

# **1st Asian Colloquium of Soil Zoology ACSZ 2024, Nara**



Yoshihiko Sato ©

## **Program Book**

Nara Centennial Hall  
(7-1 Sanjo-Miyamae-cho, Nara City, Nara 630-8121,  
Japan)

22 (Thursday) –24 (Saturday), August 2024  
Nara, Japan.

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**Program of ACSZ 2024**

time	Thursday	Friday	Saturday
	22-Aug	23-Aug	24-Aug
9:00		9:00 opening (the doors)	9:00 opening (the doors)
9:30		<b>Sopark Jantarit</b> Prince of Songkla University, Thailand	<b>Chih-Han Chang</b> National Taiwan University, Taiwan
10:00	10:00 Bussiness Meeting	<b>Oral Presentation #3</b>	<b>Oral Presentation #4</b>
10:30			
11:00			
11:30	12:00 opening (the doors)	<b>11:20 Poster Presentation</b>	
12:00		12:30 close	12:30 close
12:30	12:50 Opening Ceremony		
13:00	<b>Donghui Wu</b> Northeast Normal University, China	Field Trip	
13:30	<b>Oral Presentation #1</b>		
14:00			
14:30	14:30 Break		
15:00	14:50 <b>Oral Presentation #2</b>		
15:30			
16:00	16:30 close		
16:30			
17:00	Welcome Mixier		

**1st Asian Colloquium of Soil Zoology [ACSZ 2024], Nara**

**Program Book**

**Published by Local Committee, 14 August 2024**

**Nara Centennial Hall**

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# **ABSTRACTS**

**Oral Session:**

**[22-Aug Thursday]**

**13:00–13:30 Keynote #1**

**O-1. Wu Donghui:** SINO-BON and Soil Animal Biodiversity Data Collection in China

**13:30–13:50**

**O-2. Ting-Wen Chen:** Linking community, trait and phylogenetic ecology to understand soil animal diversity across space.

**13:50–14:10**

**O-3. Md Ekramul Haque, Maria Rinke, Ting-Wen Chen, Mark Maraun, Stefan Scheu:** Multidimensional traits avoid local extinction across microarthropod taxa

**14:10–14:30**

**O-4. Anna Zueva:** Properties of microbiomes associated with termites of a tropical monsoon forest in the Cát Tiên National Park (Vietnam)

**14:30–14:50**

**Break**

**14:50–15:10**

**O-5. Po-Wei Yu, Jen-Pan Huang, Chih-Han Chang:** Systematics, biogeography, and evolution of the endemic *Metaphire formosae* species group (Crassiclitellata: Megascolecidae) in Taiwan and the Southern Ryukyus

**15:10–15:30**

**O-6. Jeongwon Choi, Jimin Shin, Dohyeon Jeong, Nakyeong Lee, Yun Ji Kim, Aslan Hwanhwi Lee, Yun-Sik Lee:** A Study on food switching time of *Allonychiurus kimi* (Collembola: Onychiuridae): from fungi to bacteria.

**15:30–15:50**

**O-7. Jo Kutsukake:** Diversity, dispersal, and evolutionary history of symphylans by molecular phylogenetic analysis (Myriapoda: Symphyla)

**15:50–16:10**

**O-8. Rena Matsuyama, Mitsuki Fukushima, Katsuki Morimoto, Akira Miyake, Eri Nishihara:** Analysis of elytral microstructure and elemental composition in *Phelotrupes auratus* with geographic color differences

**[23-Aug Friday]**

**9:30 Keynote #2**

**O-9. Sopark Jantarit:** Soil cave fauna in Thailand, with special focus on cave springtails (Hexapoda: Collembola).

**10:00**

**O-10. I-Chih Sha**, Yu-Pei Tseng, Po-Ju Ke, Chih-Han Chang: Arthropod communities in the suspending soil of *Asplenium nidus* in a *Cryptomeria japonica* forest in Taiwan

**10:20**

**O-11. Hui-Ming Zhong**, Da-Li Lin, Chih-Han Chang: The earthworm communities and the ecological groups in pomelo orchards under different agricultural management

**10:40**

**O-12. Asuka Segawa**, Yudai Kitagami, Yosuke Matsuda: Morphological characteristics and viability of *Tuber himalayense* spores after pass through millipede guts

**11:00**

**O-13. Kento Nagata**, Taizo Nakamori: Laboratory observations of terrestrial flatworm predation on two species of pillbugs

**11:20 – 12:20**

**Poster Session**

**[24-Aug Saturday]**

**9:30 Keynote #3**

**O-14. Chieh Kao**, Huei-Ping Shen, **Chih-Han Chang**: Taxonomy, morphological variations, and phenology of a group of large-bodied epi-endogeic earthworms endemic to Taiwan

**10:00**

**O-15. Sao Cheng Lao** and Chih-Han Chang: *Pontoscolex corethrurus* (Müller, 1857): a pan-tropical invasive earthworm with co-occurring cryptic diversity

**10:20**

**O-16. Toshimichi Nagai**: Integrative taxonomic research of the genera *Nesticus* and *Cyclocarcina* in and around Kanto-Mountains

**10:40**

**O-17. Reina Takaesu**, Taizo Nakamori: Salt tolerance of *Archisotoma* (Collembola, Isotomidae) inhabiting shore of sea, brackish lake, or freshwater lake

**11:00**

**O-18. Satoshi Shimano**, Tobias Pfingstl, Shimpei F. Hiruta: Toward a global evolutionary history of soil mites adapted to the intertidal zone.

**Poster Session:**

- P-1. Taizo Nakamori:** Revision of the genus *Halofriesea* (Collembola: Neanuridae) in the fauna of Japan
- P-2. Atsuko Ohira, Taizo Nakamori:** An undescribed luminous species of Lobellini (Collembola: Neanuridae) from Japan
- P-3. Nongnapat Manee, Areeruk Nilsai and Sopark Jantarit:** Climate change and its impact on tropical cave fauna, a preliminary study in Collembola of genus *Coecobrya* (Collembola: Entomobryidae)
- P-4. Natsuki Hirakizawa, Takeyuki Nakamura, Takeo Yamauchi:** Centipedes and millipedes active in winter in eastern Japan
- P-5. Wataru Hagino, Haruka Tomoyose:** Education method based on the soil fauna of Okinawa.
- P-6. Hayato Endo, Katsuyuki Eguchi:** Taxonomic study on Japanese earthworm species morphologically similar to Korea species (Annelida: Clitellata: Megascolecidae)
- P-7. Reina Takaesu, Yukihiro Kinjo, Taizo Nakamori, Seikoh Saitoh:** Genetic diversity in the surface-dwelling Collembola *Tomocerus* cf. *ocreatus* along the Ryukyu Archipelago
- P-8. Hijiri Noda, Masaki Takenaka, Koji Tojo:** Diversity and Evolutionary History of the Order Scutigleromorpha in the Japanese Islands

## **Oral Session**



O-1

## **SINO-BON and Soil Animal Biodiversity Data Collection in China**

**Donghui Wu**<sup>1,2</sup>

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In China, Sino-Non was established by the Chinese Academy of Science following the basic principle of sound planning and unified layout for biodiversity observation at national scale. It formally became a member of AP BON on October 11, 2014. Soil animal biodiversity collection is one of the most important tasks in biodiversity networks in China. Its work plans were following in soil animal field: 1) Taxonomy and abundance of soil animal across China; 2) Patterns and maintaining of soil animal biodiversity in the habitats; 3) Ecological services of soil animal at the ecological process. Till now we have nearly finished the first time survey of soil animal biodiversity, such as earthworm, mites, Collembola, nematode, and spiders, and soon, in the farmland across China, and hope to continue to collect soil animal biodiversity data in forest and grassland in the future. Long term field monitoring plots were also included in the data collection in the network of soil animal biodiversity in China. An open database will be shared soon, and soil animal biodiversity maintenance and changes will be focused.

*Funding Source:* This work was supported by a grant (no. 2018FY100300) from the National Science & Technology Fundamental Resources Investigation Program of China.

