

**15 & 16 September 2022**  
**University of Basel, Switzerland**  
**Main building, room 120, Petersplatz 1, Basel**

**International Symposium  
in Honour of Caspar Bauhin (1560–1624)**

**400 Years Botanical Collections  
Implications for Present-Day Research**

**Inspiring and showcasing herbarium-based  
scientific research, and celebrating 400 years  
since Bauhin's pioneering Flora of Basel**

**Organizers**  
Herbaria Basel, Dept Environmental Sciences, University of Basel  
Basel Botanical Society

**Bauhin2022.ch**



University  
of Basel

Departement  
Umweltwissenschaften  
U|W

Basler  
Botanische Gesellschaft  
botges.ch



# Table of content

- 2 Introduction to the conference
- 3 Caspar Bauhin – Life, academic career, and achievements as a botanist
- 6 Symposium program
- 10 Keynote talks
- 12 Talks (abstracts in alphabetical order by presenting author)
- 35 Posters (abstracts in alphabetical order by last name)
- 52 List of participants
- 56 Impressum/Imprint
- 57 Map of conference locations

## The organizers gratefully acknowledge the support and donations received

Stiftung zur Förderung der Pflanzenkenntnis  
Basler Botanische Gesellschaft  
Freiwillige Akademische Gesellschaft Basel  
Schweizerische Botanische Gesellschaft  
Departement Umweltwissenschaften der Universität Basel



botges.ch  
Basler Botanische  
Gesellschaft BBG



Freiwillige Akademische  
Gesellschaft Basel  
seit 1835



Schweizerische  
Botanische Gesellschaft

Société Botanique  
Suisse

D | Departement  
U | Umweltwissenschaften  
W

# 400 Years Botanical Collections – Implications for Present-day Research

## International Symposium in Honour of Caspar Bauhin (1560–1624)

15 & 16 September 2022, University of Basel, Switzerland

Inspiring and show-casing herbarium-based scientific research, and celebrating 400 years of Caspar Bauhin's pioneering Flora of Basel

### Scientific Committee

**Tinde van Andel**, Clusius Professor History of botany and gardens, Leiden University and Naturalis, NL | **Freek T. Bakker**, Professor of Molecular Systematics, Wageningen University, NL | **Mark Carine** PhD, Principal Curator in Charge, Botanical Collections, Natural History Museum London, UK | **Stefan Eggenberg** PhD, Head National Data and Information Center on the Swiss Flora (InfoFlora), Bern | **Jason Grant**, Professor of Biology and Director of the Herbarium, University of Neuchatel | **Flavio Häner** PhD, Historian of Science and Collections, Cultural Property Protection Expert, Basel | **Ansgar Kahmen**, Professor of Botany, Director Botanical Garden and Herbarium, University of Basel | **Gudrun Kadereit**, Professor of Systematics, Biodiversity and Evolution of Plants, Head Botanical Garden and Herbarium, University of München, DE | **Austin Mast**, Professor of Biology and Director of the Godfrey Herbarium, Florida State University Tallahassee, USA | **Reto Nyffeler** PhD, Curator of Phanerogams, University of Zurich | **Richard B. Primack**, Professor of Biology, Boston University, USA | **Michelle Price**, Professor of Plant Systematics and Biodiversity, University of Geneva; Head of Science and Head of the Cryptogamic Herbarium, Conservatory and Botanical Garden of Geneva, Vice-Chair of the Consortium of European Taxonomic Facilities (CETAF) | **Verena Schünemann**, Professor of Paleogenetics, University of Zurich & University of Vienna | **Yvonne Willi**, Professor of Ecology, University of Basel

### Organizing Committee

**Jurriaan M. de Vos** PhD, Curator Herbaria Basel and Botanical Garden, University of Basel  
**Jürg Stöcklin**, Professor emeritus of Botany, President of the Basel Botanical Society  
**Sylvia Martinez** MSc, Dept of Environmental Science – Botany, University of Basel

### Organizers

Herbaria Basel, Department of Environmental Sciences – Botany, University of Basel  
Basel Botanical Society, Basel, Switzerland

