In this study, we collected these three varieties from all over Japan and examined the genetic differentiation among the three varieties using the genome-wide SNPs by MIG-seq.

Analyses based on the SNPs showed that the populations of *A. margaritacea* var. *angustifolia* and var. *yedoensis* were monophyletic, respectively and these lineages were contained with *A. margaritacea* var. *margaritacea*, suggesting that they are of a single origin from *A. margaritacea* var. *margaritacea*. Population genetics analyses showed that the *A. margaritacea* complex comprised three clades as a whole: “*A. margaritacea* var. *margaritacea* in Hokkaido” clade, “*A. margaritacea* var. *margaritacea* in Honshu” clade, and “*A. margaritacea* var. *yedoensis* in Hokkaido” clade. *Anaphalis margaritacea* var. *angustifolia* was included in “var. *margaritacea* in Honshu” clade. On the other hand, it is revealed that *A. margaritacea* var. *yedoensis* in Honshu have a admixture of the two clades of *A. margaritacea* var. *margaritacea* in Honshu and *A. margaritacea* var. *yedoensis* in Hokkaido. Based on these results, we will discuss differentiation processes among the three varieties of *A. margaritacea*.

## List of scientific papers in 2022 published by field science group in Graduate School of Agricultural Science, Tohoku University

### *The Forest-Andisols Group*

- Cardoni, S., Piredda, R., Denk, T., Grimm, G.W., Papageorgiou, A.C., Schulze, E-D., Scoppola, A., Shanjani, P.S., Suyama, Y., Tomaru, N., Worth, J.R.P. and Simeone, M.C. (2022) 5S-IGS rDNA in wind-pollinated trees (*Fagus* L.) encapsulates 55 million years of reticulate evolution and hybrid origins of modern species. *Plant J.*, **109**(4): 909-926.
- Fukasawa, Y. (2022) Does coexistence of diverse fungi retard wood decomposition?: Fundal diversity-decomposition relationship. *Kagaku to Seibutsu*, **60**(7): 319-326. (in Japanese)
- Fukasawa, Y. (2022) Mushroom thinking. *Seibutsukougaku*, **100**: 251. (in Japanese)
- Fukasawa, Y. and Kaga, K. (2022) Surface area of wood influences the effects of fungal interspecific interaction on wood decomposition—A case study based on *Pinus densiflora* and selected white rot fungi. *J. Fungi*, **8**: 517.
- Fukasawa, Y. and Kitabatake, H. (2022) Which is the best substrate to regenerate? a comparative pot experiment for tree seedling growth on decayed wood and in soil. *Forests*, **13**: f13071036.
- Higashi, Y., Hirota, S.K., Suyama, Y. and Yahara, T. (2022) Geographical and seasonal variation of plant taxa detected in faces of *Cervus nippon yakushimae* based on plant DNA analysis, in Yakushima Island. *Ecol. Res.*, **37**: 582-597.
- Hirota, S.K., Yahara, T., Fuse, K., Sato, H., Tagane, S., Fujii, S., Minamitani, T. and Suyama, Y. (2022) Molecular phylogeny and taxonomy of *Hydrangea serrata* complex (Hydrangeaceae) in western Japan including a new subspecies of *H. acuminata* from Yakushima. *PhytoKeys*, **188**: 49-71.
- Ishii, N.I., Hirota, S.K., Matsuo, A., Sato, M.P., Sasaki, T. and Suyama, Y. (2022) Species-genetic diversity correlations depend on ecological similarity between multiple moorland plant species. *Oikos*, **2022**: e09023.
- Ishii, N.I., Hirota, S.K., Tsunamoto, Y., Matsuo, A., Abe, H. and Suyama, Y. (2022) Extremely low level of genetic diversity in *Gentiana yakushimensis*, an endangered species in Yakushima Island, Japan. *Plant Species Biol.*, **37**: 315-326.
- Islam, J. Tanimizu, M., Shimizu, Y., Goto, Y., Ohtani, N., Sugiyama, K., Tatezaki, E., Sato, M., Makino, E., Shimada, T., Ueda, C., Matsuo, A., Suyama, Y., Sakai, Y., Furukawa, M., Usami, K., Yoneyama, H., Aso, H., Tanaka, H. and Nochi, T. (2022) Development of a rational framework for the therapeutic efficacy of fecal microbiota transplantation for calf diarrhea treatment. *Microbiome*, **10**(1): 31.
- Komagata, Y., Fukasawa, Y. and Matsuura, K. (2022) Low temperature enhances the ability of the termite-egg-mimicking fungus *Athelia termitophila* to compete against wood-decaying fungi. *Fungal Ecol.*, **60**: 101178.
- Kurata, S., Vasques, D.T., Hirota, S.K., Kurashima, O., Suyama, Y., Nishida, S. and Ito, M. (2022) From East Asia to Beringia: reconstructed range dynamics of *Geranium erianthum* (Geraniaceae) during the last glacial period in the northern Pacific region. *Plant Syst. Evol.*, **308**: 28.
- Kusuma, Y.W.C., Matsuo, A., Suyama, Y., Wanke, S. and Isagi, Y. (2022) Conservation genetics of three *Rafflesia* species in Java Island, Indonesia using SNP markers obtained from MIG-seq. *Conserv. Genet.*, **23**: 1039-1052.
- Makino, T. (2022) Study on dynamics of hazardous elements in soil and reduction of crop absorption. *J. Jpn. Soc. Soil Sci. Plant Nutr.*, **93**(5): 243-246. (in Japanese)
- Makishima, D., Ishii, N., Sutoh, R., Goto, A., Kawai, Y., Taniguchi, H., Uchida, K., Shimazaki, M., Nakashizuka, T., Suyama, Y., Hikosaka, K. and Sasaki, T. (2022) Predicting diversity changes in subalpine moorland ecosystems based on geometry of species distributions and realistic area loss. *J. Veg. Sci.*, **33**(5): e13150.
- Nakahama, N., Hanaoka, T., Itoh, T., Kishimoto, T., Ohwaki, A., Matsuo, A., Kitahara, M., Usami, S., Suyama, Y. and Suka, T. (2022) Identification of source populations for reintroduction in extinct populations based on genome-wide SNPs and mtDNA sequence: a case study of the endangered subalpine grassland butterfly *Aporia hippia* (Lepidoptera; Pieridae) in Japan. *J. Insect Conserv.*, **26**: 121-130.
- Nakahama, N., Okano, R., Nishimoto, Y., Matsuo, A., Ito, N. and Suyama, Y. (2022) Possible dispersal of coastal and subterranean carabid beetle *Thalassoduvallius masidai* (Coleoptera) by ocean currents. *Biol. J. Linn. Soc.*, **135**(2): 265-276.



