VII International Rubiaceae and Gentianales Conference

Copenhagen, Denmark

11 – 14 September 2017

Natural History Museum of Denmark
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Organizing committee

Brecht Verstraete, Natural History Museum of Denmark
Nina Rønsted, Natural History Museum of Denmark

Scientific committee

Maria Regina de V. Barbosa, Universidade Federal da Paraíba
Petra De Block, Botanic Garden Meise
Charlotte Taylor, Missouri Botanical Garden
Helga Ochoterena, Universidad Nacional Autónoma de México
Sylvain Razafimandimbison, Swedish Museum of Natural History

Contact during the conference

Brecht Verstraete +45 71 64 91 31
Nina Rønsted +45 23 81 12 03
General information

Venue
The conference is held at the Pompeii conservatory of the Carlsberg Academy, which is located in the Vesterbro neighbourhood of Copenhagen. The address is Gamle Carlsberg Vej 15 and the Google Maps coordinates are 55.663883, 12.531746. See also on the map.

Public transport
Plan your trip on www.rejseplanen.dk or with the “Rejseplanen”-app. You can buy a City Pass in advance on www.citypass.dk or download the “DOT Mobilbilletter”-app.
Train: the nearest stop is “Carlsberg St.” and the S-trains run very frequent, in the morning even every 5 minutes (or less). Walk along the tracks on Carlsbergruten to the venue.
Bus: the nearest stop is “Bjerregårdsvej” and you can take bus 8A or 26. Walk down Bjerregårdsvej to the venue.

Registration
Registration is open on Monday between 09.00 and 09.45.

Presentations and symposia
Presentations are held on Monday, Tuesday, and Wednesday between 09.00 – 15.00. The Next Generation Sequencing symposium is held on Monday between 15.30 – 17.00, and the World Flora Online symposium is held on Tuesday between 15.30 – 17.00.

Posters
Posters can be mounted on Monday between 09.00 – 09.45. There is no formal poster session but everyone is encouraged to look at the posters during the breaks and lunches.

Lunch
Lunch is served each day between 12.00 – 13.30 in the winter garden of the Carlsberg Academy.

Reception
The reception is scheduled for Monday between 18.00 – 20.00 at the Geological Museum. The address is Øster Voldgade 5-7 and the Google Maps coordinates are 55.687347, 12.576486. See also on the map.

Dinner
The conference dinner is scheduled for Wednesday from 19.00 and is held at “Toldboden”. The address is Nordre Toldbod 18-24 and the Google Maps coordinates are 55.689744, 12.599782. See also on the map.

Excursion
The excursion to Møns Klint is scheduled for Thursday between 09.00 – 18.00. The bus leaves from Ingerslevgade and the Google Maps coordinates are 55.670109, 12.565362. See also on the map.
Please see further details inside the program.

Post-conference activity
A visit to the Herbarium C is scheduled for Friday between 09.00 – 16.30. The bus pick-up location will be announced later. Please see further details inside the program.
Route to the Carlsberg Academy from the Carlsberg train station and the nearest bus stop.
Location of the Carlsberg Academy (venue), the bus to Møn (excursion), the Geological Museum (reception), and the restaurant Toldboden (dinner).
PROGRAM
Program at a glance

Monday 11 September
09.00 – 09.45  Registration
09.45 – 10.30  Presentations
10.30 – 11.00  Break
11.00 – 12.00  Presentations
12.00 – 13.30  Lunch
13.00 – 15.00  Presentations
15.00 – 15.30  Break
15.30 – 17.00  NGS symposium
18.00 – 20.00  Reception at the Geological Museum

Tuesday 12 September
09.00 – 10.30  Presentations
10.30 – 11.00  Break
11.00 – 12.00  Presentations
12.00 – 13.30  Lunch
13.00 – 15.00  Presentations
15.00 – 15.30  Break
15.30 – 17.00  WFO symposium

Wednesday 13 September
09.00 – 10.30  Presentations
10.30 – 11.00  Break
11.00 – 12.00  Presentations
12.00 – 13.30  Lunch
13.00 – 15.30  Presentations
19.00 –        Dinner at Toldboden

Thursday 14 September
09.00 – 18.00  Excursion to Møns Klint

Friday 15 September
09.00 – 16.30  Visit Herbarium C
### Monday 11 September

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<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>09.00 – 09.45</td>
<td>Registration</td>
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</table>
| 09.45 – 10.00 | Brecht Verstraete and Nina Rønsted, Natural History Museum of Denmark  
*Opening address*  
Chair: Brecht Verstraete |
| 10.00 – 10.30 | Aaron Davis, Royal Botanic Gardens, Kew  
The resilience potential of wild and cultivated Arabica coffee (Coffea arabica) in Ethiopia |
| 10.30 – 11.00 | Break                                                                                           |
| 11.00 – 11.30 | Perla Hamon, UMR DIADE  
*GBS coffee phylogeny and the evolution of caffeine content* |
| 11.30 – 12.00 | Andreas Berger, University of Vienna  
*New insights into the phytochemical differentiation within Psychotrieae and Palicoureeae (Rubiaceae)* |
| 12.00 – 13.30 | Lunch                                                                                           |
|          | Chair: Charlotte Taylor                                                                           |
| 13.30 – 14.00 | Carla Maldonado, Herbario Nacional de Bolivia  
*Can phylogeny predict the quantity of alkaloids in plants? A case study in the iconic Yellow Cinchona bark (Rubiaceae)* |
| 14.00 – 14.30 | Niklas Wikström, Bergius Botanic Garden  
*Conflicting phylogenies for Rubiaceae revealed by chloroplast phylogenomic data* |
| 14.30 – 15.00 | Catarina Rydin, Stockholm University  
*Mitochondrial genomic data challenge current views of Rubiaceae phylogeny* |
| 15.00 – 15.30 | Break                                                                                           |
| 15.30 – 17.00 | Next Generation Sequencing symposium  
Olivier Maurin, Royal Botanic Gardens, Kew  
*Completing the plant tree of life*  
Discussion |
| 18.00 – 20.00 | Reception at the Geological Museum  
Øster Voldgade 5-7 (See map) |
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<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>09.00 – 09.30</td>
<td>Steven Janssens, Botanic Garden Meise</td>
<td><em>What is the impact of heterostyly on the diversification of species? A case study within the Rubioideae subfamily</em></td>
</tr>
<tr>
<td>09.30 – 10.00</td>
<td>Elmar Robbrecht, Botanic Garden Meise</td>
<td><em>Where and when did tropical Rubiaceae migrate towards the temperate zones?</em></td>
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<tr>
<td>10.00 – 10.30</td>
<td>Petra De Block, Botanic Garden Meise</td>
<td><em>Different ways to obtain similar results. The development of the corolla and epipetaly in herbaceous Rubioideae (Rubiaceae)</em></td>
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<tr>
<td>10.30 – 11.00</td>
<td>Break</td>
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<tr>
<td>11.00 – 11.30</td>
<td>Roberto Salas, Instituto de Botánica del Nordeste</td>
<td><em>Spermacoce in the Americas: small group, small flowers but great taxonomic problems</em></td>
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<tr>
<td>11.30 – 12.00</td>
<td>Johan Rova, University of Gothenburg</td>
<td><em>Can ITS and rps16 data be used to delimit species and morphological groups in Pentagonia (Rubiaceae)</em></td>
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<tr>
<td>12.00 – 13.30</td>
<td>Lunch</td>
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<tr>
<td>13.30 – 14.00</td>
<td>Piero Delprete, Herbier de Guyane</td>
<td><em>Taxonomic revision of Simira (Rubiaceae, Condamineeae)</em></td>
</tr>
<tr>
<td>14.00 – 14.30</td>
<td>Xiaoming Guo, South China Botanical Garden</td>
<td><em>Integrative taxonomy and phylogeny-based species delimitation of Leptodermis (Rubiaceae), a genus with rich species complex?</em></td>
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<tr>
<td>14.30 – 15.00</td>
<td>Olivier Lachenaud, Botanic Garden Meise</td>
<td><em>The Rubiaceae of Gabon</em></td>
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<tr>
<td>15.00 – 15.30</td>
<td>Break</td>
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<tr>
<td>15.30 – 17.00</td>
<td>World Flora Online symposium</td>
<td><em>Rubiaceae in the World Flora Online</em></td>
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<td>Chair: Elmar Robbrecht</td>
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<td></td>
<td><em>Discussion</em></td>
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# Wednesday 13 September

