

Posters of 2023 Annual Meeting of SPP1991 Taxon-Omics

The presenting scientist of each poster is underlined.

Poster title	Authors	Project
1 New kid on the block - proteomic fingerprinting as quick and easy molecular tool for species identification in monitoring of marine communities	Janna Peters ¹ , Sven Rosse ¹ , Pedro Martinez Arbizu ² , Silke Laakmann ³ , Sabine Holst ¹ , Sahar Khodami ² , Jasmin Renz ¹	Proteomic fingerprinting for species identification – discriminatory power and optimal analyses procedures for integrated molecular and morphological datasets in zooplankton biodiversity assessments
2 Phylogeny and species delimitation in <i>Albinaria</i> from western Crete (Gastropoda: Clausiliidae) using genomic markers	<u>Elisa Becher</u> ⁴ and Bernhard Hausdorf ⁴	Exploring genomic methods for delimiting species in radiations of terrestrial snails
3 Mining <i>Hypoxylon</i> Genome Data for Total Biosynthesis	Russel Cox ⁵ , Yunlong Sun ⁵ , Katharina Schmidt ⁵ , Henrike Heinemann ⁵ , Eric Kuhnert ⁵ , Kevin Becker ⁵ , Dong-Song Tian ⁵	
4 Coprophilous fungi: a source of biological and chemical diversity	Karen Harms ⁶ , Esteban Charria-Giron ⁶ , <u>Yasmina Marin-Felix</u> ⁶	Phylogenomics of the genus <i>Hypoxylon</i> based on 50 new high-quality genomes and with special emphasis on the <i>H. rubiginosum</i> complex
5 Evolution in the Taxonomy of <i>Hypoxylon</i> - from Morphological Species Concept to Phylogenomics	<u>Marjorie Cedeño-Sánchez</u> ⁶ , Bart Verwaaijen ⁷ , Marc Stadler ⁶	
6 A genomic sequencing effort to expand the Phylogeny of the genus <i>Hypoxylon</i> – Phase 2	Bart Verwaaijen ⁷ , Eric, Kuhnert ² , Marjorie Cedeño ⁶ , Tian Cheng ⁶ , Tobias Busche ⁷ , Russell Cox ⁵ , Marc Stadler ⁶ , Jörn Kalinowski ⁷	

7	<p>A novel target-enriched multilocus assay for sponges (<i>Porifera</i>)</p>	<p><u>Joëlle van der Sprong</u>⁸, Nicole J. de Voogd⁹, Grace P. McCormack¹⁰, Kenneth Sandoval¹⁰, Simone Schätzle⁸, Oliver Voigt⁸, Dirk Erpenbeck⁸, Gert Wörheide⁸, Sergio Vargas⁸</p>	Sponge TaxonOMICs V2
8	<p>The phylogenetic relationships and wing-pattern evolution of burnet moths (<i>Zygaena</i>) using museum specimens</p>	<p>Eduardo Marabuto^{11,12}, Sneha Bhansali¹², Franziska Patzold¹², Lars Podsiadlowski¹¹, Axel Hofmann¹³, Anna K. Hundsdoerfer¹², <u>Marianne Espeland</u>¹¹</p>	
9	<p>Wing pattern and phylogenomics in the Lepidoptera genus <i>Hyles</i> - status quo</p>	<p><u>Anna K. Hundsdoerfer</u>¹², Franziska Patzold¹², Ilyos Amirov⁴², Ozodbek Turg'unboye⁴², Bakhtiyor Kholmatov⁴², Eduardo Marabuto^{11,12}, Lucas Langer¹², Michael San Jose¹⁴, Dan Rubinoff¹⁴, Alberto Zilli⁴⁴, Jean Haxaire⁴³, Claudia Paetzold¹²</p>	Comparative and experimental wing pattern genomics in Lepidoptera
10	<p>Integrative species delimitation in <i>Xanthium</i> sect. <i>Acanthoxanthium</i></p>	<p><u>Salvatore Tomasello</u>¹⁵, Eleonora Manzo¹⁵, Diego G. Gutiérrez</p>	Resolving intricate taxonomies by using type material, Hyb-Seq and geometric morphometrics.
11	<p>The decline of the native <i>Xanthium strumarium</i> L. and the invasiveness of the American <i>X. orientale</i> L. Are competition and allelopathy triggering factors?</p>	<p><u>Eleonora Manzo</u>¹⁵, Chiara-Sophie Epifanio, Julius Friedemann Pahl, Salvatore Tomasello¹⁵</p>	– A proof-of-concept from the nasty <i>Xanthium</i> L.
12	<p>Molecular evidence for sectional classification of shrub willows (<i>Salix</i> L. subg. <i>Chamaetia/Vetrix</i>) based on RAD sequencing data</p>	<p>Pia Marincek¹⁵ and Natascha Wagner¹⁵</p>	Molecular evidence for sectional classification of shrub willows (<i>Salix</i> L. subg. <i>Chamaetia/Vetrix</i>) based on RAD sequencing data
13	<p>The CARRARA approach: species delimitation in intensively hybridising plant genera based on herbarium specimens</p>	<p><u>Marco Dorfner</u>¹⁶, Lara Escherich¹⁷, Frank H. Hellwig¹⁷, Robert Vogt¹⁸, Christoph Oberprieler¹⁶</p>	The CARRARA pipeline: Using machine-learning techniques for automated species delimitation in intensively hybridising plant genera based on herbarium specimens