O-2

**Linking community, trait and phylogenetic ecology to understand soil animal diversity across space**

**Ting-Wen Chen<sup>1,2</sup>**

*<sup>1</sup>J. F. Blumenbach Institute of Zoology and Anthropology, University of Göttingen, Göttingen, Germany*

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Recent developments in phylogenetic and functional ecological concepts, together with molecular and trait methods, have advanced our understanding of the mechanisms driving and maintaining biodiversity. Here I present the ‘CTPE framework’ and use Collembola and Oribatida as examples to show how integrations of community (C), trait (T), phylogenetic (P) and environmental (E) data will help to understand spatial distributions of soil animal diversity at different scales: (1) Traits are proposed to be functional only if species in communities differ in their traits across gradients or between sites. (2) Trait evolutions are random processes, i.e. they have no specific directions but follow the Brownian motion model; however, this results in a non-random phylogenetic signal in trait values across species. (3) Community assembly processes (i.e. filtering and partitioning) are revealed by trait similarities in local communities. (4) Combinations of different traits representing multidimensional niches of species can reveal both filtering and partitioning processes operating simultaneously in the same communities. (5) In stable habitats with ample resources, niche partitioning is expected to dominate community assembly over filtering processes. (6) In multidimensional niche space, rare species are likely to occupy niches vacated by dominant species. Although this framework appears promising for predicting soil animal distributions in response to environmental change and for enabling more effective conservation strategies for soil ecosystems, some research gaps remain regarding the evolution and ecology of relevant functional traits of soil animals and the scales of communities in ecosystem processes.

**Multidimensional traits avoid local extinction across microarthropod taxa****Md Ekramul Haque<sup>1</sup>**, Maria Rinke<sup>1</sup>, Ting-Wen Chen<sup>1</sup>, Mark Maraun<sup>1</sup>, Stefan Scheu<sup>1,2</sup>

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The persistence of microarthropods (Oribatida, Collembola, and Mesostigmata) in intertidal salt marsh ecosystems is subject to variable tidal inundation. It depends on a set of multidimensional functionally analogous traits that perform similar ecological functions across taxa and are critical for preventing local extinctions and maintaining ecosystem stability. This study tests four key traits related to their morphology, body size, shape, and surface cover with putative functions across different taxa to preventing extinctions in salt marsh communities in the Wadden Sea of Spiekeroog, Germany. We investigated local extinction of microarthropods by establishing two experimental systems: the first on the seashore from the pioneer zone through the lower salt marsh to the upper salt marsh and the second at the same tidal height on artificial islands 500 m from the seashore. Natural salt marshes with microarthropods from the lower salt marsh were transplanted to the two most extreme environments (i.e. the upper salt marsh exposed to occasional flooding and the pioneer zones inundated twice a day) and were exposed for five years to observe changes in community structure. Local extinction of microarthropods was consistently higher on the artificial islands than on the seashore, with the extinction rate being higher in the pioneer zone than in the upper salt marsh, regardless of microarthropod taxa. Results indicate strong effects of environmental filtering, with different microarthropod taxa using different functional traits and strategies to avoid local extinction in the face of increasing inundation frequency. Species with larger empodium (Collembola) and multiple claws (Oribatida), but reduced number of pedipalp forks (Mesostigmata) avoided local extinction in pioneer zones. Although no correlations were found between body size and the extinction rate, variations in community body size of Mesostigmata reflected species sorting, with smaller species suffering from more frequent inundations. However, increased proportions of elongate Collembola and Oribatida, and seed-like armored Mesostigmata towards the pioneer zones indicate that they are able to survive inundation by better floating on water due to a higher surface to volume ratio. Furthermore, increased proportions of hairy Collembola, waxy Oribatida, and cerotegumental Mesostigmata in the communities towards the pioneer zones indicate that their survival in water is largely dependent on plastron respiration. Overall, the results document the main mechanisms that confer survival advantages to different microarthropod taxa in the intertidal habitats.

O-4

**Properties of microbiomes associated with termites of a tropical monsoon forest  
in the Cát Tiên National Park (Vietnam)**

**Anna Zueva<sup>1,2</sup>**

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Termites (Blattodea, Isoptera) are the most important decomposers of dead organic matter in tropical ecosystems (Bourguignon et al., 2011). In our investigations we aim at characterizing termite-associated microbiomes and determining factors defining their characteristics. We focus on fungi, bacteria, and viruses of termites of a tropical monsoon forest in the Cát Tiên National Park (Vietnam).

The study on the termite-associated yeast communities was performed on five species of termites: *Globitermes sulphureus* (Haviland), *Microcerotermes burmanicus* Ahmad (= *M. crassus* Snyder), *Macrotermes carbonarius* (Hagen), *Macrotermes gilvus* (Hagen), and *Odontotermes* sp. Termite-associated yeasts showed low alpha diversity, formed mycelial or pseudomycelial structures, and were able to ferment glucose and assimilate salicin and simple products of wood degradation (Zueva et al., 2021).

The investigation of viruses of three species of termites (*Hospitalitermes bicolor* (Haviland), *M. carbonarius* (Hagen) and *O. wallonensis* (Wasmann)) resulted in the assembling of four genomes of the novel viruses. The contig close to fungi-infecting viruses was also detected. This virus is likely to infect fungi cultivated by termites (Litov et al., 2022).

Though soil animals influence soil microbiomes (Scheu et al., 2002), the study on prokaryotes of soils of the Cát Tiên National Park showed no notable effect of differences in soil macro- and mesofauna composition on the diversity of prokaryotes (Zhelezova et al., 2021). More detailed research on the termite-associated bacteria is supposed to be done.

We plan simultaneous study of fungal, bacterial, and viral components of microbiomes of termites along with the assess of the trophic position of termites using bulk stable isotope analysis and genetic diversity via cytochrome C oxidase analyses. We expect to improve our knowledge about factors forming soil macro- and mesofauna microbiomes.

**Systematics, biogeography, and evolution of the endemic *Metaphire formosae* species group (Crassiclitellata: Megascolecidae) in Taiwan and the Southern Ryukyus**

Po-Wei Yu<sup>1</sup>, Jen-Pan Huang<sup>2</sup>, Chih-Han Chang<sup>1,3</sup>

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The *Metaphire formosae* species group is a clade of giant earthworms with 17 described species or subspecies endemic to Taiwan and the Southern Ryukyus. Previous studies have suggested that the endemism and diversity of these earthworms resulted from a series of speciation events taking place during the formation of the Taiwan Island, presumably several million years ago. However, their phylogeny is still poorly resolved, hindering divergence time estimation and our understanding on the mechanisms leading to this diversity. In addition, although some potential hybrid individuals were previously collected, whether there is inter-specific gene flow or not remains unknown. In this study, we applied double-digest restriction-site associated DNA sequencing (ddRAD-seq) techniques to unearth the phylogeny, the biogeography, and the evolutionary history of the *Metaphire formosae* species group. We discovered one potential new species based on morphology and DNA barcoding, and obtained a well-supported phylogenetic tree using 804,601 SNPs from ddRAD-seq data. Furthermore, population structure inferred using fineRADstructure revealed that there was higher coancestry between *M. paiwana liliumfordi* and *M. glareosa*, between *M. feijani* and *M. tengjihensis*, as well as between *M. bununa* and *M. tahanmonta*, suggesting the occurrence of potential incomplete lineage sorting (ILS) and/or gene flow among these closely relative species. In addition, Procrustes analysis indicated that geographical barriers of the Central Mountain Range and altitudes-related adaption might be the main factors that shaped the geographical structure of this species group. Future analyses will focus on divergence time estimation, ecological niche modeling, and evaluating mechanisms leading to previous speciation events. We anticipate that future research endeavors will further enhance our understanding on the historical biogeography of these earthworms.

O-6

**A Study on Food Switching Time of *Allonychiurus kimi* (Collembola: Onychiuridae): From Fungi to Bacteria.**

**Jeongwon Choi<sup>1</sup>, Jimin Shin<sup>1</sup>, Dohyeon Jeong<sup>1</sup>, Nakyeong Lee<sup>2</sup>, Yun Ji Kim<sup>2</sup>, Aslan Hwanhwi Lee<sup>2</sup> and Yun-Sik Lee<sup>1,3</sup>**

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Changes in food conditions in habitat due to environmental alterations lead a specific species to undergo food switching to maintain population density. *Allonychiurus kimi* has been reared in laboratory conditions for approximately 20 years, feeding on the fungus *Saccharomyces cerevisiae*, and this fungus has been employed as a food source in various experiments using *A. kimi*. This study investigates the potential of food switching and the switching time from fungus to bacteria in *A. kimi*, a predator of soil microorganisms. A control group was fed with *S. cerevisiae* while the treatment groups were fed three types of bacteria (*Nostoc neudorfense*, *Pseudoaaliinostoc* sp., *Nostoc* sp.). The time at which egg production in each treatment group equaled that of the control group statistically was measured. The three types of bacteria may need to take over eight weeks for food-switching. This result suggests the possibility of *A. kimi*, experimentally fed exclusively on fungi, switching to bacteria as a food source. Furthermore, it indicates that the time required for food switching in environments where microbial diversity diminishes may be a crucial factor in maintaining of Collembola populations.