- Narukawa, T., Makino, T., Kanno, H., Hamamoto, T., Kimura, K. and Yamasaki, S. (2022) The changes in the chemical forms of thallium, cobalt and manganese with air-drying of soils. *Soil Sci. Plant Nutr.*, **68**(4): 429-433.
- Ngoc, N.V., Binh, H.T., Son, H.T., Suyama, Y. and Yahara, T. (2022) A new species of *Quercus* genus (Fagaceae) from Son Tra Peninsula, Central Vietnam. *PhytoKeys*, **206**: 61-73.
- Ngoc, N.V., Son, H.T., Binh, H.T., Tagane, S., Suyama, Y. and Yahara, T. (2022) A new species of Lithocarpus (Fagaceae) from Ca Dam Mountain of Quang Ngai Province, Vietnam. *Syst. Bot.*, **47**: 729-737.
- Nota, K., Klaminder, J., Milesi, P., Bindler, R., Nobile, A., Steijn, T., Bertilsson, S., Svensson, B., Hirota, S.K., Matsuo, A., Gunnarsson, U., Seppä, H., Valiranta, M., Wohlfarth, B., Suyama, Y. and Parducci, L. (2022) Norway spruce postglacial recolonization of Fennoscandia. *Nat. Commun.*, **13**(1): 1333.
- Saito, T., Sasaki, T., Tsunamoto, Y., Uchida, S., Satake, K., Suyama, Y. and Chiba, S. (2022) Even short-distance dispersal over a barrier can affect genetic differentiation in *Gyraulus*, an island freshwater snail. *Freshwater Biol.*, **67**: 1971-1983.
- Sakaguchi, S., Oishi, M., Takahashi, D., Matsuo, A., Hirota, S.K., Suyama, Y. and Setoguchi, H. (2022) *Ribes fujisanense* (Grossulariaceae): a new species of obligate epiphytic gooseberry discovered in central Japan. *Acta Phytotax. Geobot.*, **73**(1): 49-56.
- Sasaki, T., Ishii, N.I., Makishima, D., Sutou, R., Goto, A., Kawai, Y., Taniguchi, H., Okano, K., Matsuo, A., Lochner, A., Cesarz, S., Suyama, Y., Hikosaka, K. and Eisenhauer, N. (2022) Plant and microbial community composition jointly determine moorland multifunctionality. *J. Ecol.*, **110**(10): 2507-2521.
- Suetsugu, K., Hirota, S.K., Nakato, N., Suyama, Y. and Serizawa, S. (2022) Morphological, ecological, and molecular phylogenetic approaches reveal species boundaries and evolutionary history of *Goodyera crassifolia* (Orchidaceae, Orchidoideae) and its closely related taxa. *PhytoKeys*, **212**: 111-134.
- Suetsugu, K., Okada, H., Hirota, S. and Suyama, Y. (2022) Evolutionary history of mycorrhizal associations between Japanese *Oxygyne* (Thismiaceae) species and Glomeraceae fungi. *New Phytol.*, **235**(3): 836-841.
- Suyama, Y., Hirota, S.K., Matsuo, A., Tsunamoto, Y., Mitsuyuki, C., Shimura, A. and Okano, K. (2022) Complementary combination of multiplex high-throughput DNA sequencing for molecular phylogeny. *Ecol. Res.*, **37**(1): 171-181.
- Takahashi, D., Isagi, Y., Li, P., Qiu, Y-X., Setoguchi, H., Suyama, Y., Matsuo, A., Tsunamoto, Y. and Sakaguchi, S. (2022) Stable persistence of relict populations involved evolutionary shifts of reproductive characters in the genus *Tanakaea* (Saxifragaceae). *J. Syst. Evol.*, **60**: 1405-1416.
- Takahashi, K. and Fukasawa, Y. (2022) Association between corticolous myxomycetes and tree vitality in *Cryptomeria japonica*. *Mycoscience*, **63**: MYC563.
- Teramura, A., Koeda, K., Matsuo, A., Sato, M.P., Senou, H., Ho, H-C., Suyama, Y., Kikuchi, K. and Hirase, S. (2022) Assessing the effectiveness of DNA barcoding for exploring hidden genetic diversity in deep-sea fishes. *Mar. Ecol. Prog. Ser.*, **701**: 83-98.
- Toji, T., Hirota, S.K., Ishimoto, N., Suyama, Y. and Itino, T. (2022) Intraspecific independent evolution of floral spur length in response to local flower visitor size in Japanese *Aquilegia* in different mountain regions. *Ecol. Evol.*, **12**(3): e8668.
- Tsuzuki, Y., Sato, M.P., Matsuo, A., Suyama, Y. and Ohara, M. (2022) Genetic consequences of habitat fragmentation in a perennial plant *Trillium camschatcense* are subjected to its slow-paced life history. *Popul. Ecol.*, **64**(1): 5-18.
- Uemura, R., Asakawa, A., Fujii, S., Matsuo, A., Suyama, Y. and Maki, M. (2022) Can *Rumex madaio* (Polygonaceae) be threatened by natural hybridization with an invasive species in Japan? *Nord. J. Bot.*, **2022**(5): e03543.
- Wagatsuma, S., Imanishi, J., Suyama, Y., Matsuo, A., Sato, M.P., Mitsuyuki, C., Tsunamoto, Y., Tominaga, T. and Shimono, Y. (2022) Revegetation in Japan overlooks geographical genetic structure of native *Artemisia indica* var. *maximowiczii* populations. *Restor. Ecol.*, **30**(7): e13567.
- Watanabe, K., Yaneshita, M., Denda, T., Yokota, M., Hirota, S.K., Suyama, Y. and Tsumura, Y. (2022) Genetic structure of the *Liriope muscari* polyploid complex and the possibility of its genetic disturbance in Japan. *Plants*, **11**: 3015.
- Zhang, J., Liu, G. and Fukasawa, Y. (2022) Editorial: Fungal genetics in plant biomass conversion. *Front. Microbiol.*, **13**: 875768.