14	MUSEOMICS VERSUS THE TAXONOMIC GAP: Type-specimen explicit species delimitation to resolve cophyline taxonomy	Alice Petzold ^{19,20} , Clara Keusgen ¹⁹ , Michaela Preick ¹⁹ , Carl R. Hutter ²¹ , Frank Glaw ²² , Miguel Vences ²³ , Michael Hofreiter ¹⁹ , Mark D. Scherz ²⁴	FrogCap for the Taxonomic Gap: Harnessing Hybrid Enrichment for Next-Generation Taxonomy
15	Meristic co-evolution and genomic co-localization of the lateral line and vertebrae in Central American cichlid fishes	Nicolas Ehemann ²⁵ , Paolo Franchini ²⁵ , Axel Meyer ²⁵ , C. Darrin Hulsey ²⁵	Genomics of Hybridization and Species Delimitation in Cichlid Fishes
16	Sex-biased demographic patterns and migration of the big European firefly (<i>Lampyris noctiluca</i>)	Ana Catalán ⁸ and Sebastian Höhna ⁸	New approaches for species delimitation from genome data with examples to two widespread fireflies (<i>Lamprohiza splendidula</i> and <i>Photinus pyralis</i>)
17	Ophiuroid phylogenomics: Illuminating “dark” abyssal biodiversity	Angelina Eichsteller ² , Magdalini Christodoulou ²⁶ , Tim O’Hara ²⁷ , Pedro Martinez Arbizu ²	Ophiuroid phylogenomics: Illuminating “dark” abyssal biodiversity
18	Developing a Standardized Multilocus Marker Set - From Field to Museum: The First Experimental Marker Set	Yannis Schöneberg ²⁸ , Christoph Mayer ¹¹ , Stefan Prost ² , Henrik Krehenwinkel ²⁸ , Susan Kennedy ²⁸	From field to museum: Harnessing the power of third generation sequencing to establish a simple and cost-effective multiplex approach for spider taxonomy
19	Reference genomes greatly improve the resolution of GBS-analyses in Ukrainian Veronica.	Mareike Daubert ²⁹ , Christoph Nehrke ²⁹ , Dirk C. Albach ²⁹	Making efficient use of herbarium specimens – Hybrids in Veronica as case example
20	HybSeq or GBS for herbarium specimens? A battle of reduced representation datasets.	Christoph Nehrke ²⁹ , Mareike Daubert ²⁹ , Dirk C. Albach ²⁹	

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AfriTTax: Innovative integration of high-throughput DNA barcoding, transcriptome-based constrained phylogenetics, hyperspectral imaging, and morphology to assess and characterize a poorly known fauna

Ernesto Rázuri-Gonzales³⁰,
Roger J. Blahnik³¹, M. Francois
Ngera, Oskar Schröder³⁰,
Wolfram Graf³², Steffen U.
Pauls³⁰

Innovative integration of high-throughput DNA barcoding, transcriptome-based constrained phylogenetics, hyperspectral imaging, and morphology to assess and characterize a poorly known fauna

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Resolving species diversity of marine loricate choanoflagellates using different taxonomical approaches

Frank Nitsche³³ and Sabine
Schiwitza³³

New approaches for high throughput species discovery and delimitation within unicellular eukaryotes exemplified by choanoflagellates

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Insights into the diversity of the *Vampyrellida* (Rhizaria) through culture-based, environmental sequencing and genomic approaches.