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker(s)</th>
<th>Institution(s)</th>
<th>Presentations</th>
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<tbody>
<tr>
<td>09.00 – 09.30</td>
<td>Mary Endress, University of Zurich&lt;br&gt;Sex, drugs and pupusas: relationships in Echiteae (Apocynaceae) – it’s complicated</td>
<td>Chair: Helga Ochoterena</td>
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<tr>
<td>09.30 – 10.00</td>
<td>Ulrich Meve, University of Bayreuth&lt;br&gt;Early evolution of Ceropegieae (Apocynaceae-Asclepiadoideae)</td>
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<td>10.00 – 10.30</td>
<td>André Simões, Universidade Estadual de Campinas&lt;br&gt;Phylogenetic and systematic studies in Aspidosperma Mart. &amp; Zucc. (Apocynaceae, Rauvolfioideae)</td>
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<tr>
<td>10.30 – 11.00</td>
<td>Break</td>
<td>Arne Sinnesael, KU Leuven</td>
<td>Microscopic evidence for vertical transmission of the leaf nodulated endosymbiont in Psychotria punctata</td>
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<tr>
<td>11.00 – 11.30</td>
<td>Brecht Verstraete, Natural History Museum of Denmark&lt;br&gt;Bacterial leaf symbiosis promotes the evolutionary success of its host plants</td>
<td>Chair: Erik Smets</td>
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<tr>
<td>11.30 – 12.00</td>
<td>Sylvain Razafimandimbison, Swedish Museum of Natural History&lt;br&gt;Historical biogeography of the pantropical Psychotrieae alliance (Rubiaceae) in the Western Indian Ocean Region</td>
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<tr>
<td>12.00 – 13.30</td>
<td>Lunch</td>
<td>Chair: Erik Smets</td>
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<tr>
<td>13.30 – 14.00</td>
<td>Arnaud Mouly, Université Bourgogne Franche-Comté&lt;br&gt;New Caledonia, an isolated flora within a web of Pacific archipelagos: the Gardenieae (Rubiaceae) model</td>
<td>Chair: Helga Ochoterena</td>
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<tr>
<td>14.00 – 14.30</td>
<td>Brecht Verstraete, Natural History Museum of Denmark&lt;br&gt;Closing address and next meeting</td>
<td>Chair: Helga Ochoterena</td>
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<tr>
<td>14.30 – 15.00</td>
<td>Sylvain Razafimandimbison, Swedish Museum of Natural History&lt;br&gt;New Caledonia, an isolated flora within a web of Pacific archipelagos: the Gardenieae (Rubiaceae) model</td>
<td>Chair: Helga Ochoterena</td>
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<tr>
<td>15.00 – 15.30</td>
<td>Helga Ochoterena, Universidad Nacional Autónoma de México&lt;br&gt;A phylogenetic diversity overview of Rubiaceae in the Greater Antilles based on evidence from the petD intron</td>
<td>Chair: Helga Ochoterena</td>
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<tr>
<td>19.00 – 19.30</td>
<td>Conference dinner at Toldboden&lt;br&gt;Nordre Toldbod 18-24 (See map)</td>
<td>Chair: Erik Smets</td>
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### Thursday 14 September

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09.00 – 11.00</td>
<td>Bus to Møns Klint</td>
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<tr>
<td>11.00 – 13.00</td>
<td>Guided tour</td>
</tr>
<tr>
<td>13.00 – 14.00</td>
<td>Lunch</td>
</tr>
<tr>
<td>14.00 – 16.00</td>
<td>Free time</td>
</tr>
<tr>
<td>16.00 – 18.00</td>
<td>Bus to Copenhagen</td>
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</tbody>
</table>

#### Pick-up & drop-off location
A bus from the company “Lyngby Turistfart” will pick us up at “Ingerslevsgade” behind the central train station. The location is indicated on the map and the Google Maps coordinates are 55.670109, 12.565362. The company usually has busses that are gold and red but there will be a sign in the window and both Brecht and Nina will be there. Brecht mobile: +45 71 64 91 31 and Nina mobile: +45 23 81 12 03.

#### Guided tour
When we arrive at Møns Klint, we will split up in two groups. Each group will have a nature guide from the Møns Klint Geocenter who will tell us more about the area. See also on the website [http://moensklint.dk/uk?lang=en](http://moensklint.dk/uk?lang=en).

#### Lunch
Lunch is included and will be served at Café Sommerspiret.

#### Free time
After lunch, you are free to walk around on your own. You can walk along the coastline with its steep white stretches of cliff or stroll in the beautiful beech forest growing on the calcareous soil. The area is also known for its diversity of orchids. Inside, you can visit the exhibition at the Geocenter (note: not included in the fee; 140 DKK).
Friday 15 September

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
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<tbody>
<tr>
<td>09.00 – 09.30</td>
<td>Bus to the herbarium</td>
</tr>
<tr>
<td>09.30 – 10.15</td>
<td>Welcome, history, and tour of the herbarium, instructions for work in herbarium C by Olof Ryding and Nina Rønsted</td>
</tr>
<tr>
<td>10.15 – 12.00</td>
<td>Work in the herbarium</td>
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<tr>
<td>12.00 – 13.00</td>
<td>Lunch</td>
</tr>
<tr>
<td>13.00 – 15.45</td>
<td>Work in the herbarium</td>
</tr>
<tr>
<td>15.45 – 16.00</td>
<td>Conclusion, re-identifications, other comments, and requests for loans (types excluded) and high-resolution scans</td>
</tr>
<tr>
<td>16.00 – 16.30</td>
<td>Bus to Copenhagen</td>
</tr>
</tbody>
</table>

We are very happy and honoured to have you visiting the herbarium and helping us improving our collections.

**Pick-up & drop-off location**
Bus pick-up location to be confirmed later. Nina Rønsted mobile: +45 23 81 12 03.

**Lunch**
Lunch is included.

**Guided Tour**
Olof Ryding and Nina Rønsted will tell you about the history and highlights of the herbarium C.

**Herbarium C** ([http://botanik.snm.ku.dk/english/Samlinger/Herbarier/](http://botanik.snm.ku.dk/english/Samlinger/Herbarier/))
Herbarium C is currently relocated to Priorparken in Glostrup, 30 min outside Copenhagen while a new Natural History Museum is being built in the Botanical Garden.

The General Herbarium includes ca. 1,323,000 specimens of non-Danish flowering plants, gymnosperms, and pteridophytes, including 20,800 type specimens, organised by family, genera, species, and geographic location. The General Herbarium collections are representing well Europe, Thailand, eastern Africa, and temperate South America (Argentina, Brazil). In addition, we have separate herbaria for the Danish and Arctic (mainly Greenland) collections.

All Rubiaceae material will be accessible for this event. A form will be available during registration so you can list your taxa of interest to ensure we have them taken out for you. You are also welcome to send an email to the curatorial staff at curator@snm.ku.dk, preferably with copy to nronsted@snm.ku.dk. Spirit collections are stored at a different address, so if you need these, it is important to let us know in advance. All Indet. materials will be displayed for everybody to help improve IDs.

As part of improving IDs and increase awareness of the importance of the herbarium, we will collect data on how many collections have been looked at, how many Indet. specimens have been identified during this event, and of course any potential new species or overlooked types. The event will go on twitter, the museum’s web news, etc.

_Nina Rønsted, Scientific Curator of the General Herbarium_  
_Olof Ryding, Karen Back, and Frank Barham, Curatorial Managers_
ABSTRACTS
Completing the plant tree of life

William J. Baker¹, Abigail Barker¹, Steven Dodsworth¹, Wolf L.T. Eiserhardt¹, Ester Gaya¹, Jan Kim, Olivier Maurin¹, Joe Parker¹, Lisa Pokorny¹, Felix Forest¹

¹ Royal Botanic Gardens, Kew, United Kingdom
* o.maurin@kew.org

Evolutionary trees are powerful tools for prediction, species discovery, monitoring and conservation. Through comparative analysis of DNA sequence data, the backbones of the plant and fungal trees of life are relatively well understood, and many subcomponents have been studied in great detail. However, DNA data are still lacking for numerous genera and the vast majority of species of plants and fungi, preventing their accurate placement within this evolutionary framework and hindering downstream science. To better understand how the world’s plants and fungi are related to each other and how they have evolved, we have initiated a project at the Royal Botanic Gardens, Kew to complete the Plant and Fungal Trees of Life (PAFTOL). We will utilise our collections and work with our collaborative networks to produce extensive new DNA sequence data (whole plastid genomes, 100s of nuclear loci) for a representative species from each genus of plant and fungus using high-throughput sequencing technologies. This comprehensive investigation of phylogenetic relationships will be a rich resource enabling the discovery and study of evolutionary patterns in the plant and fungal kingdoms, and will provide a unifying framework for comparative research. The project is an essential step towards the compilation of genomic data for all known species. This talk will focus on the plant tree of life component of the project (focusing on angiosperms), highlighting current progress in sampling, phylogenomic methodologies, bioinformatic approaches and collaborative opportunities.
In 2010, the updated Global Strategy for Plant Conservation (GSPC) identified its Target 1 as “An online flora of all known plants”. In 2012, four botanical institutions organized a world collaboration to create the World Flora Online (WFO), <www.worldfloraonline.org>. The WFO is an open-access, web-based compilation of the information electronically available about the world’s plant species, built through international collaboration. Its information is compiled from various sources and organized by a nomenclatural backbone. This contains all published plant names and a synonymy (accepted names and synonyms). The WFO’s basic nomenclatural backbone is The Plant List, which itself is an electronic compilation of taxonomic information that calculates accepted names based on several arbitrary parameters. The Plant List is not regularly updated, and ca. 20% of its names are currently unresolved. IPNI and the Kew World Checklist are now being combined and will support a new version of The Plant List, but that will still be out of date for some groups. Many of the world’s plant species have never been studied since their description. The WFO would like updated taxonomies from specialists for particular groups, and help with unresolved names. The WFO has an option to upload a new taxonomic backbone for a particular group, and replace that part of The Plant List. Specialist taxonomies must be comprehensive for names of each genus treated. The WFO has an outline for contributions but no specified format. TROPICOS data can be incorporated, and its Rubiaceae Project will provide updated taxonomies for selected groups along with commentary, images, and specimen records that can be mapped interactively. Information that is not digitized in some accessible way cannot be included in the WFO.
New insights into the phytochemical differentiation within Psychotrieae and Palicoureeae (Rubiaceae)

Andreas Berger¹, Lothar Brecker², Johann Schinnerl¹, Karin Valant-Vetschera¹

¹ Department of Botany and Biodiversity Research, University of Vienna, Austria
² Department of Organic Chemistry, University of Vienna, Austria
* andi.berger@univie.ac.at