### ***The Ruminant Production Group***

- Bando, H., Fukuda, Y., Watanabe, N., Olawale, J.T. and Kato, K. (2022) Depletion of intracellular glutamine pools triggers *Toxoplasma gondii* stage conversion in human glutamatergic neurons. *Front. Cell. Infect. Microbiol.*, **11**: 788303.
- Fukasawa, M. and Takahashi, R. (2022) The seasonal and diurnal expression pattern of sleep like posture in milking Holstein cows. *Ani. Behav. Manage.*, **58**(2): 37-49. DOI: 10.20652/jabm.58.2\_39
- Fukasawa, M. and Takeda, K. (2022) Chapter 2, Welfare of livestock. Section 2, Cattle. In: *Animal Welfare Science*, edited by Shinmura, T. Showa-do. Kyoto. pp. 129-143. (in Japanese)
- Fukuda, Y., Akematsu, T., Bando, H. and Kato, K. (2022) Snf2 Proteins Are Required to Generate Gamete Pronuclei in *Tetrahymena thermophila*. *Microorganisms*, **10**(12): 2426.
- Gotoh, Y., Kakihara, H., Shishido, T., Fukuda, Y., Takizawa, S., Suyama, Y., Matsuo, A., Nakano, M. and Ogura, S. (2022) Effect of plant species diversity in pasture on ruminal and fecal bacterial community of grazing Japanese Black cows. The 19th Asian-Australasian Association of Animal Production Animal Science Congress, Jeju, Korea.
- Islamuddin, M., Ali, A., Afzal, O., Ali, A., Ali, I., Altamimi, A.S.A., Alamri, M.A., Kato, K. and Parveen, S. (2022) Thymoquinone Induced Leishmanicidal Effect via Programmed Cell Death in *Leishmania donovani*. *ACS Omega*, **7**(12): 10718-10728.
- Islamuddin, M., Ali, A., Khan, W.H., Ali, A., Hasan, S.K., Abdullah, M., Kato, K., Abidin, M.Z. and Parveen, S. (2022) Development of Highly Sensitive Sandwich ELISA for the Early-Phase Diagnosis of Chikungunya Virus Utilizing rE2-E1 Protein. *Infect. Drug Resist.*, **15**: 4065-4078.
- Islamuddin, M., Mustfa, S.A., Ullah, S.N.M.N., Omer, U., Kato, K. and Parveen, S. (2022) Innate Immune Response and Inflammasome Activation During SARS-CoV-2 Infection. *Inflammation*, **45**(5): 1849-1863.
- Kabir, M.H.B., Recuenco, F.C., Mohd, Zin, N.K., Watanebe, N., Fukuda, Y., Bando, H., Watanabe, K., Bochimoto, H., Xuan, X. and Kato, K. (2022) Identification of potent anti-Cryptosporidium new drug leads by screening traditional Chinese medicines. *PLoS Negl. Trop. Dis.*, **16**(11): e0010947.
- Kakihara, H. and Ogura, S. (2022) Effect of soil acidification on regrowth of orchardgrass (*Dactylis glomerata*) under application of grazing cattle dung, cattle manure compost, and chemical fertilizer. *Grassl. Sci.*, **68**(3): 255-262. DOI: 10.1111/grs.12361
- Kakihara, H. and Ogura, S. (2022) Relationship between orchardgrass (*Dactylis glomerata*) dominance and the soil chemical characteristics of non-allophanic Andosol under cutting and cattle grazing. *Grassl. Sci.*, **68**(2): 165-173.
- Kume, H., Shishido, T., Kakihara, H., Fukasawa, M., Sato, K. and Ogura, S. (2022) The effect of the demand for oral behavior on salt block intake of sheep. The 19th Asian-Australasian Association of Animal Production Animal Science Congress, Jeju, Korea.
- Masuda, C., Morikawa, Y., Masaka, K., Koga, W., Suzuki, M., Hayashi, S., Tada, C. and Seiwa, K. (2022) Hardwood mixture increases stand productivity through increasing the amount of leaf nitrogen and modifying biomass allocation in a conifer plantation. *For. Ecol. Manage.*, **504**: 119835.
- Masuda, C., Morikawa, Y., Masaka, K., Koga, W., Suzuki, M., Hayashi, S., Tada, C. and Seiwa, K. (2022) Hardwood mixtures facilitate leaf litter decomposition and soil nitrogen mineralization in conifer plantations. *For. Ecol. Manage.*, **507**: 120006.
- Matsubara, R., Murakoshi, F., Tada, C., Fukuda, Y. and Nakai, Y. (2022) Synergistic oocysticidal effect of Ortho-reagent and saturated calcium hydroxide solution against *Cryptosporidium parvum*. *J. Ani. Prod. Environ. Sci.*, **21**(1): 32-38.
- Morikawa, Y., Hayashi, S., Negishi, Y., Masuda, C., Watanabe, M., Watanabe, K., Masaka, K., Matsuo, A., Suzuki, M., Tada, C. and Seiwa, K. (2022) Relationship between the vertical distribution of fine roots and residual soil nitrogen along a gradient of hardwood mixture in a conifer plantation. *New Phytol.*, **235**(3): 993-1004.
- Okaze, T. and Tada, C. (2022) Development and performance evaluation of a micro anaerobic digestion system for household use. *Jpn. Archit. Rev.*, **5**(4): 644-648. DOI: 10.1002/2475-8876.12289
- Sakurai, R., Yokoyama, Y., Fukuda, Y. and Tada, C. (2022) Quantification of free and esterified long-chain fatty acids without extraction by high-performance liquid chromatography in anaerobic