O-7

**Diversity, Dispersal, and Evolutionary History of Symphylans  
by Molecular phylogenetic analysis (Myriapoda: Symphyla)**

**Jo Kutsukake**

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Symphylans are a major component of soil animal communities found in various types of soil such as sand and loam in regions excluding Antarctica, with population densities often exceeding 22,000 individuals per square meter. So far, in taxonomy, mainly morphological insights have been accumulated, but molecular phylogenetic analysis has almost never been performed. In this study, molecular phylogenetic analysis was introduced through improved methods such as the Chelex-TE boiling, a new non-destructive DNA extraction that improved from Aoyama (2015). Between August 2018 and December 2023, over 3,500 symphylans were collected from approximately 250 locations across Japan, some of which were analyzed. COI barcoding and putative species determination based on genetic distances using ASAP revealed at least 128 putative species existing in Japan. Given that only three species from Europe and a few species in an undetermined state were previously believed to live in Japan, and that there are only 220 described species worldwide, these results suggest that previous classifications relying solely on morphological information have greatly underestimated diversity. Distinct distribution ranges were observed for each provisional species, and some were distributed across oceans and mountain ranges. Correlation analysis using original indices showed that lower environmental selectivity was associated with higher dispersal in Scolopendrellidae, suggesting the possibility of passive dispersal. However, further research is needed to identify direct migratory dispersal factors. The results of phylogenetic analysis using COI and 28S sequences of 13 putative species in six genera identified by molecular and morphological methods showed an evolutionary history different from the morphological phylogenetic analysis presented by Camacho (2009), and the monophyly of the family was again supported. However, this phylogenetic hypothesis requires further analysis including at least the remaining eight genera of symphylans.

O-8

**Analysis of elytral microstructure and elemental composition in *Phelotrupes auratus* with geographic color differences**

**Rena Matsuyama<sup>1</sup>, Mitsuki Fukushima<sup>1</sup>, Katsuki Morimoto<sup>2</sup>, Akira Miyake<sup>3</sup>, Eri Nishihara<sup>1</sup>**

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The geotrupid dung beetle, *Phelotrupes auratus*, feeds on the dung of deer and large wild mammals and inhabits montane forests throughout Japan. The body's surface exhibits structural colors that arise from the multi-layered structure of the elytra, predominantly red nationwide; however, in some regions, it is known to show regional variations of colors (indigo, green, and red). Interestingly, the variation is particularly pronounced in Nara Prefecture and its neighboring areas, where all three colors can be observed. Therefore, we focused on the structure and composition of the elytra to investigate why color variations occur depending on the region.

First, the reflectance spectra of specimens with three colors confirmed that the actual values closely matched the visually observed colors. Corresponding to the experiments, we conducted reflectance spectrum calculations using transfer-matrix methods, revealing that the colors varied numerically with changes in layer thickness. Furthermore, we observed the multi-layered structure using transmission electron microscopy (TEM). These results were consistent with those previously reported (Akamine, *et al.*, 2011).

Finally, we investigated the elemental composition of the multi-layered structure using TEM-energy dispersive X-ray spectroscopy (TEM-EDS). We observed two types of layers with different elemental compositions that are alternately stacked. One type is rich in several elements (O, Na, Mg, Ca, K), while the other is not.

In summary, we reconfirm that the colors are influenced by distinct structural differences in the elytra and speculate that the elemental composition is related to the colors exhibited. The observed elemental composition possibly relates to the beetle's diet of dung and soil, which form its habitat during larval development. This may link to the geographic color variation, as the characteristics of the dung and the soil vary based on the region.



O-9

**Soil cave fauna in Thailand, with special focus on cave springtails (Hexapoda: Collembola)**

**Sopark Jantarit**

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Located in the heart of the Asian region and a biodiversity hub, Thailand is one of the richest biodiversity on earth. Thailand also has extensive cave-containing karsts throughout the region. However, the soil cave fauna in Thailand is still poorly known. In this work, terrestrial soil cave fauna is focused on and analyzed. At least 3 phyla, 9 classes, 29 orders, 68 families, 112 genera and 207 known species of soil fauna are recognized. Among these, Diplopoda is the most known taxa, of which 47 species are reported, followed by Collembola and Insecta (44 species each), Arachnida (41 species), Chilopoda and Malacostraca (5 species each), Reptilia (3 species) and Mammalia (2 species).

Diversity surveys, taxonomic knowledge and biogeographical data for cave Collembola in Thailand have gained a rapid increase in recent years. More than 300 caves (including subterranean habitats) have been sampled throughout the country. The results reveal that Collembola is today among the most common and diverse invertebrate groups in caves, and by far the most diverse of terrestrial hexapods in Thailand and Southeast Asia caves. A total of 4 orders, 11 families, 36 genera and at least 300 species (including morphospecies) are recognized from Thai caves. Morphology and molecular evidence confirm that each karstic unit has its own, well-differentiated species of Collembola especially the family Entomobryidae (*Coecobrya*, *Cyphoderopsis*, *Cyphoderus*, *Lepidocryptus* and *Troglopedetes*) which is extremely diversified and has a huge local radiation. Most of them are unknown to science. The discovery of several highly troglomorphic species and the endemism of subterranean Collembola in Thailand support the importance of caves for sustaining biodiversity and raise concerns about their conservation status and vulnerability. It also points to the need for developing sound cave conservation strategies in the country as well as increasing awareness of the vulnerability of the subterranean ecosystem.

**Arthropod communities in the suspending soil of *Asplenium nidus* in a *Cryptomeria japonica* forest in Taiwan**

**I-Chih Sha<sup>1</sup>, Yu-Pei Tseng<sup>2,3</sup>, Po-Ju Ke<sup>2</sup>, Chih-Han Chang<sup>1,2,\*</sup>**

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Metacommunity is a set of local communities linked by the dispersal of multiple potentially interacting species. It gives ecologists a view to explain community assembling and biodiversity patterns, such as the species-area relationship. Bird's nest fern (*Asplenium nidus* L.) is a common epiphyte in tropic and subtropic forests. Due to their spatial isolation among each other in the forest canopy, *A. nidus* individuals can be regarded as habitat patches for arthropod communities. In this study, we apply the metacommunity concept to study the arthropod community in *A. nidus* individuals. We aim to (1) survey the arthropod species diversity and update the taxonomy of Acari and Collembola in bird's nest ferns in Taiwan, (2) investigate the species-area relationship of arthropods living in *A. nidus* individuals, and (3) evaluate whether the arthropod communities are influenced by the age and size of their *A. nidus* hosts. We sampled 24 *A. nidus* individuals, which belong to three different sizes groups, in a *Cryptomeria japonica* plantation. We separated the organic substrate from each *A. nidus* individuals into the outer and the inner layer to study how fine-scale environmental heterogeneity influence arthropod communities. Arthropods were collected by Winkler bags and identified to morphospecies. We found 159 morphospecies, including 35 Insecta, 18 Collembola, 23 Oribatida, 21 Gamasida, and 61 species of other or uncertain arthropod groups. We standardized samples to the same sampling coverage using the rarefaction curve, and found that there is no significant difference in the estimated species diversity with regards to different sizes of the *A. nidus* individuals. However, species diversity and abundance of arthropod in the outer layer were significantly higher than those in the inner layer. We are planning to estimate the  $\beta$  diversity of arthropod communities to evaluate the influence of the age and size of *A. nidus*.