Palicoureeae and Psychotrieae (Rubiaceae) are species-rich sister tribes of mostly understory shrubs with a pantropical distribution. Since the initial studies on Ipecacuanha, a growing number of studies have reported a diverse array of alkaloids and other secondary metabolites from various species included therein. However, the generic limits within the tribes have long been unclear and only recently, genera have been segregated from a once broadly circumscribed Psychotria (Psychotrieae). This has hampered a better understanding on phytochemical differentiation and biosynthetic capabilities within the group, which is of major importance in drug discovery and for studying plant-animal interactions such as herbivory. In order to provide a framework for answering such questions, a revision of published literature in combination with the phytochemical study of >100 spp. was performed. It was found that nearly all studies published on secondary metabolites of Psychotria actually pertain to species now included in other genera and that all these are unique in their chemical complement. This challenges the common perception of Psychotria as an „alkaloid genus” which largely accumulates iridoids and condensed tannins. The only exception is the ethnobotanically important P. viridis containing psychoactive N,N-dimethyltryptamine (DMT). In turn, many different types of alkaloids are present in the tribe Palicoureeae: Palicourea is characterized by strictosidine-derived monoterpane-indole i.e. tryptamine-iridoid alkaloids. Carapichea is characterized by emetine-type and Rudgea by alstrostine-type monoterpane-indole alkaloids. Eumachia contains cyclotryptamines and Notopleura appears to be devoid of alkaloids instead accumulating quinones. These insights could pave the way for future studies addressing the evolution and ecological importance of secondary metabolite differentiation in the fascinating group of plants.
The resilience potential of wild and cultivated Arabica coffee (*Coffea arabica*) in Ethiopia

Aaron P. Davis

1 Royal Botanic Gardens, Kew, United Kingdom
* a.davis@kew.org

Ethiopia generates around a quarter of its export earnings from coffee, which in turn provides livelihoods for around 15 million farmers. Ethiopia is also the main home of indigenous (wild) Arabica coffee (*Coffea arabica*), the only other indigenous populations being in nearby South Sudan. Against a country-wide backdrop of rapidly increasing temperatures and decreasing rainfall, there is an urgent need to understand the influence of climate change on coffee production. Using a modelling approach in combination with remote sensing, supported by rigorous ground-truthing, we project drastic reductions in suitability for coffee farming under various climate change scenarios. Conversely, relocation of coffee areas, in combination with forest conservation and re-establishment, could see an increase in suitable coffee farming areas. We identify key coffee growing areas, and wild coffee forests, that are vulnerable to climate change and likely to disappear regardless of intervention, but also locate areas with climatic resilience. The differences between niche modelling of wild vs. farmed coffee are discussed.
ORAL

Phylogenetic and systematic studies in *Aspidosperma* Mart. & Zucc. (Apocynaceae, Rauvolfioideae)

Andreza S. de Souza Pereira¹, Ana C. Devides Castello¹, Ana L. Scudeler¹, André O. Simões², Ingrid Koch²

¹ Programa de Pós-Graduação em Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas – UNICAMP, Brazil
² Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas – UNICAMP, Brazil
* aosimoes@unicamp.br

*Aspidosperma* Mart. & Zucc. currently comprises 48 species, of which 44 occur in Brazil. It is distributed throughout tropical America, from Mexico to Argentina, with the highest number of endemic species in Brazil (13). Current classifications of the genus are based entirely on morphology and recognize two subgenera, *Aspidosperma* and *Coutinia* (Vell.) Marc.-Ferr. The typical subgenus is divided into nine sections (*Aspidosperma* – 18 spp., *Nobilia* – 11 spp., *Polyneura* – 5 spp., *Excelsa* – 4 spp., *Pungentia* – 2 spp., *Inundata* – 1 sp., *Ramiflora* – 1 sp., *Rrigida* – 1 sp., and *Schultesia* – 1 sp.). *Aspidosperma* has been studied by several authors in the last century, however, the delimitation of its species is still difficult, with taxonomically complex groups, morphological overlapping, as well nomenclatural problems. In this context, our aim is to provide a well-resolved phylogeny of *Aspidosperma* and also conduct a taxonomic revision. The phylogeny will be based on six molecular markers, four from the cpDNA (*rps16* and *rpl16* introns, *trnS-G* intergenic spacer, and *matK* gene), and two from the nDNA (ITS and ETS). So far, we have amplified and obtained preliminary sequences for *rps16* and *trnS-G* for species from sections *Aspidosperma* – 4 spp., *Nobilia* – 5 spp., *Polyneura* – 1 sp., and *Schultesia* – 1 sp. Our partial results suggest that *Aspidosperma* and *Nobilia* are not monophyletic, but more sequences are needed to verify these findings. Based on taxonomical studies, we are accepting five more species than the last published work for *Aspidosperma*. We are also describing two new species from Brazil, one endemic to the Goiás state and the other one widely distributed in the country. We also proposed the conservation of *Aspidosperma cuspa* (Kunth.) S.F. Blake, which is the species with the broader distribution in the genus.
Integrative taxonomy and phylogeny-based species delimitation of *Leptodermis* (Rubiaceae), a genus with rich species complex

Xiaoming Guo\textsuperscript{1,2}, Ruijiang Wang\textsuperscript{1}

\textsuperscript{1} Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences, China
\textsuperscript{2} University of Chinese Academy of Sciences, China
* wangrj@scbg.ac.cn

The genus *Leptodermis* Wall. includes ca. 40 species, of which 30 species are endemic to China. It is a taxonomically challenging plant taxon. Specimen examination and extensive field observation revealed that the morphological variation patterns of *Leptodermis* are very complicated and most diagnoses used for species delimitation are actually uninformative in previous works. In addition, the infrageneric classification and the phylogenetic relationship within the genus are also unclear.

Based on the about 10 years’ successive field collection and examination of about 2700 herbarium specimens, characters such as the length of flowering bracteole, calyx and capsule, the number of stigmas lobes, and the shape of calyx apex, stipules and leaf are evaluated as informative diagnosis.

Phylogenetic analysis was subsequently conducted based on either combined or independent datasets of six chloroplast (\textit{matK}, \textit{rbcL}, \textit{rpl32-trnL}, \textit{rpoB-trnC}, \textit{trnL-trnF}, and \textit{trnS-trnG}) and two nuclear DNA (ITS, ETS) fragments sequenced from 453 individuals of 38 taxa, covering most of the geographical range of the genus in China and Japan.

The integrative analysis of phylogenetic trees and morphological characters, as well as geographical distribution showed that it is reasonable to recognize sixteen species and three species complexes, the *L. scabrida* complex, the *L. pilosa* complex, and the *L. glomerata* complex. *L. yangshuoensis* and *L. vestita*, from karst habitat in the Nanling mountains, occupy a basal position, being sister to all other clades. The *L. scabride* complex is found from South Xizang to Nepal and India. The *L. pilosa* complex and the *L. glomerata* complex occur in the East Himalaya-Hengduan Mountains and have overlap in geographical region, where the biodiversity hotspots and the speciation center is.

The high morphological variation and rich species complex may imply that *Leptodermis* is a young clade and is undergoing species differentiation, but these need for further study on their population genetics, speciation mechanism, and polyploidy diversification.
A comprehensive and meaningful phylogenetic hypothesis for the commercially important coffee genus (*Coffea*) has long been a key objective for coffee researchers. For molecular studies, progress has been limited by low levels of sequence divergence, leading to insufficient topological resolution and statistical support in phylogenetic trees, particularly for the major lineages and for the numerous species occurring in Madagascar. We report here the first almost fully resolved, broadly sampled phylogenetic hypothesis for coffee, the result of combining genotyping-by-sequencing (GBS) technology with a newly developed, lab-based workflow to integrate short read next-generation sequencing for low numbers of additional samples. Despite the fact that there is uncertainty on the likely ancestral locality for the origin of the coffee genus, independent radiations across Africa, Asia, and the Western Indian Ocean Islands (including Madagascar and Mauritius) appear clearly. The evolution of caffeine, an important trait for commerce and society, was evaluated in light of our phylogeny. High and consistent caffeine content is found only in species from the equatorial, fully humid environments of West and Central Africa, possibly as an adaptive response to increased levels of pest predation. Moderate caffeine production, however, evolved at least one additional time recently (between 2 and 4 Mya) in a Madagascan lineage, which suggests that either the biosynthetic pathway was already in place during the early evolutionary history of coffee, or that caffeine synthesis within the genus is subject to convergent evolution, as is also the case for caffeine synthesis in coffee versus tea and chocolate.
Where and when did tropical Rubiaceae migrate towards the temperate zones?