digestion sludge. *J. Mater. Cycles Waste Manage.*  
DOI: 10.1007/s10163-022-01561-z

Takizawa, S., Asano, R., Fukuda, Y., Baba, Y., Tada, C. and Nakai, Y. (2022) Shifts in xylanases and the microbial community associated with xylan biodegradation during treatment with rumen fluid. *Microb. Biotechnol.*, **15**(6): 1729-1743.

Wada, S., Konno, S., Terada, F., Ogura, S. and Fukasawa, M. (2022) The effect of early stroking on calf behavioural response and plasma cortisol concentration during later managements. *Bull. Integr. Field Sci. Cent.*, **36**: 1-5. (in Japanese)

### **The Rice Production Group**

Akamatsu, Y., Tajima, R., Uno, T., Ito, T., Nishida, M. and Saito, M. (2022) Characterization of root traits for phosphorus deficiency tolerance using chromosome segment substitution lines. *Plant Root*, **16**: 21-30.

Ito, C., and Nishida, M. (2022) Regional Trends: Tohoku. *J. Jpn. Soc. Soil Sci. Plant Nutr.*, **93**(2): 91. (in Japanese)

Matsuoka-Uno, C., Uno, T., Tajima, R., Ito, T. and Saito, M. (2022) Liming and Phosphate Application Influence Soil Carbon and Nitrogen Mineralization Differently in Response to Temperature Regimes in Allophanic Andosols. *Agriculture*, **12**(2): 142.

Susilawati, P. N., Tajima, R., Giamerti, Y., Yang, Y., Yufdy, M. P., Lubis, I. and Homma, K. (2022) Application of consecutive polyethylene glycol treatments for modeling the seminal root growth of rice under water stress. *Sci. Rep.*, **12**: 2096.

Tokonami, Y., Funao, T., Oga, T., Nishida, M., Takahashi, T. and Asakawa, S. (2022) Estimation of turnover time of microbial biomass potassium in paddy field soil. *Soil Sci. Plant Nutr.*, **68**(2): 275-283.

Yamashita, Y., Nishida, M., Akita, K., Ito, T., Saito, M., Honjo, H., Shinohara, M. and Asakawa, S. (2022) Pool size of microbial biomass potassium in various farmland soils. *Soil Sci. Plant Nutr.*, **68**(3): 400-408.

### **Marine Bio-Production Group**

Kurihara, H. and Ikeda, M. (2022) Screening of microsatellite DNA markers for population genetic analysis of sailfin sandfish *Arctoscopus japonicus*. *Aquat. Anim.*, AA2022-14. (in Japanese)

Obayashi, T., Ando, D. and Ikeda, M. (2022) Permutation tests of likelihood ratios for estimating kinships

in wild populations of olive flounder *Paralichthys olivaceus*. *IPSJ SIG Tech. Rep.*, **56**: 1-7. (in Japanese)

Oki, Y., Kitazato, H., Fujii, T. and Yasukawa, S. (2022) Habitat mapping for human well-being: a tool for reducing risk in disaster-prone coastal environments and human communities. *Geol. Soc., London, Spec. Publ.*, **505**: 271-282.

Takeda, M. and Ikeda, M. (2022) Distribution of *Palaemon paucidens* C type in Amami-Oshima and Kakeroma Islands with the data for the genetic characteristics and seawater requirement of the larvae. *Aquat. Anim.*, AA2022-2.