**The earthworm communities and the ecological groups in pomelo orchards under different agricultural management**

**Hui-Ming Zhong<sup>1</sup>, Da-Li Lin<sup>2</sup>, Chih-Han Chang<sup>1</sup>**

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Agricultural management usually leads to soil compaction, and applying soil ameliorants and chemicals can reduce soil fertility and soil fauna diversity. Earthworms, categorized into six ecological groups, can differentially affect soil attributes. However, limited research exists on earthworm communities in Asian agricultural fields with little focus on perennial orchards. This study aims to explore the impact of different agricultural management on earthworm communities in orchards and establish a local dataset of stable isotopes for earthworms in Taiwan. Four conventional and four organic pomelo orchards were investigated. Earthworms were categorized into ecological groups based on stable isotopes <sup>13</sup>C and <sup>15</sup>N. We collected 6,446 individuals belonging to 15 species between August 2022 and July 2023, including 19% sexually mature. Stable isotope analysis on 231 specimens in February 2023 categorized 12 species into four ecological groups. Generalized linear mixed models indicated that agricultural management did not significantly affect earthworm abundance and biomass, except in August 2022, in which conventional orchards had higher earthworm abundance than organic orchards ( $p < 0.05$ ). Water holding capacity and soil pH were positively associated with earthworm abundance, while rock fragment content was negatively associated, whereas bulk density showed no apparent trend. Non-metric multidimensional scaling showed significant differences in earthworm community structures between agricultural management in November 2022, likely driven by the invasive *Pontoscolex corethrurus*. Earthworm ecological group compositions also differed between conventional and organic orchards in November and June. Our study highlights that organic management may not increase earthworm abundance and biomass potentially due to similar management intensity in both management types. Soil properties, particularly water holding capacity and rock fragment content, may appear more influential. Maintaining grass cover and preserving plant residues may enhance conditions for earthworm communities.

O-12

**Morphological characteristics and viability of *Tuber himalayense* spores after pass through millipede guts**

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Soil animals contribute to spore dispersals by feeding fungal fruitbodies and excreting spore aggregates. Soil-dwelling macrofauna, such as Diplopoda, are sometimes found near fruitbodies, and their guts as well as fecal pellets contain many intact spores. Thus, soil animals can carry spores to distant locations from fruiting positions. However, the effect of feeding by soil animals on morphological characteristics and viability of hypogeous fungal spores such as truffles is unknown. We aimed to record the feeding, morphology and viability of hypogeous fungal spores by millipedes. Ten millipedes (*Anaulaciulus* spp.) were collected next to the truffles of *Tuber himalayense* in a secondary *Quercus serrata* forest. *T. himalayense* spores were found in the hindgut of nine out of the ten millipedes. Based on the number of *T. himalayense* spores retrieved from a 10% length of hindgut, the total number of spores contained in the entire hindgut was estimated. For the observation of spore morphologies, 40 fresh spores collected from *T. himalayense* fruitbodies and 40 spores contained fecal pellets of millipedes were examined using both a light and a scanning electron microscope. The total number of spores was estimated ranging from 210 to 10070 spores per individual (n=9), with an average of  $3262 \pm 3010$  spores. Microscopies showed that all non-feeding spores remained encased in asci while feeding ones were present individually without asci. Moreover, 72.5% spores (n=29) were intact shapes and the remaining ones (n=11) were collapsed partially in spiny or spinose-reticulate ornamentations in a hindgut. These results suggest that millipede feeding can change the shape of hypogeous fungal spores though most of the spore shape remained intact. In this presentation, we will discuss the importance of millipede feeding adding with currently ongoing examination of the viability and colonizing potential of spores.

O-13

**Laboratory observations of terrestrial flatworm predation on two species of pillbugs**

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Pillbugs are one of the most common soil animals, but their ecology is still largely unknown. Because predators can affect prey distribution, competition, and the evolution of defense strategies in a species-specific manner, understanding the relationship between pillbugs and their predators is important. Although flatworms are known to prey on pillbugs, it has not yet been clarified whether they have different effects on pillbug species. In this study, we aimed to determine whether there were species differences in the predatory pressure exerted by flatworms on pillbugs in the laboratory. Two pillbug species, *Armadillidium vulgare* and *Spherillo obscurus*, were collected from Kannonzaki, Kanagawa, Japan, and kept in total darkness at 20°C for 24 h. Subsequently, a treatment container was prepared in which single individuals of the two species of pillbugs and flatworms were contained. A control container was prepared in the same manner as the treatment container, except that flatworms were not included. The survival of pillbugs was observed for 3 days. The results showed that the survival rate of *A. vulgare* was significantly lower in the presence of flatworms and was significantly lower than that of *S. obscurus*. The content of all dead pillbug carcasses was lost in the presence of the flatworm, suggesting that the pillbugs were predated by the flatworm. These results indicate that *A. vulgare* is more susceptible to predation by flatworms than is *S. obscurus*. This may be because flatworms prefer to prey on *A. vulgare*, or because of differences in defense mechanisms between the two pillbug species. Future studies should examine the ecological implications of the different susceptibilities of the two pillbug species to flatworms in the field.

**Taxonomy, morphological variations, and phenology of a group of large-bodied epi-endogeic earthworms endemic to Taiwan**

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The *Amyntas sexpectatus* species complex is a group of large-bodied earthworms endemic to Taiwan. With a mean body length of 20 cm and brownish or greenish yellow coloration, these organisms have a unique appearance among epi-endogeic species. Our field surveys suggest that these organisms have a continuous, north-south distribution throughout the hill regions in western Taiwan. So far, five species in this species complex have been described, but they cannot be reliably identified using diagnostic characters documented in the literature. In this study, we aim to revisit the taxonomy of this species complex and investigate its phenology. Molecular phylogeny based on mitochondrial genes suggests seven lineages with an allopatric distribution, with five of which corresponding to five nominal species. However, nuclear gene haplotype networks show a pattern indicating incomplete lineage sorting, providing little support for the seven-species hypothesis. Three molecular species delimitation methods (Assemble Species by Automatic Partitioning, Bayesian implementation of the Poisson tree processes, and Bayesian Phylogenetics and Phylogeography) result in inconsistent outcomes. Factor analysis of mixed data (FAMD) based on external and internal morphological characters failed to separate the seven mitochondrial lineages, indicating that these lineages are morphologically indistinguishable. We conclude that there is only one species in the *A. sexpectatus* species complex, and *A. binoculatus*, *A. fusing*, *A. lioujia*, and *A. majia* are all junior synonyms of *A. sexpectatus*. Monthly field sampling during 2021–2022 indicates that this giant earthworm is an annual species. Individuals can be found for 6–7 months throughout spring, summer, and fall, with the first mature individual appearing in as early as June in northern populations. Presumably, the species survives through winter-early spring (from December to March/April/May) as cocoons. Populations in the south have a “delayed” phenology compared to those in the north, likely due to different temporal patterns in precipitation.

***Pontoscolex corethrurus* (Müller, 1857): a pan-tropical invasive earthworm with co-occurring cryptic diversity**

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*Pontoscolex corethrurus* (Müller, 1857), originally from Brazil, is the most widespread invasive earthworm species in the tropical and sub-tropical regions. This dominant invader has been known to dramatically change soil structure, carbon dynamics, nutrient cycling, and may potentially interact with both aboveground and belowground communities. A recent study from analyzing 792 specimens over 25 countries showed that *P. corethrurus* is a species complex composed of four morphologically indistinguishable lineages (L1, L2, L3, and L4), and further concluded that they represent three distinct species. Additionally, some of these cryptic lineages, specifically L1, L3, and L4 were found to co-occur in Taiwan and Brazil, suggesting potential niche differences. This species is often the dominant earthworm species in human-disturbed environments in Taiwan. However, the ecological impact of this species in Taiwan remains poorly understood, and it is also unclear how the cryptic lineages differ ecologically. The objectives of this study are to understand the genetic structure in the *P. corethrurus* species complex, and to further investigate the potential ecological differences among the co-occurring cryptic lineages using stable isotopes. We found three cryptic mitochondrial lineages in 5 out of 25 sampled sites investigated at the central, southern and eastern part of Taiwan, suggesting that co-occurrence of cryptic lineages of *P. corethrurus* in the same earthworm community may be common in Taiwan. Our findings can conclude that there is not only one species of *Pontoscolex corethrurus*, but included three cryptic species L1, L3 and L4. Moreover, one of the cryptic species L1 is widely distributed in Taiwan.