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Although most Rubiaceae species occur in tropical and subtropical regions worldwide, a substantial amount is also present in more temperate areas on the northern and southern hemisphere. Simultaneous to the change in climate preference within certain lineages of the Rubiaceae family, there is also a shift from woody shrubs and trees to a more herbaceous habit. Here, we aim to investigate these adaptations and migrations. Seven cpDNA data sets were used to construct a tree of the Rubiaceae. In this tree, the temperate tribe Rubieae is the terminal clade of the herbaceous lineage (supertribe Rubiidinae) of the Rubioideae. Using Takhtajan’s “Floristic Regions” (slightly adapted), all taxa of the Rubiidinae were chorologically characterized. Apart from Kelloggia, the clades most closely related to Rubieae (Theligonum and the tribe Putorieae) nowadays are centered in the Mediterranean Region. The hypothesis therefore that Rubiaceae migrated towards the Circumboreal Region through a Mediterranean belt is tested by ancestral area reconstruction using BioGeoBears.
ORAL

What is the impact of heterostyly on the diversification of species? A case study within the Rubioideae subfamily

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Heterostyly is a form of reciprocal herkogamy that is frequently linked with self-incompatibility and outbreeding. This genetically controlled floral polymorphism is observed in over 25 angiosperm families. Most of the heterostylyous species currently recognized belong to the Rubiaceae (coffee family) and more specific to the Rubioideae subfamily. Here, we investigate the impact of heterostyly on the evolutionary dynamics within the Rubiaceae family. Using a combined molecular-morphological approach, we inferred the ancestral breeding system, as well as the transition rate from heterostyly to other breeding systems in the coffee family. In addition, we investigated whether habitat shifts and long-distance dispersal events had an effect on the distribution of heterostylos lineages. From our results, it is clear that the most recent common ancestor of both Rubioideae and Rubiaceae was heterostylos and that breeding systems have an effect on diversification patterns within certain lineages of the Rubioideae subfamily. Also, habitat shifts and long-distance dispersal events have an influence on the type of breeding system that occurs in a certain region of the world (temperate vs. tropical, island vs. continent). Although a large range of ecological factors had an impact on the evolutionary dynamics of the coffee family, shifts in breeding system most likely also shaped the current species diversity in Rubiaceae.
ORAL

**The Rubiaceae of Gabon**

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Gabon is situated on the Atlantic coast of Central Africa, and covers around 267,000 km\(^2\), which is about half the size of France. More than 80% of its territory consists of equatorial rainforest, the rest being mostly savanna. It is thus the most forested country in tropical Africa. It has a very rich flora with around 5175 species of vascular plants recorded to date, more than 10% of which are considered endemic; however, the botanical exploration of the country is not yet complete, and these numbers are still increasing. Rubiaceae are the largest plant family in Gabon, with an estimated 640 species in 81 genera; the most diverse of these are *Psychotria* (106 species), *Sabicea* (47 species), *Pavetta* (c. 30 species), *Pauridiantha* (26 species), *Tricalysia* (23 species), *Chassalia* (22 species), and *Chazaliella* (22 species). Many species are still undescribed and new discoveries are regularly made. The talk will present an overview of the diversity of Gabonese Rubiaceae, with a particular focus on recent discoveries and ongoing taxonomic revisions. Around one third of the genera have been treated in volumes 12 and 17 of the *Flore du Gabon*, while for the rest, no recent national treatment is available. The Botanic Garden Meise is currently planning to finalize the *Flore du Gabon* series, and in this context, contributions are welcome.
ORAL

Can phylogeny predict the quantity of alkaloids in plants? A case study in the iconic Yellow Cinchona Bark (Rubiaceae)

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Considerable inter- and intraspecific variation with respect to the quantity and composition of plant natural products exists. The processes that drive this variation remain largely unknown. Understanding which factors determine chemical diversity has the potential to shed light on plant defenses against herbivores and diseases and accelerate drug discovery. For centuries, Cinchona alkaloids were the primary treatment of malaria. Using Cinchona calisaya as a model, we generated genetic profiles of leaf samples from four plastid (trnL-F, matK, rps16, and ndhF) and one nuclear (ITS) DNA regions from 22 C. calisaya stands sampled in the Yungas region of Bolivia. Climatic and soil parameters were characterized and bark samples were analyzed for content of the four major alkaloids using HPLC-UV to explore the utility of evolutionary history (phylogeny) in determining variation within species of these compounds under natural conditions. A significant phylogenetic signal was found for the content of two out of four major Cinchona alkaloids (quinine and cinchonidine) and their total content. Climatic parameters, primarily driven by changing altitude, predicted 20.2% of the overall alkaloid variation, and geographical separation accounted for a further 9.7%. A clade of high alkaloid producing trees was identified that spanned a narrow range of altitudes, from 1,100 to 1,350 m. However, climate expressed by altitude was not a significant driver when accounting for phylogeny, suggesting that the chemical diversity is primarily driven by phylogeny. Comparisons of the relative effects of both environmental and genetic variability in determining plant chemical diversity have scarcely been performed at the genotypic level. In this study, we demonstrate that there is an essential need to do so if the extensive genotypic variation in plant biochemistry is to be fully understood.
Taxonomic revision of *Simira* (Rubiaceae, Condamineeae)

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The taxonomic revision of *Simira* is presented. *Simira* is a Neotropical genus of about 40 species distributed in Central and South America, with two main centers of diversity in Northeastern and Southern Brazil. The revision was accomplished with the study of specimens from numerous herbaria, field studies, and gathering of specimens in several Brazilian localities. After comparative studies, four names were newly reduced to synonymy, and 15 lectotypes were designated. The revision includes a morphological characterization of the genus and infrageneric groups, a dichotomous key for species identification, full synonymy, species descriptions, specimens examined, distribution maps, observations, and illustrations.
Early evolution of Ceropegieae (Apocynaceae-Asclepiadoideae)

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Within the Ceropegieae, the hyperdiverse subtribe Stapeliinae with around 700 often arid-adapted/succulent species attracted most attention in the family. In contrast, the first branching subtribes Anisotominae, Leptadeniinae, and Heterostemminae are much less investigated and poorly understood. Limited species numbers and low abundance of most their species might explain this, although otherwise the diversity of fascinating floral structures can compete with Stapeliinae like Ceropegia or the stapeliads. For phylogenetic reconstruction 34 samples from southern and (north)eastern Africa and Asia for the nuclear internal transcribed spacer (ITS) region, and five plastid markers (trnT-L, trnL-F, and trnH-psbA intergenic spacers, trnL and rps16 introns) were analyzed. The sister-group of Stapeliinae, the Anisotominae, show a strictly African distribution of the ca. 30 species with the tropical liana Neoschumannia in sister-group position to the remaining genera, Anisotoma, Emplectanthus, Riocreuxia, and Sisyranthus. Especially in Sisyranthus and Riocreuxia torulosa s.l., sequence data reveal low genetic variation pointing to an actively radiating and speciating group, possibly in adaptation to pollinator pressure. In Leptadeniinae, sister to the Stapeliinae–Anisotominae clade, the position of the strictly Asian, rheophytic Pentasachme could be resolved as sister to the remaining genera of Leptadeniinae. The position of the South Asian/Australasian wet forest lianas of the genus Heterostemma as sister to the remaining Ceropegieae indicates a humid Asian origin for the Ceropegieae.
Apocynaceae are widely used in traditional medicine around the world due to their rich array of bioactive secondary metabolites, including complex indole alkaloids, steroidal alkaloids, and cardenolides. Although toxic secondary metabolites in plants have arisen as a means of phytochemical protection for the plant against herbivores, in diverse insect groups certain lineages have become adapted to the toxins, which they then use as protection against predators. In a few genera of apocynoids, a fascinating association has evolved between plants containing pyrrolizidine alkaloids (PAs) and certain Lepidoptera. The poisons are ingested by the larvae as they feed on leaves of the host plants, or in a more derived behavior known as pharmacophagy, adult insects imbibe PAs from injured or withered plant parts. Two groups of Lepidoptera – arctiid moths and danaid butterflies – have evolved an even more specialized use of PAs. Males use them as the chemical basis for male-mating pheromones. In Apocynaceae, the largest number of PA-producing genera is found in Echiteae. We did a molecular phylogenetic analysis, including representatives of all subtribes and 17 of the 19 recognized genera. Echiteae and four of its subtribes (Echitinae, Parsonsiiinae, Peltastinae, and Prestoniinae) were shown to be non-monophyletic. The fifth subtribe, Pentalinoninae, though monophyletic, was resolved as sister to a clade of Odontadenieae. Two genera, Fernaldia and Peltastes, were nested within Echites and Macropharynx, respectively, and were synonymized. Fourteen genera were maintained, divided among five subtribes. Species reported to have associations with PA-adapted insects were found in all subtribes except one, for which no data on secondary compounds was available. Since the characteristic secondary metabolites in the closest relatives of Echiteae, Odontadenieae, and Mesechiteae are cardenolides, we hypothesize that an evolutionary shift took place in the ancestors of Echiteae, in which these were replaced by parsonsine type PAs as the predominant defense compounds.
New Caledonia, an isolated flora within a web of Pacific archipelagos: the Gardenieae (Rubiaceae) model

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New Caledonia is a hotspot of biodiversity in the world. Among the most diverse families of plants there, Rubiaceae consists of 30 genera containing 220 species, with a level of endemism of 93%. The tribe Gardenieae is represented by three genera, \textit{Gardenia} (8 species), \textit{Aidia} (2 species), and \textit{Atractocarpus} (10 species). Also, since \textit{Randia} was restricted to the Neotropics, eight New Caledonian species remain unplaced within the tribe. Recent studies for the region on the large genus \textit{Psychotria} led to an interesting pattern of affinities, where the New Caledonian lineage is phylogenetically isolated and geographically surrounded by the \textit{Psychotria} Pacific clade species on the proximate islands. The aim of the present study is first to test the phylogenetic placement of the remaining \textit{Randia} species of the New Caledonian flora in order to find their generic affiliation; and second, to assess the pattern of phylogenetic isolation of the New Caledonian Gardenieae as observed in \textit{Psychotria}. To solve these problems, we investigated c. 40 species of Pacific Gardenieae, with a focus on the \textit{Porterandia} group, in a Bayesian phylogenetic reconstruction based on two chloroplast markers, \textit{trn}T-F and \textit{rpl}32, and the nuclear ribosomal marker ITS. The results of our study provide a supported consensus tree topology. There, five \textit{Gardenia} and the eight \textit{Randia} species merge within a subclade of the \textit{Porterandia} group that comprises the New Caledonian \textit{Atractocarpus} species, rending both \textit{Atractocarpus} and \textit{Gardenia} polyphyletic. This subclade is sister to the other Pacific Islands \textit{Atractocarpus} species, providing evidence for the New Caledonian \textit{Atractocarpus s.l.} lineage isolation in the Pacific Ocean as observed in \textit{Psychotria}. Interestingly, the two New Caledonian endemic \textit{Aidia} species belong to the \textit{Porterandia} group, as sister species to \textit{Tamilnadia uliginosa}, and not to the \textit{Aidia} group of Gardenieae, as further evidence for the New Caledonian flora singularity.
A phylogenetic diversity overview of Rubiaceae in the Greater Antilles based on evidence from the petD intron