### **Integrated Field Control Group**

Furuya, S., Oishi, T., Hasegawa, K. and Yonezawa, C. (2022) Estimation of tea yield and quality during the first crop season using UAV remote sensing data. Proceedings of the 73rd (Autumn 2022) Conference of the Remote Sensing Society of Japan, pp. 47-48. (in Japanese)

Furuya, S., Yonezawa, C., Ishitsuka, N. and Kojima, S. (2022) A Preliminary Study of Paddy Rice Yield Estimation Using Full Polarimetric Air-borne X-band Sar Data. Proceedings of 2022 IEEE International Geoscience and Remote Sensing Symposium, pp. 1129-1132.

Kunii, D., Yonezawa, C., Okaze, T. and Minami, K. (2022) Challenges and Considerations for Preserving the Windbreak Forests "Igune" as a Community — A case study in Osaki City, Miyagi Prefecture, Japan — . Proceedings of the JASS 2022 Annual Meeting, pp. 51-52. (in Japanese)

Minami, K., Yonezawa, C. and Okaze, T. (2022) A Study of Effects of Wind Speed Reduction by "Igune" as Homestead Trees around Rural House in Osaki Koudo based on Large-Eddy Simulation. *J. Jpn. Agric. Syst. Soc.*, **38**(2): 37-42. (in Japanese)

Minami, K., Yonezawa, C. and Okaze, T. (2022) Investigation of Windbreak Characteristics by Shrubs and Tall Trees Constituting "Igune" in Osaki Koudo Based on Numerical Fluid Dynamics Analysis. Proceedings of the JASS 2022 Annual Meeting, pp. 49-50. (in Japanese)

Minami, K., Yonezawa, C. and Okaze, T. (2022) Qualification of Value of "Igune" in Osaki Koudo as Windbreak Planting (Part 1) Large-Eddy Simulation Considering Leaf Area Density Distribution. AIJ HOKKAIDO 2022, 41021.

Murata, H. and Yonezawa, C. (2022) Detection of Submerged Aquaculture Raft Using a Drone-based Multispectral Camera. Proceedings on

- Asian Conference on Remote Sensing (ACRS) 2022.
- Murata, H., Fujii, T. and Yonezawa, C. (2022) Creation of orthomosaic maps from drone-based multispectral camera images: a case study in a ria coast of Ago Bay, Mie Prefecture, Japan. Proceedings of the 73rd (Autumn 2022) Conference of the Remote Sensing Society of Japan, pp. 131-132. (in Japanese)
- Mutatisse, A.A., Magezi, E.F. and SUMITA, T. (2022) Analysis on Banana Consumers' Attitudes: Exploring Farmers' Local Markets in Response to Exports Restrictions in Mozambique. *J. Integr. Field Sci.*, **19**: 30.
- Muxiye and Yonezawa, C. (2022) Analysis of Time Series Satellite Images for Pasture Area in Kawatabi Field Science Center, Osaki City, Japan. The 43rd Asian Conference on Remote Sensing (ACRS) 2022. (oral presentation)
- Muxiye, Yonezawa, C., Nishida, M., Tajima, R., Yokoyama, R., Okada, K., Takamura, K., Amaya, K. and Ichikawa, K. (2022) Investigation of the Possibility of Monitoring Paddy Rice Growth Using ALOS-3. Proceedings of the JASS 2022 Annual Meeting, pp. 33-34. (in Japanese)
- Nakamura, K., Sakurai, H., Sumita, T. and Fujii, Y. (2022) Issues of Human Resource Management for External Employment on Community-based Farming Corporation. *J. Rural Soc. Econ.*, **40**(1): 94-104. (in Japanese)
- Nakano, Y. and Magezi, E.F. (2022) How Can We Achieve Green Revolution in Sub-Saharan Africa? The Case of Tanzania. In *Agricultural Development in Asia and Africa*, Emerging-Economy State and International Policy Studies, edited by Estudillo, J.P., Kijima, Y. and Sonobe, T. Springer, Singapore, pp. 75-86. DOI: 10.1007/978-981-19-5542-6\_6
- Nawano, M., Fujii, T., Murata, H. and Yonezawa, C. (2022) Evaluation of Temporal Variability in Surface Chlorophyll-a Concentration Estimated by GCOM-C/SGLI in Onagawa Bay. *J. Integr. Field Sci.*, **19**: 36. (abstract)
- Nawano, M., Fujii, T., Murata, H. and Yonezawa, C. (2022) Evaluation of Temporal Variability in Surface Chlorophyll a Concentration Estimated by GCOM-C/SGLI in Onagawa Bay, Japan. Proceedings of International Symposium on Remote Sensing 2022, pp. 268-271.
- Nguyen, T.C.V., Magezi, E.F. and SUMITA, T. (2022) Smallholders Inclusion in Staple Food Contract Farming: Collective Action Approach and its Impact on Farmers Income in Vietnam. *J. Integr. Field Sci.*, **19**: 29.
- Saito, M., Matsunami, T. and Yonezawa, C. (2022) Examining the applicability of UAV and satellite remote sensing data for soybean cultivation. *J. Integr. Field Sci.*, **19**: 34. (abstract)
- Sugawara, Y. and Sumita, T. (2022) An Analysis of Attitude of Tourists toward Agriculture-related Experiences in a Package Tour: The Properties of Favorable Guests. *J. Rural Soc. Econ.*, **39**(2): 97-106. (in Japanese)
- Sugawara, Y. and Sumita, T. (2022) Significance and Issues of the Agritourism during and after the COVID-19 Pandemic: Analysis of the Tourists' Needs on a Day Trip to Nearby Places. *J. Rural Soc. Econ.*, **40**(1): 105-113. (in Japanese)
- Sumita, T. (2022) The Relation Between the Farm and the Community in Japan. *J. Integr. Field Sci.*, **19**: 6-7.
- Suzuki, H. and Sumita, T. (2022) Success Factors of the Project to Secure Successors for the Revitalization of Vegetable Production Area: A Case Study of the Production Area Formation Process of Yamagata Cellie. *J. Rural Soc. Econ.*, **39**(2): 107-115. (in Japanese)
- Yonezawa, C. and Miura, Y. (2022) Development of automatic extraction methods of windbreak forests by using SPOT6 image — A case study in Osaki City, Miyagi Prefecture — . *J. Jpn. Agric. Syst. Soc.*, **37**(4): 77-85. (in Japanese)
- Yonezawa, C. and Miura, Y. (2022) Extraction of Igune, a Traditional Japanese Windbreak Forest, Based on K-means Clustering of Spot6 Imagery. Proceedings of 2022 IEEE International Geoscience and Remote Sensing Symposium, pp. 6232-6235.
- Yonezawa, C. and Okubo, T. (2022) A Preliminary Study for Extraction Windbreak Forest from Aerial Photographs Using a Deep Learning Approach in Miyagi Prefecture, Japan. Proceedings of International Symposium on Remote Sensing 2022, pp. 19-22.