O-16

**Integrative taxonomic research of the genera *Nesticus* and *Cyclocarcina*  
in and around Kanto-Mountains**

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The family Nesticidae Simon, 1894 is a small family of spiders of the order Araneae, comprising 16 genera and 292 species and distributed worldwide, except in polar regions. This family is divided into two tribes, Nesticini that have larger body and the smaller Nesticellini, and tribe Nesticini inhabiting Japan is known to undergo species diversification within narrow geographical regions.

Although taxonomic classifications based on genital morphology are conducted in the 20th century, there has been little molecular phylogenetic organization of the genera and species of the Japanese Nesticini. Especially, the genera *Nesticus* Thorell, 1869 and *Cyclocarcina* Kishida, 1942 within this tribe lack sufficient basis for existing taxonomic systems and recognition of species and subspecies, resulting in confusion at various taxonomical ranks. Additionally, some species exhibit significant variation in genital morphology within the species.

Therefore, this study has been conducted to discover new species and reevaluate the taxonomic system of the genera *Nesticus* and *Cyclocarcina* inhabiting the Kanto Mountains and its surrounding areas, employing Integrative Taxonomy, which combines morphological species identification with molecular phylogenetics.

Specimens were mainly collected from around Kanto region. At the morphological observations, various morphospecies were defined based on the genital morphology using only adult individuals among the collected and provided specimens. Due to differing reliability of genital morphology in species identification between males and females within this tribe, males and females were treated as separate species at the morphospecies level. For molecular phylogenetic analysis, DNA extraction, amplification of the mitochondrial *COI* gene barcode region using PCR, and sanger sequencing were conducted. Using obtained sequences, phylogenetic analysis by ML methods were conducted. Based on the sequence and morphological information, species delimitation hypotheses have been obtained using ASAP. In addition, taxonomic validity of the 2 genera in Kanto region have been reexamined by pairwise distances and those linages.



O-17

**Salt tolerance of *Archisotoma* (Collembola, Isotomidae) inhabiting shore of sea, brackish lake, or freshwater lake.**

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Lake Biwa is the third oldest lake in the world and is a freshwater lake that has never been flooded by seawater. Despite this, more than ten species of marine flora and fauna have been identified within it. In our study, we discovered a previously undescribed species of the genus *Archisotoma* of Collembola from the shore of Lake Biwa. Collembola (springtails) are wingless terrestrial arthropods with a body length of 1 to 5 mm. They are commonly found in a variety of terrestrial environments, including seashores. Certain species inhabiting seashores are confirmed to exhibit halotolerance, likely as an adaptation to saline environments. The genus *Archisotoma* is globally distributed in marine littoral habitats and comprises 29 species, two of which are found in Japan. The occurrence of *Archisotoma* on the shores of a freshwater lake, Lake Biwa, is unique in the world. The aim of this study was to investigate the halotolerance of *Archisotoma* sp. inhabiting Lake Biwa. The *Archisotoma* spp. inhabiting the shore of Lake Biwa, a brackish lake shore and seashores were tested for salt tolerance. The specimens were incubated at 20°C for 24 hours on ionized water with salinity levels set at 0.0%, 1.7%, 3.4%, and 6.8%, representing freshwater, brackish water, seawater, and double seawater, respectively. The number of surviving individuals was subsequently counted. Individuals from all types of shores showed higher survival rates at all salinities, except at 6.8%. These findings suggest that individuals of the genus *Archisotoma* inhabiting the shore of Lake Biwa likely arrived from some seashore relatively recently. Furthermore, the habitats of the genus *Archisotoma* might be restricted to shores by environmental factors other than salinity.

**Toward a global evolutionary history of soil mites adapted to the intertidal zone.**

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Oribatida is a taxon with an ancient origin that already constituted part of terrestrial ecosystems during the early Devonian (ca. 416 mya) and middle Devonian (e. g., Hirst 1923; Norton et al. 1988; Kethley et al. 1989; Dunlop & Selden 2009; Dunlop et al. 2020). Superfamily Ameronothroidea Vitzthum, 1943, is the only group that has successfully adapted to intertidal environments and has been thought to be monophyletic.

However, our mitochondrial genomic data indicate that we have shown that the family is polyphyletic, with land-to-sea adaptations occurring three independent times.

The common ancestor of the "tropical" family Fortuyniidae Hammen, 1963 and Selenoribatidae Schuster, 1963 first adapted to the tidal environment during the Triassic and Jurassic periods (ca. 225 mya). The divergence age of the two families is estimated by using the same dataset. The current distribution ranges of the two families suggest that this event occurred early in the Triassic when the supercontinent Pangaea was still in existence.

The ancestor of the cold "northern hemisphere only" Ameronothroidea Vitzthum, 1943, was adapted to the tidal environment from the Late Jurassic to the Early Cretaceous (ca. 170 mya), suggesting an ancient distribution along the coast of Laurasia.

The ancestor of Podacaridae Grandjean, 1955, which inhabits the cold "southern hemisphere only," adapted to the tidal environment of Gondwana about 30 million years after the former family (ca. 140 mya).

## **Poster Session**

**P-1**

**Revision of the genus *Halofriesea* (Collembola: Neanuridae) in the fauna of Japan**

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The genus *Halofriesea* was described in 1997 with the type species *Halofriesea kuroshio* Yoshii & Sawada, 1997, from Japan. Currently, two species are known worldwide: *H. kuroshio* from Japan and *H. kai* (Christiansen & Bellinger, 1992) from Hawaii, USA. Members of this genus are halophilous, known only from seashore habitats. The genus is distinguished from other genera in the subfamily Friesenae by the presence of a pair of perturbations on the pleural parts of thoracic segments I, II, and III. However, this trait might have been overlooked in species described before 1997. The present study examined the presence or absence of perturbations in halophilous species of Friesenae in Japan, based on the lectotype, paralectotypes, and newly collected topotypes. Results showed that two species currently not assigned to *Halofriesea* have perturbations on thoracic segments I, II, and III, suggesting that a taxonomic revision is needed for these two species and that a reexamination is required for other halophilous species of Friesenae.

P-2

**An undescribed luminous species of Lobellini (Collembola: Neanuridae) from Japan**

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The tribe Lobellini is a large group comprising 17 genera, mainly found in Southeast Asia, East Asia, and the Australian–Oceania region. Seven genera of Lobellini have been recorded in Japan. Here, we report a previously undescribed species of Lobellini from Miyako Island, Okinawa Prefecture, Japan. This undescribed species can be distinguished from known species by its DNA barcode and chaetae length. This species emitted light from the tubercles on its abdominal and thoracic terga in response to stimuli. This bioluminescence is greenish. In the present study, we recorded a third luminous species of Lobellini. The phylogenetic position of this Lobellini sp. is also discussed.

**Climate change and its impact on tropical cave fauna, a preliminary study in  
Collembola of genus *Coecobrya* (Collembola: Entomobryidae)**

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Climate change poses significant challenges to biodiversity worldwide, particularly affecting temperature-sensitive species such as subterranean fauna. This study investigates the impact of climate change on a species of springtail, *Coecobrya* sp., one of the dominant Collembola genus in Thai caves. Laboratory experiments exposed *Coecobrya* sp. to different tested temperatures ranging from 27°C (the controlled temperature) to 36°C, simulating projected climate scenarios. The results demonstrated that *Coecobrya* sp. could not survive at the temperature higher than 32°C after exposure to heat experiments for 7 and 14 consecutive days. Specifically, exposure to heat experiment at 32°C (5°C above the controlled temperature), though they survived, appeared to induce sterility in the F1 generation, underscoring the vulnerability of these species to thermal stress. Furthermore, developmental studies indicated accelerated growth rates significantly from egg to adult stages as temperatures rose ( $P < 0.001$ ), emphasizing the species' adaptation to fluctuating environmental conditions. However, prolonged exposure beyond thermal thresholds ( $>34^{\circ}\text{C}$ ) has proved lethal, highlighting the precarious balance between adaptation and survival in warming climates. This research contributes novel insights into the physiological responses of cave-dwelling Collembola to temperature variations, which is crucial for understanding the broader implications of climate change on tropical cave ecosystems. The findings underscore the urgent need for conservation strategies aimed at preserving thermal refuges and enhancing resilience among vulnerable subterranean species.