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The Caribbean Islands represent one of the ten insular hotspots of biodiversity in the world mainly significant by its level of endemism. In this region, it is estimated that there are 12 300 vascular plant species. This high diversity is related to the complex geological and environmental history of the region, where various tectonic and climatic events have affected species divergence, combined with disjunction, migration and extinction in the region over time. The Rubiaceae family is by far the most diverse in the region (887 taxa of which 856 are native) and it has the highest level of endemism (730 taxa). This family is therefore an excellent model for understanding plant radiation in the area and illustrates the importance of these insular systems for evolutionary and conservation purposes. We performed a petD intron phylogenetic analysis including more than 300 terminals mainly from Cuba and other Caribbean islands to estimate their phylogeny and to review the taxonomic representativeness of Rubiaceae lineages in the Greater Antilles. The current classification of Rubiaceae includes 29 tribes present in the Neotropics of which 24 tribes occur in the Greater Antilles. Of the 24 tribes, 22 have endemic taxa, with 16 of them having endemic species and six endemic genera. The tribe Chiococceae has the largest number of endemic genera (13), followed by Rondeletieae (7) and Spermacoceae (4). At species level, the Rondeletieae tribe has the highest number of endemic taxa (177), followed by Chiococceae (163), Guettardeae (146) and Psychotrieae (119). The phylogenetic framework allows us to estimate dispersal events to the Caribbean islands from the continental area. We conclude that among the insular hotspots, the Caribbean Islands harbor the most significant amount of phylogenetic diversity of Rubiaceae.
ORAL

Historical biogeography of the pantropical Psychotrieae alliance (Rubiaceae) in the Western Indian Ocean Region

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The Western Indian Ocean Region (WIOR) is an insular biodiversity hotspot encompassing Madagascar and the nearby Comoros, Mascarene, and Seychelles archipelagos. The region contains many islands of various sizes and ages with high levels of diversity and endemism of plants and animals. The biodiversity of the WIOR constitutes a mix of species that have been evolving there as a result of vicariance and those that arrived there via dispersals during the Cenozoic, 65 Ma to present.

The Psychotrieae alliance (subfamily Rubioideae) is the most species-rich lineage of the coffee family (Rubiaceae) in the WIOR, with about 300 species currently that are classified in five of its nine tribes (Craterispermeae, Gaertnereae, Morindeae, Palicoureeae, and Psychotrieae). The high level of endemism and wide distribution of the alliance across the WIOR make this group of plants and the region an ideal model and geographic setting, respectively, for investigating the origins of insular biodiversity and dynamics of island colonization. The alliance is distributed pantropically, with the exceptions of some members of the East Asian and North and Central American tribe Mitchelleae. Members of the alliance are ubiquitous components of many terrestrial ecosystems, and typically produce small, fleshy, drupaceous fruits, which are an important resource for numerous frugivorous, tropical birds and mammals. We aim to investigate the origins of the WIOR Psychotrieae alliance and the dynamics (i.e., timing, direction or sequence) of its colonization events within the region.
ORAL

Can ITS and rps16 data be used to delimit species and morphological groups in *Pentagonia* (Rubiaceae)?

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The genus *Pentagonia* (Rubiaceae) occurs from Guatemala to Peru and comprises about 40 species of small to medium sized trees. Interesting morphological features in the genus include calyx shape (five-lobed vs. spathaceous calyx), leaf size (some species have leaves that exceed 2 m in length), and leaf form (entire, lobed and compound leaves are found in the genus). About 60 species have been described in *Pentagonia*, but the genus lacks a revision and several names should most likely be synonymized. Circumscription of the type species, *P. macrophylla*, has been particularly problematic, and there are different views whether this species occurs all the way from Costa Rica to Ecuador, or if it should be considered having a much more restricted distribution. In this project, we present rps16 and ITS phylogenies of *Pentagonia*, we discuss whether there is molecular support for a clade of lobed-leaved species, and we try to use molecular data to solve the circumscription of *P. macrophylla*. 
Mitochondrial genomic data challenge current views of Rubiaceae phylogeny

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Current knowledge on plant phylogeny is often based mostly on data from the chloroplast. Less problems with for example allelic variation and paralogy (compared to using nuclear data), and readily available universal primers for amplification of informative gene regions paved the way for numerous chloroplast-based phylogenetic studies on all groups of plants. The mitochondrion has, in contrast, rarely been used to infer phylogeny of plants, conceivably because of an assumed information poverty and demonstrated lateral transfer of gene regions. Using the species-rich and biologically diverse coffee family as study system, we show that the mitochondrial genome can provide structured and well-supported information on plant phylogeny. Furthermore, some surprising and statistically significant conflicts between results based on mitochondrial data and plastid data emerge, and our study demonstrates with striking clarity that relying solely on plastid data yield biased results that do not provide a complete picture of plant evolution. Among possible biological processes responsible for the conflicting results in Rubiaceae are horizontal transfer of genetic material and ancient hybridization events.
ORAL

**Spermacoce in the Americas: small group, small flowers but great taxonomic problems**

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The genus *Spermacoce* belongs to tribe Spermacoceae s.l. Together with 23 other genera it forms the monophyletic *Spermacoce* clade. Several genera of this *Spermacoce* clade are well supported by molecular data (e.g. *Mitracarpus*, *Richardia*, *Galianthe*), while others are paraphyletic (e.g. *Borreria* and *Spermacoce*). The generic boundaries of *Spermacoce* are problematic and currently strongly discussed. There are two concepts, the most comprehensive one includes other genera (*Borreria* and parts of *Diodia*), whereas the narrow one includes only the type *S. tenuior*, and seven closely related species. Based on our molecular dataset (ITS and ETS), the genus comprises American and Australian species divided into three lineages: *Spermacoce* s.s. (including type species), *S. eryngioides* group (ex B. sect. *Pseudodiodia*), and an Australian group. In the Americas, *Spermacoce* differs from its closest relatives in having small urceolate corolla, lobes internally pilose, stamens and stigma included, and pollen grains with tectate exine, long colpi, and endocingulum. In this continent, as defined above, it comprises 35 species, of which five are new to science. The review, based on over 1900 specimens, provides nomenclatural and taxonomic discussion about the type species, the *S. ocyroides* complex, and the geographic distributions. Species within *Spermacoce* can be distinguished from each other based on calyx lobes/corolla length ratio, internal indumentum of the corolla, morphology of the ventral face of the seeds, exotesta patterns, and pollen characters such as shape, number of colpi, distribution of perforations, and supratectal elements.
Microscopic evidence for vertical transmission of the leaf nodulated endosymbiont in *Psychotria punctata*

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Symbiotic interactions between microorganisms and plants are ubiquitous and crucial for the survival of plants. These mutualistic associations enhance plant fitness by increasing the uptake of nutrients or boosting plant defence, while the endophytes obtain shelter and carbohydrates in return. It is in the plant’s benefit to maintain this positive interaction for the next generations by transferring the beneficial microorganisms to their offspring. Vertical transmission of microorganisms from the mother plant to the next plant generation via the seed is relatively unknown, but interest is growing. Previous research has revealed that seed microbiomes can be fundamental for the germination and growth of seedlings.

In Rubiaceae, several plant species belonging to three genera (*Psychotria*, *Pavetta*, and *Sericanthe*) house a specific bacterial endosymbiont of the genus *Burkholderia* in leaf nodules. In previous research, only one endophytic species was identified in the leaves of a host plant. Due to this specificity, the interaction seems to have an obligatory character, but most of the benefits of the interaction are still unresolved. One of the advantages of the interaction for the host is the production of insecticidal secondary metabolites, which increase the defence of the host plant. To increase the survival chances of the offspring, these endophytes should be transferred vertically to the next generation of plants. This was already hypothesised in previous research due to its specific and obligatory character.

Our research aims to clarify the transfer of the endophyte of *candidatus* Burkholderia kirkii throughout the floral and seed development of *Psychotria punctata* using Fluorescence In Situ Hybridisation. This microscopic technique allows detection of specific endophytes in plant organs and tissues, and is the most suitable approach to elucidate the vertical transmission of the endosymbiont. *In situ* location of the endophytes in the context of floral and seed development is key to a mechanistic understanding of the (obligatory nature of) microbial endosymbiosis in *Psychotria*.
Every plant species on Earth interacts in some way or another with microorganisms and it is well known that certain forms of symbiosis between different organisms can drive evolution. Within some clades of Rubiaceae (coffee family), a specific plant-bacteria interaction exists in which non-pathological endophytes are present in the leaves of their hosts. It is hypothesized that the bacterial endophytes, either alone or by interacting with the host, provide chemical protection against herbivory or pathogens by producing toxic or otherwise advantageous secondary metabolites. If the bacteria indeed have a direct beneficial influence on their hosts, it is reasonable to assume that the endophytes may increase the fitness of their hosts and therefore it is probable that their presence also has an influence on the long-term evolution of the particular plant lineages. In this study, the possible origin in time of non-nodulated bacterial leaf symbiosis in the Vanguerieae tribe of Rubiaceae is elucidated and dissimilarities in evolutionary dynamics between species with endophytes versus species without are investigated. Bacterial leaf symbiosis is shown to have most probably originated in the Late Miocene, a period when the savannah habitat is believed to have expanded on the African continent and herbivore pressure increased. The presence of bacterial leaf endophytes appears to be restricted to Old World lineages so far. Plant lineages with leaf endophytes show a significantly higher speciation rate than plant lineages without endophytes, while there is only a small difference in extinction rate. The transition rate shows that evolving towards having endophytes is twice as fast as evolving towards not having endophytes, suggesting that leaf symbiosis must be beneficial for the host plants. We conclude that the presence of bacterial leaf endophytes may also be an important driver for speciation of host plants.
Different ways to obtain similar results. The development of the corolla and epipetaly in herbaceous Rubioideae (Rubiaceae)

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Rubiaceous flowers are described as having a calyx with basally fused lobes and a tubular corolla with epipetalous stamens. In several tropical Rubiaceae, floral developmental investigations revealed that the corolla is early sympetalous and that a stamen corolla tube develops from an annular primordium. Other species showed late sympetalal with a rudimentary or absent stamen corolla tube and no epipetaly. Payer observed individual petal primordia postgenitally fusing with the filaments in herbaceous European Rubiaeae. A floral cup results with only the distal parts of the filaments free. In this study, we want to test the hypothesis that rubioid tubular corollas result from three developmental processes; 1) the development of a stamen-corolla tube from a common annular primordium, 2) the development of a corolla tube sensu stricto from an annular intercalary meristem, and 3) postgenital fusion of petals or corolla lobes. Following Goethes “Prinzip der variablen Proportionen”, we hypothesize that these processes are differently expressed depending on the species. We investigate the development of the perianth and androecium in herbaceous species within Rubioideae.