<https://bauhin2022.ch>

<https://herbarium.unibas.ch/de/bauhin2022/>



## What lies behind and what lies ahead – Introduction to the conference

The year 2022 marks the four hundredth anniversary of Caspar Bauhin's renowned regional flora of Basel (*Catalogus Plantarum circa Basileam sponte nascentium*): time to take stock of four centuries of herbarium-based research, and to look ahead. Bauhin's *Catalogus* (in those times, the word Flora was restricted to mythology!) arose as a spin-off product of Bauhin's lifelong effort to assemble a herbarium that reflected the entire known diversity of plants, in order to name them unambiguously and to end the systematic confusion among different authors. He taught his medical students on the "virtues" of plants and encouraged them to get to know them in their native habitat around Basel, so he indicated which plant grew where. His primary work, however, was of much larger scope: his herbarium reflected the order of his *Pinax Theatri Botanici* (1623), an index of all known plant species that he planned to monograph in *Theatri Botanici*, of which only one part was published (posthumously in 1658). The *Pinax* formed an important pillar for Linnaeus' *Species Plantarum* (1753). Thus, Caspar Bauhin's herbarium provided key contributions to the birth of modern plant nomenclature. Read more about his work as a botanist in the next pages and more extensively on the conference website.

Early botanists in Basel and elsewhere may have never realized the lasting value of their herbaria, much beyond their original scope. Crucially, the permanent preservation of accurately labeled plants not only enables the research of the present, but also secures inference that transcends generations. In our time of climate change and radically altered land use, long time-series of specimens provide direct evidence of how the world changes. **Richard Primack's** keynote address on symposium day 1 centers around this theme and echoes throughout the conference.

The revolutionary progress in botany in Bauhin's time was preceded by the technological innovation of pressing plants between sheets of paper. Today, we also live in a pivotal time with technological innovations revolutionizing herbarium-based research. First, with dedicated clean labs and advances in DNA sequencing techniques,

it is now possible to sequence large portions of ancient genomes. **Hernán Burbano's** keynote on day 2 highlights important progress, with several talks employing these methods later that day.

The second groundbreaking innovation is that of the digital specimen. Specifically, digital representations of specimens in appropriately structured databases allow to consult and query specimens in ways and magnitudes unthinkable just a few years ago. The afternoon of day 1 focuses on inspiring progress from globally leading herbaria and remarkable historic collections. Also, remember that specimen selection for many molecularly-oriented case studies, presented later, would not be feasible without digital specimens! These new uses of herbaria complement their original taxonomic, systematic, and biogeographic uses, which remain ever important. Finally, the form of herbaria is intimately associated with its use, enabling important cultural-historic research to better understand how we – as humans, as teachers, as scientists – perceive the world. The relevance of herbaria thus keeps expanding.

I am sure no participant doubts the importance of herbaria. But we might have different views on why they are important: be it as a source of aDNA, a record of past plant distribution, a plant identification tool, a preserved physiological state, protected cultural heritage, or a document on the scientific process itself, to name a few. Hence, the overarching goal of this conference is to bring us all together – physically, in one room – to let new synergies arise and to stimulate further herbarium-based endeavors. And consequently, this symposium is also a call to continue collecting herbarium specimens to document current diversity for future comparison.

*Jurriaan M. de Vos*  
on behalf of the organizers

## Caspar Bauhin (1560–1624) – Life, academic career, and achievements as a botanist

### Biographical data and origin

Caspar Bauhin was born on January 15, 1560 in Basel, where he died on December 5, 1624 at the age of 64. He originated from a distinguished Protestant family from Picardy (France), whose members held high offices in Paris. His father Johann Bauhin (1511–1582) fled the political persecution of the Huguenots and arrived in Basel in 1543, where he practiced as a wound surgeon and became a naturalised citizen. As a medical doctor, Caspar Bauhin's father showed great interest in medicinal plants and even maintained a small, private botanical garden. Caspar Bauhin was the seventh and youngest child and the second son of the Bauhin couple. His brother Johann Bauhin (1541–1613), who was almost 20 years older, became a city doctor in Lyon (France) and also made a name for himself as a botanist.