## Centipedes and millipedes active in winter in eastern Japan

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When snow cover is above a certain level, the temperature at the ground below the snow cover remains stable at around 0°C due to the shielding effect of the snow cover layer. Therefore, the snow cover protects the organisms living below from lethal temperatures. Various taxa such as small mammals, arthropods, and fungi are active in the space between the snow cover and the ground. A major part of subnivean invertebrate studies by pitfall trap below the snow is from North America, Europe, and a part of northeast China, with particular reports of mites, spiders, springtails, beetles, and flies. Centipedes and millipedes are classified in the subphylum Myriapoda. They have a large biomass of soil animals and are ecologically important. However, little is known about their winter activities, and there are very few reports of their activities below snow cover. We set up pitfall traps at eleven sites in eastern Japan to survey centipedes and millipedes active during the winter snow season. Ten pitfall traps were set at each study site from October to April 2017-2022 (120 traps in total). As a result, 421 individuals of three orders and seven families of centipedes (including unknown families) and 386 individuals of four orders and seven families of millipedes (including unknown families) were collected during the snow season. Particularly high numbers of individuals were collected in the family Schendylidae (Chilopoda), Diplomaragnidae (Diplopoda), Lithobiidae (Chilopoda), and Conotylidae (Diplopoda) in the study sites. The present study shows that a wide variety of centipedes and millipedes are active below snow cover in the heavy snowfall and cold regions of Japan.

**Education method based on the soil fauna of Okinawa.**

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The Ryukyu Archipelago, which is located in the southwest of Japan and belonging to the subtropical maritime climate, has been actively studied for its soil fauna. Many references are suitable for field observations of vegetation, soil fauna including oribatid mites, and other insect fauna. As part of environmental education at the technical college, where the presenter is affiliated, a course called “Environmental Science Experiments” was established to cover topics such as regional biodiversity, material cycles, and the relationship between organisms and the environment. Over the past five years, this course has utilized these materials and the soil fauna of the northern region of Okinawa Island in its educational program, and has also been used in various science events and outreach classes. Students enrolled in this program will investigate and discuss local biodiversity, the relationship between vegetation and the soil environment, and the associated changes in biota through observation of soil fauna. Meanwhile, soil animal samples collected through this educational program will be preserved as immersion specimens for subsequent taxonomic and ecological studies. Currently, we are focusing on oribatid species in the northern region of Okinawa Island, with the aim of examining taxonomy and elucidating species diversity. This presentation introduces the efforts to enhance the environmental education program, which has led students to develop a strong interest in soil animals through soil animal observation classes, and to connect this series of activities to research activities. It also introduces several species of oribatid mites obtained through these activities.



**Taxonomic study on Japanese earthworm species morphologically similar to Korea species (Annelida: Clitellata: Megascolecidae)**

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At least one validly named species, *Amyntas tappensis*, and three morphospecies of the earthworm genus *Amyntas* are distributed in Japan. These species are very similar to Korean species. This earthworm lineage, hereafter referred to as the *A. tappensis* lineage, involves eight species and two subspecies from Korea: *A. sanchongensis*, *A. songaesiki*, *A. gucheonensis*, *A. odaesanensis*, *A. righii*, *A. fasciiformis*, *A. bangtaesan*, *A. bangtaesan*, *A. bangtaesan confines*, *A. seoraksan seoraksan* and *A. seoraksan iti*. All of these species are characterized with the distribution and number of genital marking in the male pore and spermathecal pore regions. However, these morphological traits often show intraspecific variations and less reliable as diagnostic characters at species or higher taxonomic levels. In this study, I examine the taxonomic status of the Japanese morphospecies belonging to the *A. tappensis* lineage to address these issues.

The three Japanese morphospecies of the *A. tappensis* lineage can be determined to be three Korean species, *A. righii*, *A. seoraksan*, and *Amyntas* sp., respectively, by referring to taxonomic articles on Korean species. On the other hand, many aspects of each species are still not fully understood based only on the original description. In addition, since there are so many similar species in the *A. tappensis* lineage, an integrative taxonomic approach using DNA sequence data is also essential. In order to solve these issues, it is essential to establish a cooperative relationship with Korean researchers. Analyses of specimens obtained from overseas, especially from neighboring countries, are essential for understanding and conserving the biota of our own countries and regions. We need to ensure proper compliance with international rules such as Access-Benefit-Sharing (ABS) and national rules on biodiversity conservation in each country and region, and to foster equal, mutually beneficial, and friendly relations.

**Genetic Diversity in the Surface-Dwelling Collembola *Tomocerus cf. ocreatus* along the Ryukyu Archipelago**

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Collembola, a group of tiny, wingless, soil-dwelling animals with limited dispersal ability, are expected to have geographically isolated populations even on neighboring islands. This isolation can lead to genetic diversification and potential speciation. In this study, we examined the genetic divergence and phylogeny of the surface-dwelling collembolan species *Tomocerus cf. ocreatus* along the Ryukyu Archipelago, located in southern Japan. We sequenced six genetic markers from both mitochondrial and nuclear genomes of specimens collected from six islands spanning 800 km. Our results indicated that the Ryukyu specimens formed a monophyletic clade, which is a sister group to a clade consisting of *T. qinae* and *T. pseudocreatus* from mainland China. The genetic divergence suggested that the Ryukyu populations could be speciated into two or three distinct species. Additionally, we observed that genetic divergence at each locus increased with the geographical distance between sampling sites. We also sequenced the mitochondrial genomes from two populations on Okinawa Island—one from the northern part and one from the southern part of the island. Each genome contained 37 genes (13 protein-coding, 2 ribosomal RNA, and 22 transfer RNA genes). The mean sequence identity between the two mitochondrial genomes was 92.5% for CDS, 96.0% for rRNA genes, and 98.0% for tRNA genes, indicating considerable genetic divergence within the island. This finding also suggested that the mitochondrial cytochrome c oxidase subunit I gene, commonly used for animal DNA barcoding, has limited ability to identify conspecific specimens from different sites within this group due to its high genetic diversity in the mitochondrial genomes. These results highlight the significant genetic differentiation among populations of *Tomocerus cf. ocreatus* within and across the islands of the Ryukyu Archipelago.

## Diversity and Evolutionary History of the Order Scutigleromorpha in the Japanese Islands

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The Japanese Islands is known for its high biodiversity. This is due to a combination of various factors, including its elongated north-south orientation, thereby belonging to multiple climatic zones, and being affected by climatic change and geological events. Despite their limited dispersal ability, widely distributed species groups are suitable for estimating the process of evolution in the Japanese Islands. Centipedes, which are non-flying but widely distributed, have attracted much attention in phylogeography, but there has been little focus at the species-level of studies within the order Scutigleromorpha. In the highly species-diverse Japanese Islands, only two species are recorded of the Order Scutigleromorpha: *Thereuopoda clunifera* and *Thereuonema tuberculata*. In this study, we analyzed three mtDNA regions and three nDNA regions of both Japanese species to reveal the unknown diversity level of these species in the Japanese Islands and to reveal their evolutionary history and diversification process. The results revealed the presence of several undescribed species among the Scutigleromorpha of the Japanese Islands. We suggested that molecular phylogenetic analyses of the phylogenetically conserved morphological characteristics of Scutigleromorpha will lead to the discovery of previously overlooked species diversity. Also, *Thereuopoda* spp. is highly differentiated between islands and/or regions. This is thought to be due to the lack of flight ability, which has resulted in the population fragmentation because of their inability to overcome strait barriers. In other words, the results suggest that the straits act as a major dispersal barrier for *Thereuopoda* spp. However, some inconsistencies have been detected that cannot be explained by these factors alone. These include the presence of certain lineages that have traversed biogeographical barriers and others that show genetic similarities despite being geographically isolated, suggesting the possibility of oceanic dispersal. These findings reveal a previously overlooked level of diversity within Japanese Scutigleromorpha and uncover their interesting evolutionary history.

## **General Information**

General Information

**1st Asian Colloquium of Soil Zoology (ACSZ)**

**- General Information -**

**Venue**

Nara Centennial Hall

(7-1 Sanjo-Miyamae-cho, Nara City, Nara 630-8121, Japan)

<https://maps.app.goo.gl/fp8seg3ayNuZWkv39> Map

[http://www.nara100.com/introduce\\_3.html](http://www.nara100.com/introduce_3.html). Website

**Transportation**

On Foot

It is only 4 minutes' walk from the Exit West entrance of JR Nara station.