In temperate Phuopsis and tropical Richardia, a stamen-corolla tube with epipetalous stamens is formed. In contrast, in Asperula, Galium, and Rubia, the floral cup results from postgenital fusion of initially free petals and filaments, as also reported by Payer.

In Phuopsis, the stamens are inserted half-way in the corolla tube because of the development of a corolla tube sensu stricto, which is absent or rudimentary in Richardia. The development in these two species concurs with our hypothesis, but in Asperula, Galium and Rubia a stamen-corolla tube and corolla tube sensu stricto are absent and the floral cup results from postgenital fusion between filaments and petals. Consequently, the tube is a compound structure, composed from two different whorls with pseudo-epipetaly.
ORAL

Conflicting phylogenies for Rubiaceae revealed by chloroplast phylogenomic data

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Reconstruction of phylogenetic relationships of Rubiaceae have until recently heavily relied on single or multi-gene data, primarily from the plastid compartment. With the availability of cost- and time-efficient techniques for generating complete genome sequences, the opportunity arises to resolve some of the relationships that up until now have proven problematic. Here we contribute new data from 60 complete chloroplast genome sequences representing 55 of the currently 65 recognized tribes of the Rubiaceae. Phylogenetic analyses are conducted on a 77-gene data set including 70,557 aligned characters. Our results clearly show that simply adding more data does not provide the universal solution to resolve problematic relationships in the Rubiaceae. The standard and commonly adopted approach of analyzing the data at the nucleotide level yields a number of well supported relationships that conflict with those obtained if analyzing the data at the amino acid level. The alternative relationships obtained are discussed in relation to those previously proposed, and possible explanations for the demonstrated conflicts are offered following a series of analyses using modified data sets.
**Safeguarding the wild gene pools of Arabica and Robusta coffee: coffee genomic research in the region of Flanders**

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Did you count the number of coffee cups that you came across today? With a global consumption of over two billion cups per day, coffee is omnipresent in our lives. This popularity contrasts sharply with the current lack of knowledge about several aspects of coffee, including the integrity of the Arabica and Robusta wild gene pool. To address these knowledge gaps, several institutes in Flanders have committed themselves to conduct research that focusses on the conservation of wild Arabica and Robusta coffee genetic resources.

Being one of the most important agronomic commodities worldwide, Arabica coffee occupies an eminent position on the global market. The source species of Arabica coffee (i.e. \textit{Coffea arabica}) occurs naturally in the Afromontane moist forests of southwestern Ethiopia. Preliminary analyses have shown the exchange of alleles between wild coffee shrubs and introduced cultivars co-occurring in the Ethiopian forest landscape. Our current research focusses on a more precise quantification of introgression patterns in \textit{C. arabica} populations, not only at neutral genetic loci, but also at genes involved in disease resistance and cup quality, along a gradient of forest management intensification in Ethiopia. \textit{Coffea} also comprises a second species of major agronomic importance: \textit{Coffea canephora}, used for the production of Robusta coffee. \textit{C. canephora} has a wide geographic range that spans several Central and East African countries. However, the Congo basin has been marked as a centre of diversity for \textit{C. canephora} and as the origin of many cultivated genotypes. A second project therefore focusses on the genetic interplay between natural populations and cultivars of \textit{C. canephora} in Yangambi (D.R. Congo). This way, both projects study the integrity of the wild gene pools of coffee and how this integrity is influenced by adjacent cultivated coffee plants.
Phylogeny and revision of *Psyllocarpus* Mart. ex Mart. & Zucc. (Rubiaceae, Spermacoceae), an endemic genus from Brazil

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*Psyllocarpus* belongs to the *Spermacoce* clade within Spermacoceae, being considered one of the morphologically well-defined genera in the tribe and preliminarily supported in phylogenetic studies. It was recovered as monophyletic with maximum support in an analysis based on two species and two nuclear regions, sister to a clade of *Spermacoce* species. In the last taxonomic revision of the genus, it was classified in two sections, based on morphology and geographic distribution. *Psyllocarpus* sect. *Psyllocarpus* is characterized by terete leaves, homostylos flowers, prolate-spheroidal pollen grains, non-perforated and spinulose along each side of the colpi exine, and bilobate stigma. This section occurs in the “cerrado” and “campos rupestres” from the Espinhaço range and the Planalto Central of Brazil, comprising five species. *Psyllocarpus* sect. *Amazonica* also presents capsules strongly compressed parallel to the septum but is characterized by planar leaves, heterostylos flowers, oblate-spheroidal pollen grains, perforated, finely and evenly spinulose exine, and bifid stigma, being restricted to white-sand Amazonian “campinas”, comprising three species. More recently, two species from the Espinhaço range were described but not classified in any section. The objectives of this study are to produce a taxonomic revision of *Psyllocarpus* and to infer its phylogeny. We consulted 28 herbaria, accounting for ca. 1500 specimens analysed. Field expeditions were carried out to collect fresh samples for the molecular study. We estimated a phylogeny based on two plastid regions (*rps16* and *trnL-F*) and nine species using Bayesian inference. We discovered four new species, which are being described. Notably, *P. laricoides* is a species complex. *Psyllocarpus* sect. *Psyllocarpus* was supported as monophyletic with maximum support. *Psyllocarpus densifolius* is not related to the other species of the genus and formed a long branch. We still need to produce sequences from nuclear regions and include the missing species in our analysis.
Towards a phylogeny of *Ladenbergia* (Rubiaceae: Cinchoneae): a preliminary hypothesis based on nuclear and chloroplast DNA sequences

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The neotropical Rubiaceae genus *Ladenbergia* Klotzsch belongs to the tribe Cinchoneae and includes ca. 35 species. Its species occur mostly in South America, with a few reaching Central America. *Ladenbergia* is centered in the Tropical Andes and is closely allied to *Remijia* due to morphological similarities. Previous phylogenetic studies in Rubiaceae suggest the monophyly of *Ladenbergia* but based on reduced sampling of species of the genus. In this study, we infer the phylogenetic intraspecific relationships of *Ladenbergia* based on sequences from nuclear (ITS) and chloroplast (*rps16* introns and *trnL-trnF* intergenic spacer) regions of 18 species of *Ladenbergia* and allied genera. Our preliminary results corroborate the monophyly of *Ladenbergia* and its sister relationship to *Remijia*. Two main clades and five subclades within *Ladenbergia* are well supported. The Andean species are paraphyletic and provide no support for previously proposed classifications. This work is an important step in elucidating relationship of *Ladenbergia* and it contributes to the understanding of the phylogenetic relationships within Cinchoneae.
**Divo, a new LTR-retrotransposons family in coffee genomes**

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LTR-retrotransposons (LTR-RTs) are omnipresent components of plant genomes. Numerous lineages and families have been described leading to a well-established classification of elements. This profusion of LTR-RTs sequences and structures were enriched with the recent discovery of non-autonomous element structures, such as LARDS, TRIM, and TR-GAG. With the availability bioinformatics tools dedicated to the LTR-RTs identification and analysis, it became reasonable to performed annotation of such transposable elements at whole-genome scale. Here, during the process of coffee genomes annotation, we described a novel family of *Copia* LTR-RT called *Divo*, belonging to the *Bianca* lineage. *Divo* are complete and relatively short elements (~5kb) carrying typical GAG and Pol *Copia* domains. However, Reverse Transcriptase (RT) and Integrase (INT) domain-based phylogenetic analysis demonstrated that *Divo*, with *Bianca* family, forms a new and well-supported group within the branch 2 of *Copia* LTR-RTs, but outside other *Copia* lineages in plants. So far, *Divo* was only found in plant genomes. In coffee trees, as well as in *Arabidopsis* and grapevine, *Divo* was present in relatively low copy numbers, but in coffee, the presence of recently inserted and complete copies and the detection of RNAseq transcription suggest that *Divo* might be active. It also could present a different evolution between *C. arabica*, the only allotetraploid genome, and its two diploid progenitors, *C. canephora* and *C. eugeniodes*. Altogether our results indicated that *Divo* is a novel *Copia* LTR-RTs family, ubiquitous in plant genomes and can highlight evolutionary events in coffee genomes.
**POSTER**