## Guidelines for Authors

**The Journal of Integrated Field Science (JIFS)** publishes articles in all areas of field science in agricultural science. The JIFS is an English journal launched in 2003 when the Integrative Field Science Center, Graduate School of Agricultural Science, Tohoku University, was officially established. The JIFS places the edit committee under which original scientific articles, including short papers, proceedings, reviews, descriptions, and data are published. An original manuscript will be peer-reviewed by two referees. In principle, our journal publishes one volume per year, and it began publication as an online journal from volume 15 (JIFS: [https://www.agri.tohoku.ac.jp/jp/center/far\\_field/activity/](https://www.agri.tohoku.ac.jp/jp/center/far_field/activity/)). We will also publish all the manuscripts on the website as an e-journal (Tohoku University Repository: <https://tohoku.repo.nii.ac.jp/>).

### Ethical Issues

#### *Authors' Responsibility*

The manuscript will not be accepted if it has been published in other periodicals or is under consideration for publication elsewhere. All authors must have participated in the conception, design, implementation, analysis, or interpretation of the data.

The submitted manuscript is predicated on the assumption that all listed authors have concurred in the submission and that the final version of the manuscript has been reviewed and approved by all authors. All authors must agree to the terms stated in the **Authors' Responsibility Form** and sign the form. The responsible author(s) are required to submit a copy of the completed **Authors' Responsibility Form** to the JIFS Editorial Office by e-mail ([jifs.grp@tohoku.ac.jp](mailto:jifs.grp@tohoku.ac.jp)).

#### *Permissions*

Authors wishing to include figures, tables, or text passages that have already been published elsewhere are required to obtain permission from the copyright owner(s) and to include evidence that shows such permission has been granted when submitting their papers. Any material received without such evidence will be assumed to have originated from the authors.

#### *Ethical Rules for Experiments and Researches*

In case the research works involve issues that require obtaining consent and/or cooperation of the third party, consideration in handling of personal information, or actions related to bioethics and/or biosafety (including the laws and regulations and the guidelines in the country/region(s) where the joint international research is to be conducted), all the works should be approved by an internal or external ethical jury. Such works may include research involving questionnaire surveys, interviews and/or behavior surveys (containing personal histories, images, and/or personal information), handling of donated specimens, human genome analysis, recombinant DNA, and experimentation with animals.

#### *Registration of Molecular Sequences*

New molecular sequences in manuscripts must be deposited in an appropriate international data bank. The database accession numbers must be included in the manuscript. For taxonomical studies based on molecular sequences, the source specimen of molecular information should be deposited in an appropriate institution.

#### *Conflict of Interest*

Authors/reviewers should clearly declare any conflicts of interest.

#### *Scientific Misconduct*

The Editorial Board of the JIFS reserves the right to reject any manuscript that contains any fraudulent activity (falsification, fabrication, plagiarism, etc.). Any research that does not meet the acceptable standards of research behavior as determined by national/local regulations, institutional review boards, or their equivalents regarding human and animal experimentation will be rejected.

The Editorial Board of the JIFS also reserves the right to withdraw a published article without the consent of the author(s), in case of any misconduct of the author(s) related to the published article. The decision of withdrawal by the Editorial Board and the reasons for the decision will be notified to the author(s) by e-mail.

### Preparing the Manuscripts

#### *General Preparation*

Times Roman or Times New Roman (+ Symbol) font with standard size (e.g., 12-point) should be used in the text and tables. Pages and lines in the text must be numbered consecutively throughout the manuscript. The file name must include the corresponding author's name. Manuscripts must be written in English and typed in double-line spacing (25–28 lines per page) with 20-mm margins. Short reports should not exceed four printed pages, including references, tables, and figures. Use the automatic page- and line-numbering function to number the pages throughout the manuscript.

- Do not use field functions.
- Use tab stops or other commands for indents, not the space bar.
- Use the table function, not spreadsheets, to make tables.
- Use the equation editor or MathType for equations.
- Footnotes to the text are not allowed, and any such material should be incorporated into the text as parenthetical matter.