### Education and academic career

In 1575, Caspar Bauhin enrolled at the medical faculty of the University of Basel. He studied medicine under Felix Platter (1536–1614) and Theodor Zwinger (1533–1588). In 1577 Caspar Bauhin went to Padua (to Jacobus Antonius Corrusius), to Bologna (to Ulisse Aldrovandi), Montpellier and Paris (among others to Jean Robin) for medical and botanical studies. In 1580 he returned to Basel, and visited Tübingen the same year. In February 1581 he publicly dissected a corpse for five days, passed his doctoral examination in April and then held his disputation. Since he demonstrated exceptional didactic skills also in a botanical course, Caspar Bauhin was commissioned to offer botanical excursions for medical students. In April 1582 he was elected professor of Greek, and now devoted himself intensively to medical practice, anatomical and botanical studies. On September 10, 1589, Caspar Bauhin was appointed the first professor of anatomy and botany at the University of Basel, a chair established at his request. A *Theatrum anatomicum* and a botanical garden (*Hortus medicus*) were set up for teaching anatomy. In the course of his life, Caspar Bauhin worked

his way up both materially and socially and gained an international reputation as a scientist. He was married three times. Caspar Bauhin's personality was characterized by diligence, meticulous work mentality and ambition. On the other hand, he lacked (according to Burckhardt 1917) the amiability and humanistic "joie de vivre" of his older colleagues Felix Platter and Theodor Zwinger.

### Merits as a physician

Caspar Bauhin must have had enormous creative power. He published around 30 works, about half with medical or botanical content. With the establishment of a *Theatrum anatomicum* and his public autopsies, he made medical anatomy in Basel a centre of attraction for foreign students. His achievements in medicine were based on the improvement and systematisation of anatomical terminology, especially in his book *Theatrum Anatomicum* (Basel 1605). This comprehensive and handy textbook of anatomy was based on his lectures and anatomical-pathological demonstrations. In this book Bauhin comprehensively arranged the anatomical knowledge of the time and illustrated it with many figures.

### Caspar Bauhin's merits as a botanist

Compared to his merits as a physician, Caspar Bauhin acquired far greater historical fame as a botanist. It is thanks to him that the University of Basel founded one of the first botanical gardens north of the Alps, offered botanical excursions and systematic botanical lectures within the medical faculty, and finally published one of the first comprehensive local floras in the world. Bauhin maintained a Europe-wide network of contacts with the leading botanists of his time. In his botanical works he aimed to give a complete overview of all plants known at the time and to arrange them systematically. In doing so, he critically examined each entry and aspired to provide the corresponding herbarium specimen to other botanists' plant names in order to clarify their taxonomic affiliation. In this way, he achieved that his herbarium finally contained about two



thirds of the plant species known at that time, many of them with the specimens collected by the corresponding authors. This herbarium formed his actual working and research tool and served as the basis for the development of his systematics. In the *Pinax Theatri Botanici* (1623), Bauhin describes 5600 plants, refers to all earlier authors, gives the plants a new name on the basis of his own observations, and lists all associated synonyms, an effort which was enormously useful for botanical science at the time and still is today. His nomenclature was a groundbreaking advance because he was the first to establish the clear distinction between genus and species. He shortened the species names, and even though they could still contain several words, they were structured hierarchically. The result of his almost immeasurable diligence over more than four decades made Caspar Bauhin a forerunner of Linné. The latter was able to rely on Bauhin for the further development of plant systematics and nomenclature. Bauhin's "*Pinax*" (1623) was intended as a preliminary work for "*Theatri Botanici*", the only volume of which appeared only posthumously in 1658.



Portrait of Caspar Bauhin from the rectorate year 1598. Rectorate register of the University of Basel, vol. 2, f. 71r.

#### Original botanical publications by Caspar Bauhin

Bauhin C (1596) *Phytopinax* seu Enumeratio Plantarum ab Herbariis nostro seculo descriptorum cum earum differentiis, cum plurimarum hactenus ab iisdem non descriptorum succinctae descriptiones et denominationes accessere: additis aliquot hactenus non sculptarum Plantarum vivis Iconibus. Basilea, per Sebastianum Henricpetri. 669 pp.  
<https://www.biodiversitylibrary.org/item/30648>

>> The "*Phytopinax*" is a plant directory of 2460 known and 164 new plants. The genera are briefly characterised. The polynomial names of the individual species were practically without exception given by Caspar Bauhin himself. For the known species, the synonyms of the authors who

described the species for the first time are listed. Here, C. Bauhin presents for the first time his innovations in botanical systematics and nomenclature.

Bauhin C (1620) *Prodromos Theatri Botanici*, in quo plantae sura sexcentae ab ipso primum descriptae cum plurimis figuris proponuntur. Francofurti a. Main, Typis Pauli Jacobi, impensi Johann. Treudelii. 160 pp.  
<https://doi.org/10.3931/e-rara-25436>

<https://www.biodiversitylibrary.org/item/14431>

>> In the "*Prodromos*" Bauhin describes 618 species, 140 of which are illustrated. Among them are many American species which Bauhin received by exchange from European colleagues. The clas-

sification and nomenclature correspond to that of "*Pinax*".