**Biogeographical patterns of genus *Galianthe* (Rubiaceae: Spermacoceae)**

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*Galianthe* is exclusive to the Neotropical region and consists of 50 species divided into two subgenera: *Galianthe*, with 39 South American species, and *Ebelia* with 11 species in Mesoamerica and South America. The aims were to establish the distribution patterns of *Galianthe* species by track analysis, and to evaluate their current distribution based on the available tectonic information and the biogeographical regionalization of the Neotropical region. A total of (±)1400 geographical records of 53 species from 57 herbaria were analysed, representing 100% of the species assigned to *Galianthe*. Individual tracks were obtained for each species by plotting localities and connecting them by minimum-spanning trees. Generalized tracks and nodes were determined from the spatial overlap among individual tracks. Individual and generalized tracks, and nodes were geographically located using DIVA-GIS. Generalized tracks and nodes were superimposed on two maps, one of them with the biogeographical provinces of the Neotropical region, and the other with the distribution of Neotropical seasonally dry forests. Five generalized tracks and four nodes were identified, all located within the Brazilian and Chacoan subregions. These nodes coincide with almost all fragments of Neotropical seasonally dry forests. The origin of the *Spermacoce* clade, where *Galianthe* belongs, was dated for the Miocene. The early dispersal of the species, along with the several vicariant events such as the rise of the Andes, the cooling and aridification during the Oligocene-Miocene, the formation of the Chacoan subregion, and the alluvial dynamics during the Pliocene-Holocene favoured the adaptive radiation of *Galianthe* species. In the same way, the intimate coincidence of the ancestral biota of *Galianthe* with the fragments of Neotropical seasonally dry forests allow us to hypothesize that those remnants of forests could serve as refugia during unfavourable geologic periods, and hence, influencing actively in the current distribution of their species.
Species delimitation in the complex *Tabernaemontana catharinensis* – *T. laeta* – *T. hystrix* (Apocynaceae, Rauvolfioideae) based on an integrative approach

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*Tabernaemontana* is a large pantropical genus of tribe Tabernaemontaneae, subfamily Rauvolfioideae, with about 120 species. The tribe has been the target of a broad phylogenetic study in 2010, in which its placement within Apocynaceae and the relationships among its constituent genera has been elucidated. Nevertheless, little is known about interspecific relationships and species delimitation within the genus. In this context, our study is the first attempt to test hypotheses on species recognition and circumscription based on an integrative approach. For that, we selected three species from *Tabernaemontana* section *Peschiera* that are morphologically alike and with areas of coincident geographical distribution (*T. catharinensis* – *T. laeta* – *T. hystrix*). We aim to integrate molecular and morphological data from plastid and nuclear DNA, and morphometrical analyses of vegetative and reproductive organs. So far, we have obtained sequences for one plastid marker (*trnS-G intergenic spacer*) for 29 taxa, and two nuclear markers (ITS1 and ITS2) for 19 taxa. In all analyzed datasets, the monophyly of *Tabernaemontana* section *Peschiera* has been strongly supported, but relationships among the *T. catharinensis* – *T. laeta* – *T. hystrix* complex are moderate to poorly resolved and sometimes incongruent. In the plastid phylogeny, the sampled specimens of *T. catharinensis* form a putative monophyletic assemblage that groups with two other species of section *Peschiera*, *T. solanifolia*, and *T. linkii*. The nuclear phylogeny, on the other hand, *T. catharinensis* and *T. hystrix* form two putative assemblages more closely related to *T. linkii* than to the other species of the section. For the morphological approach, leaves and flower buds of specimens of *T. catharinensis*, *T. laeta*, and *T. hystrix* have been measured and landmarks were added to do a geometrical morphometric analysis. Preliminary observations suggest that the sampled specimens of *T. catharinensis* form two distinct morphological groups, but more data is needed to verify this hypothesis.
Leaf anatomy of *Carajasia*, a monotypic Rubiaceae genus from “canga” vegetation on the Carajás Mountains of Brazil

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In 2015, Salas et al. described *Carajasia cangae* R.M. Salas, E.L. Cabral & Dessein, which belongs to the tribe Spermacoceae. The only habitat where this species was found is on top of iron outcrop mountains or “canga” vegetation, described as patches of saxicolous scrubs with a marked tendency to dwarfism. In order to analyze this new species in depth, the anatomy of its leaves was studied, using optical microscopy and scanning electron microscopy. Leaves are simple, patent, sessile, and spatulate with entire margins. The blade is slightly succulent, glabrous, 1.8–1.95 × 0.45–0.7 cm, narrowly ovate, attenuate at the base, acuminate at the apex. Adaxial epidermis of *C. cangae* is composed by unspecialized epidermal cells with thin walls, and straight to smoothly curved contours. Leaves are epistomatics and possess anisocytic stomata. Adaxial epidermis presents enormous idioblasts with solitary and veriform cystoliths (240 x 11 μm). The mesophyll is dorsiventral, palisade parenchyma is interrupted by substomatal chambers. A single-layered and tanniniferous hypodermis lies between the compact spongy parenchyma and the abaxial epidermis; this layer extends horizontally between vascular bundles as a paraveinal mesophyll. Abaxial epidermis is single layer occupying 50% of the thickness of the lamina, is formed by giant colorless cells, and may be aquiferous. Near the blade border there are 6-8 hydathodes per leaf. The environment of the “canga” combines high temperatures and UV radiation, which together with strong winds imply a rapid loss of water by transpiration; this combination of characteristics forces the plants to a strong adaptation. *Carajasia* possess a number of peculiar anatomical features and, perhaps more intriguingly, a combination of mesomorphic with xeromorphic leaf blades.
Litter-collecting Rubiaceae in tropical Africa

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Litter-collecting plants have the unusual ability to accumulate litter falling from the canopy, and feed on the nutrients resulting from its decomposition. This adaptation is well-documented in epiphytes (particularly ferns and Araceae). However, it has been much less studied in terrestrial species: these are usually treelets with a single stem bearing a rosette of large spatulate leaves at the apex, and show a remarkable similarity of habit even if belonging to very distant families. In Africa, around 70 species of litter-collecting treelets have been recorded in 14 families; almost two thirds of them belong to Rubiaceae, where the litter-collecting habit has arisen in no less than eight genera (\textit{Bertiera}, \textit{Chassalia}, \textit{Chazaliella}, \textit{Coffea}, \textit{Ixora}, \textit{Oxyanthus}, \textit{Pavetta} and \textit{Psychotria}, the latter alone including 30 species). Litter-collecting plants are especially sensitive to drought, and are only found in the undergrowth of very wet rainforests; they are often gregarious and locally dominant in such habitats. The other factors influencing the evolution of litter collecting in plants are unclear, but it may be an adaptation to nutrient-poor soils.
Phylogeny of Coussareeae (Rubioideae, Rubiaceae)

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Coussareeae (Rubioideae, Rubiaceae) are a Neotropical tribe comprising approximately 400 species assigned to eight genera: Coussarea (120 spp.), Coccocypselum (20 spp.), Cruckshanksia (7 spp.), Declieuxia (29 spp.), Faramea (211 spp.), Heterophyllaea (3 spp.), Hindsia (11 spp.), and Oreopolus (1 sp.).

Both vegetative and reproductive morphology in the tribe is diverse: herbs (often creeping), subshrubs, shrubs, and trees are all represented and flowers can be homo- or heterostylos and white, blue, or bright yellow. There is also a wide range of fruit types in the tribe, with schizocarps, white or blue berries, and thin- or thick-walled capsules all represented.

With the members of the tribe displaying such high level of morphological diversity it is hardly surprising that the eight genera were formally assigned to several distantly related tribes in pre-molecular classifications of Rubiaceae, with Coussareeae comprising solely Coussarea and Faramea.

In more recent classifications, based on molecular phylogenetic studies, a broadly delimited Coussareeae including all eight accepted genera have been consistently recovered as a natural group and early-diverging lineage in Rubioideae. However, Coussareeae was never the focus of molecular phylogenetic study and consequently the generic limits and relationships within the tribe are not yet fully understood.

This study aims to assess the generic limits and relationships within Coussareeae, utilizing a dense taxon sampling to produce a robust phylogeny; with an established and well-supported phylogeny in place, the aim is to investigate the evolutionary patterns of, e.g., fruit type and heterostyly.
POSTER

The monotypic Brazilian genus *Diacrodon* is a synonym of *Borreria* (Spermacoeae, Rubiaceae): morphological and molecular evidence

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*Diacrodon* is a monotypic genus of the tribe Spermacoeae (Rubiaceae), which is endemic to Brazil. The name of the only species, *Diacrodon compressus*, refers to the strongly compressed, one seeded and indehiscent fruit. This fruit type was considered enough to describe *Diacrodon* as a different genus in the tribe Spermacoeae, but its author Sprague recognized the similarity with *Borreria verticillata*. In the present study, we discuss and illustrate the morphology of flowers, fruits, seeds, and pollen grains of *Diacrodon* and the two most similar species of *Borreria*. Morphological comparisons revealed that *Diacrodon compressus* is not significantly different from *Borreria verticillata* and *B. spinosa*. Additionally, a molecular phylogenetic study was made, using ITS and ETS, to determine the position of *Diacrodon* in respect to other genera of Spermacoeae tribe. *Diacrodon compressus* appears strongly related to another species of *Borreria*. Therefore, *D. compressus* is considered as a new synonym of *Borreria*. The new combination *Borreria diacrodonta* is made and a lectotype is designated. In addition, a detailed description of the species is given with illustrations, a distribution map, and the conservation status.
A phylogenetic study of the African genus *Schumanniophyton* (Rubiaceae): revealing cryptic diversity