Each abbreviation should be defined when appearing for the first time and used consistently thereafter. Avoid abbreviations that are used only in a specific field and are unfamiliar to general readers. Insert a space between a number and a symbol, for instance, mean  $\pm$  S.D., =, <.

### ***Parts of the Manuscript***

The manuscript should be submitted in separate files: main text file (including title page, acknowledgments, and references), tables, and figures. Manuscripts should be divided into the following sections:

- 1) Title page
  - Title of the manuscript
  - The full names of all the authors
  - The author's institutional affiliations where the work was conducted, with a footnote for the author's present address if different from where the work was conducted.
- 2) Abstract and keywords
- 3) Main text
- 4) Acknowledgments (optional)
- 5) References
- 6) Tables (each table complete with title and footnotes)
- 7) Figure legends
- 8) Figures
- 9) Appendices (optional)
- 10) Supporting Information (optional)

Each figure, Appendices, and Supporting Information should be supplied as separate files.

### ***Title Page***

The title page must contain a main title, a running title, full name(s) of all the author(s), their affiliation(s) where the work was conducted, and information for the corresponding author, including complete corresponding address and e-mail address. Abbreviations should not be used in the main title, except for commonly used ones, such as DNA and RNA. A vague title must be avoided. The title should be written for readers outside the discipline. The running title must not exceed 50 characters, including spaces.

### ***Abstract and Keyword***

The abstract should state the backgrounds/rationale, objectives, findings, and main conclusions of the work in a single paragraph of 300 words or less. State the significance of your findings in the abstract. The abstract should be written for readers outside the discipline. Abbreviations should be avoided in the abstract as far as possible. A heading is not required. Tables, figures, or references are not allowed in the abstract. Provide five to seven keywords (not appearing in the title) in alphabetical order positioned beneath the abstract. Abbreviations should be avoided in the keywords as far as possible.

### ***Main Text***

Each type of papers should contain the following sections:

- Original articles: Introduction, Materials and Methods, Results, and Discussion.
- Review articles: Introduction, other optional sections, and Conclusion(s).

Authors should use headings to divide the sections of their manuscript, if appropriate: Introduction, Materials and Methods, Results, Discussion, and Conclusion(s). Regardless of the article type, the backgrounds and the aim of the study should be clearly written in the Introduction for a broad readership of the JIFS.

In cases where a study deals with human subjects or live animals, the Materials and Methods section of the manuscript must declare that all experiments were performed in compliance with the relevant laws and/or institutional guidelines, and the study was approved by the institutional review board, if necessary. A statement must also be included stating that informed consent was obtained from human subjects.

### ***Acknowledgments (Optional)***

Contributions from individuals who do not meet the criteria for authorship should be listed, with permission from the contributor, in the Acknowledgments section. All funding sources should also be mentioned. Thanks to anonymous reviewers are not appropriate.

## References

References are cited in the main text by the first author's last name and year of publication in parentheses, as shown below.

- Single author: (Aragaki, 2020)
- Two authors: (Aragaki and Ayase, 2020)
- Three or more authors: (Momota et al., 2020)
- Two or more references can be cited in the order of year of publication, such as (Takagi et al., 1993; Tamai et al., 1995; Sasaki et al., 2000; Hayami et al., 2012)

References are listed after the main text in alphabetical order under the first author's name: Last name(s), followed by initials of first and middle names; year of publication (in parentheses); title of article; title of periodical (abbreviated according to Index Medicus and italicized); number of volume (bold); and the first and last pages. Publications by the same author(s) in the same year should be listed as 2007a, 2007b, etc. In a reference with more than fifteen authors, give the first fifteen authors and then use et al.

When a book is referred to, the reference should include the author's name; year of publication (in parentheses); title of book (capitalized and italic); edition (if any); publisher; place of publication; and page(s).

Note the following examples.

1) A journal article:

Momota, K., Takagi, R., Sasaki, A., Tamai, S. and Ikeda, M. (2021) The effect of birds and cows on marine ecosystem in Miyagi Prefecture. *J. Integr. Field Sci.*, **6**: 109-115.

2) A chapter in an edited book:

Aragaki, Y. and Ikeda, M. (2021) The effect of courtship dance of fish on marine biodiversity in Onagawa Bay. In *Fish, Cattle and Biodiversity*, 2nd ed., edited by Ogura, S. and Fukasawa, M. Tohoku University Press, Sendai, pp. 108-150.

3) A book:

Ogura, S. and Fukasawa, M. (2021) *Fish, Cattle and Biodiversity*, 2nd ed., Tohoku University Press, Sendai.

## Tables

- Tables should be prepared in editable files, such as Word and Excel.
- Table(s) are placed after References.
- Number tables sequentially with Arabic numerals (e.g., Table 1) in the order in which they are cited in the manuscript.
- A large table is not welcome. The final printed size of the table, including its title, legends, and footnotes, should be less than one printed page.
- Abbreviations should not be used in the title as far as possible.
- Footnotes to the tables should be indicated by superscript lowercase letters (or asterisks for significance values and other statistical data) and included beneath the table body.
- All abbreviations used in the tables must be defined in the footnotes.

## Figures

- Figures should be prepared in PowerPoint, J-PEG, TIFF, EPS, or PDF files.
- Number figures sequentially with Arabic numerals (e.g., Fig. 1) in the order in which they are cited in the manuscript.
- Figure legends should be placed after the References.
- Authors should emphasize the most essential points in each figure by providing an understandable title and legend to each figure.
- Abbreviations should not be used in the titles as far as possible.
- Indicate the notable findings with some symbols or marks in each figure.
- Provide explanations for symbols or marks in the figure legends.
- All abbreviations used in the figures must be defined in the legends.
- High-quality photographs may be required for printing morphological data.
- Provide a scale bar in a representative morphological photograph.