Bauhin C (1622) *Catalogus Plantarum* circa Basileam sponte nascentium cum earundem Synonymiis et locis, in quibus reperiuntur: in usum Scholae Medicae, quae Basileae est. Basilea, Typus J.J. Genathii. 111 pp.

<https://doi.org/10.3931/e-rara-28834>

<https://www.biodiversitylibrary.org/item/30649>

>> The "*Catalogus*" is an index of the plants growing naturally in the vicinity of Basel (radius of a German mile, approx. 7500 m). Bauhin's *Basel Flora* contains well over 1000 species. The "*Catalogus*" is a pocket flora intended for excursions, in this form one of the first local floras worldwide.

Bauhin C (1623) *Pinax Theatri Botanici* sive Index in Theophrasti, Dioscoridis, Plinii et Botanicorum, qui a Seculo scripserunt Opera: Plantarum circiter sex millium ab ipsis exhibiturum nomina cum earundem Synonymiis et differentiis methodice secundum earum et genera et species proponens. Opus XL. annorum hactenus non editum, summopere epetum ad auctores intellegendos plurimum faciens. Basilea, Sumptibus et typis Ludovic. Regis. 522 pp.

<https://doi.org/10.3931/e-rara-26291>

<https://www.biodiversitylibrary.org/item/14431>

>> The "*Pinax*" is a plant directory of all 5640 plant species known at that time, a more careful and complete version of the "*Phytopinax*", clearly structured and more useful thanks to a detailed index. Each species is accompanied by a complete list of synonyms to overcome the Babylonian confusion of the time in naming plant species. The "*Pinax*" is Caspar Bauhin's most important work and had a great influence on Linné's "*Species Plantarum*" (1753).

Bauhin C (1658) *Theatri Botanici* sive Historiae Plantarum ex Veterum et Recentiorum placitis propriaque observatione concinnatae. Liber primus. Johann Caspar Bauhin (Hg.). Basilea, Ioannem König. 340 pp.,

<https://doi.org/10.3931/e-rara-73659>

<https://www.biodiversitylibrary.org/item/30654>

>> This is the first volume of the "*Historia plantarum universalis*", on which Caspar Bauhin worked throughout his life, and for which "*Phytopinax*", "*Pinax*" and "*Prodromus*" were only intended as preliminary work. The volume includes graminoids.

Systematics and nomenclature correspond to the "*Pinax*", the description of the species is extensive, and also contains detailed information on occurrence and (medicinal) use. This work was published by Caspar Bauhin's son, Johann Caspar Bauhin (1606–1685). What happened to the other planned volumes, of which at least the second volume was ready for printing, is not known.

#### Literature

Burckhardt A (1917) *Geschichte der medizinischen Fakultät zu Basel 1460–1900*. Verlag Friedrich Reinhardt, Basel. 494 pp.

Benkert D (2020) *Ökonomien botanischen Wissens: Praktiken der Gelehrsamkeit in Basel um 1600*. Schwabe Verlag, Basel. 352 pp

Fuchs-Eckert HP (1977–1982) *Die Familie Bauhin in Basel*. Part 1, *Bauhinia* 6: 13–48 (1977), Part 2, *Bauhinia* 6: 311–329 (1979), Part 3, *Bauhinia* 7: 45–62 (1981), Part 4, *Bauhinia* 7: 135–153

1 [https://botges.ch/bauhinia/Bauhinia\\_6\\_0013-0048.pdf](https://botges.ch/bauhinia/Bauhinia_6_0013-0048.pdf)

2 [https://botges.ch/bauhinia/Bauhinia\\_6\\_0311-0329.pdf](https://botges.ch/bauhinia/Bauhinia_6_0311-0329.pdf)

3 [https://botges.ch/bauhinia/Bauhinia\\_7\\_0045-0062.pdf](https://botges.ch/bauhinia/Bauhinia_7_0045-0062.pdf)

4 [https://botges.ch/bauhinia/Bauhinia\\_7\\_0135-0153.pdf](https://botges.ch/bauhinia/Bauhinia_7_0135-0153.pdf)