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*Schumanniophyton* is an emblematic genus of Gardenieae (Rubiaceae) that occurs in Western Africa. The genus is well known for a very special architecture with a main stem bearing only apical lateral stems, leaves seemingly arranged per three, and buds protecting a dense terminal inflorescence. From recent phylogenetic data, *Schumanniophyton* appears basal in Gardenieae and is isolated in its own lineage with important genetic drift. Nowadays, three species are placed within this genus, *S. magnificum*, *S. hirsutum*, and *S. problematicum*. The former species is divided into three infra-specific taxa with *S. magnificum* var. *magnificum*, *S. magnificum* var. *trimerum*, and *S. magnificum* var. *klaineanum*, previously considered as separate species. So far, only *S. magnificum* var. *magnificum* has been included in phylogenetic reconstructions, so that the monophyly of the genus has never been tested neither the delimitation of the infra-specific taxa within *S. magnificum*. The present study aims at assessing the monophyly of the genus and the circumscription of species within the genus. A sampling of six specimens from *S. magnificum*, two per variety, one specimen of *S. hirsutum*, and three of *S. problematicum* were sequenced for the nr-ITS and the cp-atpB-rbcL markers, associated with a dedicated outgroup sampling. Morphological data were also collected to infer a comparative table for taxa. The results provide evidence for the monophyly of the genus as the three species representatives form a well-supported clade. Within the genus, *S. hirsutum* and *S. problematicum* are sister species and the three varieties of *S. magnificum* form a supported grade at the base of the clade. Consequently, *S. magnificum* does not form a natural lineage and the three varieties should be recognized at species level, revealing two cryptic species within the genus. Morphology supports the recognition of five species within *Schumanniophyton* as morphological character combinations allow their diagnoses.
Development of pollen and anatomy of the mature anther in Argentinian species of the three subfamilies of Rubiaceae

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Rubiaceae is a cosmopolitan family that includes about 1300 species distributed in three subfamilies: Cinchonoideae, Ixoroideae, and Rubioideae. The microsporogenesis, microgametogenesis, and the structure of the mature anther were described in Argentinian species of the three subfamilies for comparative purposes. The study includes two perfect species: Cephalanthus glabratus (Cinchonoideae) and Oldenlandia salzmannii (Rubioideae) and a structurally perfect but functionally imperfect species: Randia ferox (Ixoroideae). We followed conventional techniques of optic microscopy. In the two perfect species and in the functionally staminate flowers of Randia the development of the pollen follows a normal pattern: the meiosis of the microspore mother cells originates tetrahedral and decussate tetrads. In C. glabratus and O. salzmannii, tetrads are separated in free microspores and the pollen is released in monads, while in Randia the pollen in permanent tetrads. The perfect flowers of Cephalanthus and Oldenlandia, and the staminate flowers of Randia present the anther wall only with remains of exothecium and endothecium with fibrous thickenings and show a normal dehiscence; the pollen grains are dispersed in bicellular state. In the functionally pistillate flowers of Randia, the microspore mother cells collapse and there is a progressive deterioration of the parietal strata and tapetum; the mature anther is only constituted by exothecium and endothecium without thickenings, and there is not pollen grain development. This work is a contribution to studies of reproductive anatomy, which are currently performed in Argentinian Rubiaceae species.
Pollen development and orbicule and pollen grain morphology in species of *Cephalanthus* (Rubiaceae-Naucleeae) from the Americas

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This paper is the first embryological report on the genus *Cephalanthus* L. and contributes to future studies in other genera of the tribe Naucleeae. The development of the anther wall in *Cephalanthus glabratus* (Spreng.) K. Schum. corresponds to the dicot type and microsporogenesis is simultaneous. The young wall of the anther has four layers; epidermis, endothecium, one middle layer and the secretory tapetum. The tissue of the septum has idioblasts with crystalline sand. In the wall of the mature anther, only the endothecium and remnants of epidermal cells were preserved. The occurrence and morphology of orbicules were observed in the mature anthers of all three species of *Cephalanthus* with scanning electron microscopy. The orbicules have taxonomic value at species level, since these structures allow us to distinguish between the species analyzed. The presence of a protruding oncus was observed for the first time in *Cephalanthus* in non-acetolysed pollen grains. According to our observations, this structure is not affected by the state of anther dehiscence in *C. glabratus*, because the oncus is visible and prominent in the mature pollen grains in both indehiscent and dehiscent anthers. Several authors have described that pollen grains in the Naucleeae tribe are always released in monads, we find permanent tetrads in *C. glabratus* and monads, but in a smaller proportion. This finding represents the first record for this species and the Naucleeae tribe.
Updating the genus *Elaeagia* (Rubiaceae) and its infrageneric relationships

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Rubiaceae is the 4\(^{th}\) largest family of flowering plants and includes many well-known species, several of which are used as medicine or food (e.g. quinine from *Cinchona* and coffee from *Coffea*). It is a cosmopolitan family with most of the genera and species occurring in humid tropical regions. The genus *Elaeagia* is notable for its unusually well-developed stipules and copious resin, along with its unusual intrapetiolar stipules. Molecular studies have found that *Elaeagia* belongs to the subfamily Ixoroideae in the tribe Condamineeae. In previous studies, *Elaeagia* appears to be polyphyletic with low phylogenetic support. In this study, two chloroplast DNA regions (*trnL-F* and *rps16*) and the nuclear ITS regions were analysed using Maximum Likelihood. Improved resolution of the genus was obtained compared to previous studies. *Elaeagia* is now well supported as a monophyletic group (BS=81), although the resolution of species is not clear yet and future work should include a larger number of taxa and more DNA information to resolve species concepts and relationships within the genus.
New insights into the Spermacoceae alliance phylogeny

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The Spermacoceae alliance of subfamily Rubioideae (Rubiaceae) is a group of about 3000 species currently classified in 12 tribes: Anthospermeae, Argostemmateae, Danaideae, Dunnieae, Foonchewieae, Cyanoneuroneae, Knoxieae, Paederieae, Putorieae, Rubieae, Spermacoceae, and Theligonieae. Most species in the group are herbaceous, but woody species are not uncommon. Flowers are either unisexual or hermaphroditic and their fruits are either fleshy or dry. Two tribes (Anthospermeae and Theligonieae) are unusual in that the species of those lineages have anemophilous flowers in a family otherwise characterized by having predominately zoophilous flowers. Six of the 12 tribes of the Spermacoceae alliance (Anthospermeae, Danaideae, Knoxieae, Paederieae, Rubieae, and Spermacoceae) are found in Madagascar, suggesting multiple colonization events of this group to the island. A backbone phylogeny of the Spermacoceae alliance was presented some years ago but since then, two new tribes (Foonchewieae and Cyanoneuroneae) have been described. Furthermore, the phylogenetic position of certain taxa has varied between studies. The aim of the present project is to reveal new insights into the generic limits and evolutionary relationships within the Spermacoceae alliance, and provide a basis for further studies of morphological evolution and diversification dynamics in the group. Preliminary results will be presented.
The Cinchona genome project – Testing traditional plant knowledge with phylogenomics

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Humans have explored the natural resources around them for tens of thousands of years, but how successful have they actually been in finding the best medicines? In this Swedish-Danish collaborative project we apply state-of-the-art phylogenomic tools to test a case of traditional plant knowledge. We focus on quinine, the medicine that has saved more lives than any other remedy in human history by being the only effective medicine against malaria for centuries. Quinine and related alkaloids are produced by species in the plant group Cinchoneae in the coffee family Rubiaceae. Considering this group’s high diversity (comprising over 120 related species) and wide distribution (spanning the American tropics), we initially deemed it extremely unlikely that indigenous populations with no formal botanical knowledge and only based on try-and-error would have located the species with the highest concentration of quinine. Contrary to these expectations, our preliminary results show that Native Americans were indeed able to find the very best quinine-producing species: Cinchona calisaya – a traditional knowledge that was made into a multimillion-dollar industry by colonial powers. In order to validate these first results, however, we need to increase phylogenetic resolution among the relative species in the tribe. In this project we will sequence, de novo, the genome of Cinchona calisaya, sequence four transcriptomes, and capture a large number of nuclear and plastid genes for c. 80 specimens. These data will be used to produce a highly resolved phylogenetic tree for tribe Cinchoneae, and allow us to map malaria-effective alkaloids in all clades, species and populations sampled. This project aims to revisit and settle one of the most compelling stories in the use of traditional plant knowledge.
Poster

Novelties related to the “Rondeletia complex”: resolving a taxonomic muddle

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The traditional “Rondeletia complex” (Rondeletieae) is a Neotropical artificial group that comprises approximately 250 species classified in 14 genera. Uncertainties persist in the generic circumscription and placement of some genera morphologically related to Rondeletia; some authors argue that the morphological heterogeneity of Rondeletia sensu lato should lead to the segregation of many genera, while other authors reject the splitting of Rondeletia until more evidence is available. Molecular studies are in strong overall agreement in the polyphyly of the “Rondeletia complex”: some genera are closely related to Rondeletia, while others should be placed within Guettardeae. Based on a molecular phylogenetic analysis, a morphological survey (with characters such as inflorescence position, corolla throat ornamentation, fruit type and dehiscence) and extensive field work, we produce a revised taxonomy corresponding to monophyletic groups that have morphological support. Within Guettardeae, a broad circumscription of the genus Gonzalagunia is adopted including the species formerly placed in Arachnothryx, Javorkaea, and Renistipula; the morphologically complex species related to A. buddleioides is resolved. Within Rondeletieae, a new genus Tainia was described, closely related to Acrosynanthus and Rondeletia; the genera Donnellyanthus and Rovaeanthus are accepted and moved to this tribe (the current classification considers them as synonyms of Arachnothryx and Rogiera, respectively, both in Guettardeae). We provisionally maintain the current generic status of Rondeletia and closely allied genera (Mazaea, Phyllomelia, Rachicallis, and Roigella), broader taxon sampling in this part of the phylogeny is necessary before generic circumscriptions are changed.
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