About 16 minutes' walk from Kintetsu Nara station of Kintetsu Nara line.

**Location**

Nara City, Nara Prefecture, Japan

Nara is located less than one hour from Kyoto and Osaka. Due to its past as the first permanent capital, it remains full of historic treasures, including some of Japan's oldest and largest temples (from [japan-guide.com](http://japan-guide.com)).

Historic Monuments of Ancient Nara were listed as a World Heritage site in 1998.

**Information websites**

Nara City Sightseeing Information Center

<http://narashikanko.or.jp/en/>

The tourism homepage run by Nara Prefecture

<http://www.pref.nara.jp/item/79931.htm#itemid79931>

Nara Travel Guide: Japan Guide

<http://www.japan-guide.com/e/e2165.html>

About World Heritage in Nara

<http://whc.unesco.org/en/list/870>

[https://en.wikipedia.org/wiki/Historic\\_Monuments\\_of\\_Ancient\\_Nara](https://en.wikipedia.org/wiki/Historic_Monuments_of_Ancient_Nara)

## General Information

### Registration

All participants and accompanying persons need to register immediately after arrival.

#### **Please have cash on hand.**

A certificate of attendance will be delivered along with all the ACSZ documentation upon registration.

### Internet Access

Unfortunately, the venue is **NOT** connected to the Internet due to poor cell phone and other signal conditions.

Please download the program on your own laptop or tablet and bring it with you.

### Coffee breaks

#### **Lunch boxes / Lunches**

Coffee breaks and lunches will not be provided in order to save on the participation fee; please buy your own lunch around JR Nara station.

#### **Please do your own research on vegetarian diets.**

Strict vegetarian (vegan):

<https://vegewel.com/en/prefstate/29>

Halal:

<https://www.halgourmet.jp/ja/restaurant/%E5%A5%88%E8%89%AF%E7%9C%8C/29>

### Excursion (tentative)

We will take time for excursions. There are many tourist facilities in the surrounding area, so please enjoy sightseeing on your own. As this is a small meeting, the secretariat staff will probably accompany you. Please contact us for more information.

### Colloquium dinner

The Colloquium dinner will be held on Thursday, 21<sup>th</sup> August, Dinner is not included in the registration fee. We will book a "tavern" and share the cost, but we will not be able to accommodate strict vegetarians.

### Field Trip

The Local Committee will not be making any special preparations for the field trip on the afternoon of Friday, August 23. Please use the following Nara City sightseeing guide to find a destination that you will enjoy. Nara is Japan's oldest capital and a place of historical significance.

<https://www.visitnara.jp/getting-around-nara/>

- 1) One team is planning to go to **Todaiji-Temple**. (Details of both temples are given below.
- 2) The other team will be going to **Horyu-ji Temple**. (Details of both temples are given below.
- 3) Kyoto City is also just an hour away by express train.

**Please note that it is not suitable to collect soil animals in Nara City. In particular, since Kasugayama is strictly preserved, permission to collect soil animals will never be granted.**

However, if you are interested in collaborative research using specific taxa, please discuss this with the Japanese researchers you meet at the conference.

#### A) Todai-ji temple -----

**Tōdai-ji is one of the largest wooden structures in the world.**

<https://www.todaiji.or.jp/en/access/>

##### 1) Features

Tōdai-ji is a historic temple located in Nara, Japan, and it is widely regarded as impressive for many reasons. Among these, the following points are particularly noteworthy:

**The Great Buddha Hall and the Great Buddha:** The Great Buddha Hall (Daibutsuden) at Tōdai-ji is one of the largest wooden structures in the world. Inside, it houses a colossal bronze statue of the Great Buddha (Rushanabutsu), which stands about 15 meters tall and weighs approximately 250 tons. This statue was constructed during the Nara period (8th century) and symbolizes the advanced technological capabilities of Japan at that time.

**World Heritage Site:** Tōdai-ji was registered as a UNESCO World Heritage Site in 1998 as part of the Historic Monuments of Ancient Nara. This recognition highlights the global importance of Tōdai-ji as a cultural asset.

## 2) Here's the route from JR Nara Station to Tōdai-ji:

### By Walking:

1. **Time:** About 20 to 30 minutes
2. **Directions:**
  - Exit JR Nara Station from the East Exit and head towards the roundabout in front of the station.
  - Continue straight along Omiya Street, heading east. You'll pass through areas with various shops and commercial streets.
  - Pass by Sarusawa Pond, and continue walking on Sanjo Street until you reach Nara Park.
  - Walk through Nara Park, heading further east towards Kōfuku-ji Temple and Kasuga Taisha Shrine.
  - After passing through the Nandaimon Gate (South Great Gate), you'll see the Great Buddha Hall of Tōdai-ji.

### By Bus:

1. **Time:** About 10 minutes
2. **Directions:**
  - Exit JR Nara Station from the East Exit and go to the bus terminal in front of the station.
  - Take a **Nara Kotsu Bus** from platforms 2 or 70, and get off at the "Daibutsuden/Kasuga Taisha-mae" bus stop.
  - From the bus stop, it's about a 5-minute walk to Tōdai-ji.

Walking offers a chance to enjoy the atmosphere of Nara and the scenery of Nara Park, while taking the bus is a quicker option. Both ways are convenient for sightseeing.

## B) Horyu-ji Temple -----

**Hōryū-ji houses the world's oldest surviving wooden buildings.**

<https://www.horyuji.or.jp/en/>

### 1) Features

Hōryū-ji, located in Ikaruga, Nara Prefecture, Japan, is a highly significant Buddhist temple renowned for several remarkable features:



1. **World's Oldest Wooden Structures:** Hōryū-ji houses the world's oldest surviving wooden buildings. Notably, the Five-Story Pagoda and the Main Hall (Kondō) in the Western Precinct (Sai-in Garan) were constructed in the early 7th century during the Asuka period, making them over 1,300 years old. Their preservation showcases the advanced architectural and wood preservation techniques of ancient Japan.

2. **UNESCO World Heritage Site:** In 1993, Hōryū-ji was inscribed as a UNESCO World Heritage Site, recognizing its global cultural significance as part of the "Buddhist Monuments in the Hōryū-ji Area."

## 2) Here's the route from JR Nara Station to Horyu-ji Temple.

### By Train:

1. **Time:** About 30 to 40 minutes
2. **Directions:**
  - From JR Nara Station, take the **JR Yamatoji Line** (also known as the JR Kansai Main Line) bound for Ōji or Namba.
  - Get off at **Hōryū-ji Station**. The train ride takes about 12 minutes.
  - From Hōryū-ji Station, it's about a 20-minute walk to the temple. Follow the signs or take the road heading south from the station, and you'll reach Hōryū-ji.

### By Bus (from Hōryū-ji Station):

1. **Time:** About 5 minutes by bus + 12 minutes by train
2. **Directions:**
  - After arriving at **Hōryū-ji Station** by the JR Yamatoji Line, you can take a local bus from the station to the Hōryū-ji Temple area.
  - The bus ride is about 5 minutes, and it will drop you off closer to the temple entrance.

Taking the train is the most straightforward option, and the walk from Hōryū-ji Station to the temple allows you to enjoy the surrounding area.