## Manuscript Submission

All files should be sent to the editorial board as attached files of e-mail to the Editorial Office of JIFS ([jifs@grp.tohoku.ac.jp](mailto:jifs@grp.tohoku.ac.jp)).

The manuscript files should be provided in the Word version of the manuscript (the title page, abstract, main text, references, and legends of figures), the Word or Excel version of tables, and the PowerPoint, J-PEG, TIFF, EPS, or PDF version of the figures.

The JIFS requests no submission charges.

## Peer Review

All submitted manuscripts, including the Invited Review articles, are subject to initial review by Editor(s) and iThenticate plagiarism screening. The Editor(s) will determine whether a submitted manuscript should be returned without peer review or sent for

peer review. If the manuscript is returned without peer review, the author is notified immediately.

If the manuscript warrants full peer review, the Editor assigns two independent reviewers, including the Editorial Board Members. All reviewers who review the manuscript remain anonymous to the authors. Every manuscript is treated as confidential information. The Editor-in-Chief makes the final decision based on the comments and recommendations provided by the reviewers.

### ***Submission of the Revised Manuscript***

The response letter should summarize the changes made and include a list of your point-to-point responses to the reviewers' critiques. The revised manuscript and the Word version of the response letter should be sent by e-mail to the Editorial Office of JIFS.

### ***Post Acceptance***

Once a manuscript is accepted, the corresponding author must sign the **Copyright Transfer Agreement** on behalf of all authors and return it to the editorial office. The Form will be sent to the corresponding author by e-mail from the editorial office together with a proof.

Your accepted paper may be substantially edited by the Editor(s), or requested to be partly rewritten after acceptance to ensure that your publication is accurate, clear, and understandable to the broad readership of the JIFS. Editors reserve the right to request authors to revise the manuscript when required.

A copyedited proof will be sent to the corresponding author within a few weeks. Authors should review the proof and return requested corrections within 48 hours. Tables are adapted to the JIFS style in a printing company we contract with. Authors should therefore carefully check the correctness of tables in the proof.

### **Copyright and Permissions**

#### ***Copyright***

As a condition of publication, all authors must transfer copyright to the JIFS Editorial Office. The articles published in the JIFS after volume 19 are marked by the Creative Commons (CC) License; the CC BY-NC-ND 4.0 (Attribution-NonCommercial-NoDerivatives 4.0 International) License. Anyone may download, reuse, copy, reprint, or distribute the article marked by the CC BY-NC-ND 4.0 without modifications or adaptations for non-profit purposes if they cite the original authors and source properly.

#### ***Permissions for Reuse and Reproduction***

It is our policy that authors reserve the right to reuse or reproduce their own article, in whole or in part, for non-commercial use, provided that acknowledgment is given to the original source of publication. Non-commercial use includes uses in the author's own thesis, dissertation, textbook, review article, deposit in any repository, websites, lectures at the conference or other meetings, and so on. Authors are not required to obtain permission from the Editorial Board of JIFS in such cases.

Please refer to the supplement Permissions if you request other types of permissions for reuse and reproduction.

### ***Publication Fees***

There is no publication fee, regardless of color or black and white.

### ***Reprints***

Reprints in pdf are available for free. Printed reprints amount to 200 yen per copy.

Next Publication, volume 21 of the JIFS will be published in March 2024. Please send your manuscript to us by November 30, 2023, if you want your study to appear in the forthcoming volume.

Send to: [jifs@grp.tohoku.ac.jp](mailto:jifs@grp.tohoku.ac.jp)

Submission Deadline: November 30, 2023

### **Contact**

If you have any questions about the submission process, you may contact the editorial office.

The JIFS Editorial Office

Graduate School of Agricultural Science, Tohoku University

468-1 Aramaki Aza Aoba, Aoba-ku, Sendai 980-0845, JAPAN

Tel/Fax: +81-022-757-4194

E-mail: [jifs@grp.tohoku.ac.jp](mailto:jifs@grp.tohoku.ac.jp)



## **Editorial Board**

Chief Editor: Yoshihisa Suyama, PhD (Forest Ecology)

### Members:

Toyonobu Fujii, PhD (Marine Science)

Michiru Fukasawa, PhD (Animal and Grassland Science)

Yu Fukasawa, PhD (Forest Ecology)

Yasuhiro Fukuda, PhD (Animal Science)

Minoru Ikeda, PhD (Marine Science)

Hidetoshi Kakihara, PhD (Animal and Grassland Science)

Kentaro Kato, DVM, PhD (Veterinary Microbiology)

Ayumi Matsuo, PhD (Forest Ecology)

Mizuhiko Nishida, PhD (Soil and Crop Science)

Tsuyoshi Sumita, PhD (Agricultural Economics)

Yoshihisa Suyama, PhD (Forest Ecology)

Chika Tada, PhD (Environmental Microbiology)

Ryosuke Tajima, PhD (Agronomy)

Chinatsu Yonezawa, PhD (Remote Sensing, Geographic Information Science),

### Secretary:

Chiho Nishiwaki, [chiho.nishiwaki.a3@tohoku.ac.jp](mailto:chiho.nishiwaki.a3@tohoku.ac.jp)