## Room 120, main building, University of Basel, Petersplatz 1, Basel

### Conference program

Thursday, 15 September 2022

07h45	Conference desk opens	14h30	Austin Mast, Dept of Biological Science, Florida State University, Tallahassee, FL, USA: <b>Machines can be taught to identify phenological anomalies described on herbarium labels</b>
08h30	Workshop and discussion: <b>Beyond the state-of-the-art in herbarium-based research</b> Herbarium specimens ultimately play a fundamental role in a remarkably broad range of research projects, that may or may not be based at collection-holding institutions. Different uses emphasize often different aspects of specimens. This includes physical plant material (e.g., for ancient DNA or stable isotope analysis), high-resolution digital images (such as some taxonomic, morphometric or phenological purposes), and pure label data of well-determined specimens (for instance, some floristic purposes and biodiversity assessments). Finding specimens through digitalization projects are typically critical to all, including for the history of science. Herbarium leadership is directly or indirectly responsible for enabling all this, inherently interdisciplinary, research.	14h50	Donat Agosti, Plazi, Bern, Switzerland: <b>The significance of taxonomic publications to understand biodiversity in the digital world</b>
10h00	Break	15h10	Break and poster session
10h30	Prof. Dr. Dr. h.c. Andrea Schenker-Wicki, president of the University of Basel: <b>Greeting message</b>	15h45	Urs Eggli, Sukkulenten-Sammlung Zürich, Switzerland: <b>Impossible to press? – Succulents in Renaissance herbaria: The history of the struggle to prepare succulent plants for the herbarium</b>
10h35	Dr. Jurriaan de Vos, Organizing Committee: <b>Introduction</b>	16h05	Tilman Walter, Institut für Geschichte der Medizin, Universität Würzburg, Germany: <b>Plants, gardens and herbaria. Physicians as the earliest botanists in Germany</b>
10h45	<b>Keynote talk:</b> Richard B. Primack, Boston University, USA: <b>Mobilizing herbarium specimens, botanical gardens, historical data sets and citizen science observations to investigate the biological effects of climate change</b>	16h25	Sarah T. Wagner, Institut für Botanik, Technische Universität Dresden, Germany: <b>Network analysis of the herbarium collection of the Moravian Church from the 18th century</b>
11h20	Ansgar Kahmen, Dept Environmental Sciences, Basel University, Basel, Switzerland: <b>The stable isotopes composition of herbarium specimen reveal physiological responses of plants to environmental change</b>	16h45	Jason Grant, Institut de biologie, Université de Neuchâtel, Switzerland: <b>The herbarium of Swiss naturalist Jean-Frédéric Chaillet (1747–1839) meticulously records the plants and fungi of the Neuchâtel region of the Swiss Jura</b>
11h40	Kenneth M. Cameron, Department of Botany, U Wisconsin-Madison, WI, USA: <b>A large phylo-floristic study reveals evolutionary constraints on the past, present, and future assembly of a unique regional flora in North America</b>	17h05	Anastasia Stefanaki, Biosystematics, Wageningen University & Research, Wageningen, The Netherlands: <b>Combining 16th-century botanical history and genomics to understand the complex taxonomy of the wild tulip, <i>Tulipa sylvestris</i>, in Europe</b>
12h00	Lunch break	17h25	Leisure
13h30	Mark Carine, The Natural History Museum, London, UK: <b>Documenting, understanding and opening the botanical collections of Hans Sloane (1660–1753)</b>	18h15	<b>Public lecture:</b> Prof. Richard B. Primack, Boston University, USA: <b>Climate change effects on wildflowers, trees and birds. Building on the observations of the famous American environmental philosopher Henry David Thoreau, author of «Walden»</b> Henry David Thoreau is America's most famous environmental philosopher and author of the book Walden. For the past 18 years, Professor Richard Primack and his team have been building on Thoreau's records from the 1850s and other Massachusetts data sources to investigate the earlier flowering and leafing out times of plants, the earlier flight times of butterflies, and the more variable response of migratory birds. Plants are also changing in abundance due to a warming climate. This work is now being extended to the neglected autumn season. What would Thoreau tell us to do about global climate change if he were alive today? <b>Note:</b> different location: Bernoullianum, lecture room 148, Bernoullistrasse 30, Basel.
13h50	Fred Stauffer, Conservatoire et Jardin botaniques de la Ville de Genève, Chambésy, Suisse: <b>Digitization efforts of the phanerogamic Geneva herbarium (G, G-DC, G-BOIS, G-PREL): from 2004 to present</b>	20h00	Conference dinner
14h10	Luiza Teixeira-Costa, Vrije Universiteit Brussel, Brussels, Belgium: <b>Parasitic flowering plant collections embody the extended specimen</b>		