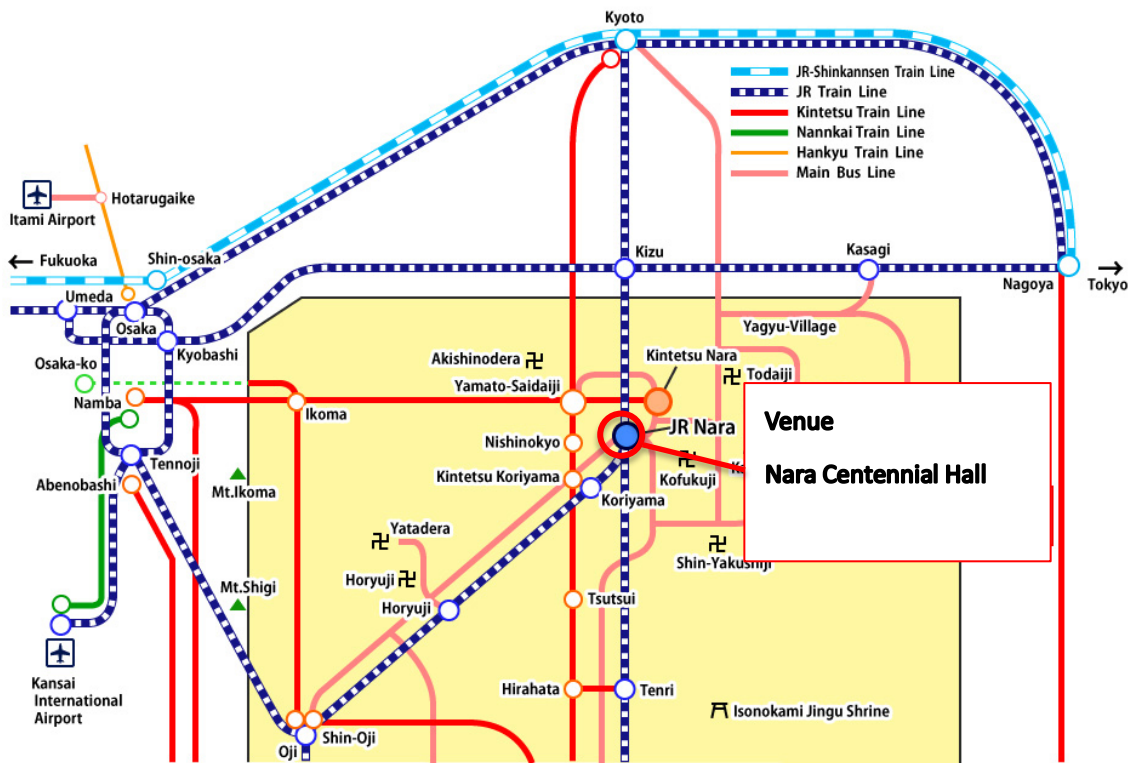
General Information

Route from Kansai International Airport

**from Kansai Int'l Airport**

 Approx. 1 h 32 min  
( JR Kansai Airport Sta. - JR Nara Sta. )

 Approx. 1 h 25 min  
( KIX Terminal 1 Bus Stop 9 - Kintetsu-Nara Sta. )





**Venue**  
**Nara Centennial Hall**



**Venue**  
**Nara Centennial Hall**

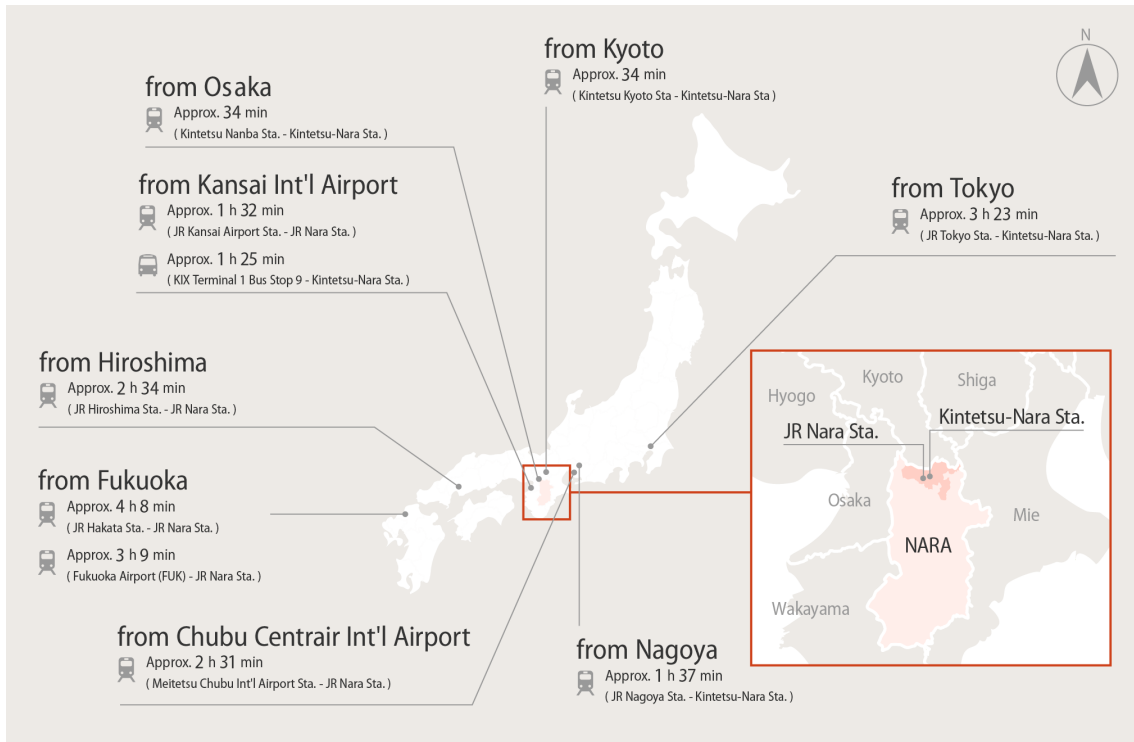
①: Nara Royal Hotel

A: Nara Kasugano International Forum IRAKA

B: JR Nara Station (JR: Japan Railways)

C: Kintetsu Nara Station

# 1st Asian Colloquium of Soil Zoology (ACSZ)



See Next Page (continued)

## General Information

### **Things to remember**

First of all in summer time, Nara city would be very hot. Participants can be affected easily by sunstroke, so we strongly recommend having water.

### **Insurance**

**Participants are advised to take out a travel insurance, as the organizing committee will assume no responsibility for personal accidents, sickness, thefts or property damage.**

### **Currency Exchange**

Only Japanese yen (JPY) is acceptable at stores and restaurants in Japan. You can exchange money at the airport, foreign exchange banks, and other authorized exchange counters upon presentation of your passport. We encourage you to exchange your money at the airport upon arrival.

### **Credit Cards and Traveler's Checks**

Visa, Master Card, American Express, Diners Club and JCB are widely accepted at hotels, department stores, shops and restaurants. Only major banks and hotels in principal cities can accept traveler's checks, but their use in Japan is not as common as in some other countries.

### **Banking**

Banks are open from 9:00 to 15:00, Monday to Friday. Post offices (Japan Post Bank) are open from 9:00 to 16:00, Monday to Friday. Post offices (Posting) are depended on a branch office, normally from 9:00 to 17:00. Post offices (Posting) are open from 9:00 to 17:00, Monday to Friday.

You can withdraw money with the credit card or cash card from the overseas institution in Japan Post Bank ATMs (Open time is depended on a branch office).

**Notice** : Following several instances of withdrawals made with stolen cards and counterfeit cards, Japan Post Bank has established a new withdrawal limit for single transactions.

**Single transaction withdrawal limit will be 50,000 Yen.**

### **Tipping**

There is no custom of tipping in Japan. Instead, at places such as restaurants, bars and hotels, 10% service charge is usually added to your bill.

#### Climate

There are four seasons in Japan: spring (March-May); summer (June-August); autumn (September-November); winter (December-February). Stretching from north to south, Japan has different climates from region to region. Also due to seasonal winds, the Japan Sea coastal area and its Pacific Ocean side have different climates respectively. The average temperature in Nara in August is 26.9° C (= 80.42° F), Highest temperature is 32.6° C (= 90.68° F), Lowest temperature is 22.6° C (= 72.68° F).

#### Electrical Appliances

Japan operates on 100 volts for electrical appliances. The frequency is 60 Hz in western Japan.

#### Consumption tax is paid by consumers.

When you purchase goods and services. The rate is currently 10%. Shops and other service providers are required to include the consumption tax in the prices shown.

#### **Contact person:**

Satoshi SHIMANO, Prof., Ph.D. sim@hosei.ac.jp

Hosei University

Please write in the subject of the mail as “[ACSZ].....”

## Participants

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1st Asian Colloquium of Soil Zoology [ACSZ 2024], Nara

Program Book

Published by Local Committee, 14 August, 2024

Nara Centennial Hall

(7-1 Sanjo-Miyamae-cho, Nara City, Nara 630-8121, Japan)

22 (Thursday) –24 (Saturday), August 2024

Nara, Japan.

[https://sim.ws.hosei.ac.jp/wp/?page\\_id=8](https://sim.ws.hosei.ac.jp/wp/?page_id=8)



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