Andreas Suthaus³³, Lubomir
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John Paul Bradican¹⁵,
Salvatore Tomasello¹⁵,
Francesco Boscutti³⁴, Kevin
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Anže Žerdoner Čalasan⁸, Kelly
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Sven Gippner²³, Christophe
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27	Publishing taxonomic data via the GFBio Submission System	<u>Barbara Wagner</u> ³⁷ , Ivaylo Kostadinov ³⁷ , Miguel Vences ²³ , Marc Weber ³⁷	Concepts, tools and support for managing, archiving, mobilizing and integrating taxonomic data
28	Metazoan-level universal single-copy orthologs (mzl-USCOs) as markers for animal taxonomy.	<u>Lars Dietz</u> ¹¹ , Jonas Eberle ³⁸ , Christoph Mayer ¹¹ , Lars Podsiadlowski ¹¹ , Bernhard Misof ¹¹ , Oliver Niehuis ¹¹ , Dirk Ahrens ¹¹	Establishing a standardized and universally applicable set of nuclear-encoded markers for genome-wide multi-locus species delimitation of metazoans
29	Fungal Phylogenomics of Freshwater Helotiales	<u>Daniel Vasconcelos Rissi</u> ³⁹ , Maham Ijaz ³⁹ , Christiane Baschien ³⁹	Molecular taxonomy of aquatic hyphomycetes by safeguarding of historical collections
30	<i>Alatospora</i> Genus Concept: Tidying up a mess	<u>Maham Ijaz</u> ³⁹ , Daniel Vasconcelos Rissi ³⁹ , Christiane Baschien ³⁹	
31	Deep molecular characterization of microorganisms' diversity and community composition in the canopy region using a metatranscriptomic approach	<u>Jule Freudenthal</u> ³³ , Kenneth Dumack ³³ , Martin Schlegel ⁴⁰ , Michael Bonkowski ³³	Continuing the deep molecular characterization of eukaryotic microorganisms' diversity and community composition in forest soils and the canopy region using a metatranscriptomics approach (micDiv II)
32	Digging treasures: Museomics for targeted sequencing in Orthosiinae (Apocynaceae) yields undescribed diversity	<u>Yam Melissa Pineda</u> ⁴¹ , Ulrich Meve ⁴¹ , Sigrid Liede-Schumann ⁴¹ , Nicolai M. Nürk ⁴¹	Elevational replacement, higher tropical mountain passes and isolated sky islands: untangling neutral and adaptive processes driving radiation of Andean Apocynaceae
33	Hybridisation in the Ustilaginales - an update	<u>Dominik Begerow</u> ⁴	The genomic basis of host specificity as tool for species recognition and delimitations in Ustilaginales - a parasite group with high gene flow
34	Understanding the evolution of effectors in Anthracideaceae by long read WGS	<u>Nils Hassel</u> ⁴ and Martin Kemler ⁴	

- 1 - Senckenberg am Meer, Hamburg
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- 3 - Helmholtz Institute for Functional Marine Biodiversity at the University of Oldenburg
- 4 - University of Hamburg
- 5 - Leibnitz University Hannover
- 6 - Hemholtzzentrum für Infektionsforschung Braunschweig
- 7 - University of Bielefeld
- 8 - Ludwig-Maximilian University Munich
- 9 - Naturalis Biodiversity Center
- 10 - University of Galway
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- 33 - University of Cologne
- 34 - University of Udine
- 35 - Western Australian Herbarium
- 36 - Nanjing Forestry University
- 37 - GFBio - Gesellschaft für Biologische Daten e.V.
- 38 - University of Salzburg
- 39 - DSMZ
- 40 - University of Leipzig
- 41 - University of Bayreuth
- 42 - Academy of Sciences of the Republic of Uzbekistan
- 43 - Muséum National d'Histoire Naturelle
- 44 - Natural History Museum, London