**Room 120, main building, University of Basel, Petersplatz 1, Basel**  
**Conference program**  
**Friday, 16 September 2022**

08h30	<b>Keynote talk:</b> Hernán A. Burbano, University College London, UK: <b>A retrospective view on plant genetic diversity using ancient DNA</b>	14h30	Meeting summary, workshop results and general discussion
09h05	Verena Schünemann, University of Vienna, Austria, and University of Zurich, Switzerland: <b>Ancient DNA analysis of medieval German grape seeds: How archaeological plant remains can contribute to the understanding of plant domestication</b>	15h00	<b>Two guided tours:</b> Caspar Bauhin and the historic treasures of the Basel herbaria, and Botanical Garden of the University of Basel
09h25	Jesse R. Lasky, Pennsylvania State University, USA: <b>Using herbarium specimens to study biogeography and response to global change in <i>Arabidopsis thaliana</i></b>	17h00	End of symposium
09h45	Donikë Sejdiu, Inst of Evolutionary Medicine, University of Zurich, Switzerland: <b>Herbarium DNA traces <i>Phytophthora infestans</i> strain that caused Irish Famine into 20th-century Europe</b>		
10h05	Break and poster session		
10h40	Tinde van Andel, Naturalis Biodiversity Center, Leiden, the Netherlands: <b>How did 16th century tomatoes look like?</b>		
11h00	Simon Aeschbacher, Dept of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland: <b>Caspar Bauhin's 400-year-old herbarium specimens reveal a mixed origin of early European tomatoes</b>		
11h20	Pablo Muñoz-Rodríguez, Department of Plant Sciences, University of Oxford, UK: <b>An integrated approach to studying tropical plant diversity: botanical monographs, herbarium specimens and sweet potato</b>		
11h40	Elizabeth M. Joyce, Faculty of Biology, Ludwig-Maximilians-Universität München, Germany: <b>Herbarium specimens reveal inter-continental migration tracks, phylogeography and taxonomic boundaries of a widespread tropical tree</b>		
12h00	Lunch Break		
13h30	Yvonne Willi, Dept of Environmental Sciences, Basel University, Switzerland: <b>Evidence for parapatric speciation in selfing <i>Arabidopsis</i> revealed by herbarium specimens</b>		
13h50	Gabriel F. Ulrich, Inst of Integrative Biology, ETH Zurich, Switzerland: <b>Harnessing herbaria to assess geographic extent and genetic consequences of habitat loss</b>		
14h10	Malene Nygaard, NTNU University Museum, Norwegian University of Science and Technology, Trondheim, Norway and Natural History Museum and Botanical Garden, University of Agder, Kristiansand, Norway: <b>Spatiotemporal monitoring of the rare Northern dragonhead, <i>Dracocephalum ruyschiana</i> (Lamiaceae) — SNP genotyping and environmental niche modelling herbarium specimens</b>		



## A retrospective view of plant genetic diversity using ancient DNA

**Hernán A. Burbano**

Centre for Life's Origins and Evolution  
University College London  
h.burbano@ucl.ac.uk

Humans have a vast transformative effect on ecosystems, which keeps shaping plants' distributions, phenotypes and genetic diversity. Tracing these changes over time is central to understand their consequences on plants' adaptability to a changing environment. Although contemporary genomes contain a record of species history, inferences based on them are uncertain, and confounded by, for instance, previous demographic history. Ancient DNA research makes it possible to directly assess historical genomes, refine demographic models, and gauge the role of natural selection in shaping the distribution of phenotypes over time.

In the first part of the talk, I will present a general overview of the technical developments that make it possible to retrieve and analyze historical/ancient genomes. In the second part of the talk, I will present a set of case studies that illustrate how the combined analysis of present-day and ancient genomes refines the population and adaptive history of plants and their pathogens through space and time.

## Mobilizing herbarium specimens, botanical gardens, historical data sets and citizen science observations to investigate the biological effects of climate change

**Richard B. Primack**

Boston University, USA  
primack@bu.edu

Over the past two decades, researchers and others involved in plant science have developed innovative and powerful methods to investigate the effects of climate change on plants. First, botanical garden staff are using their diverse collections to understand plant responses to climate change, test possible conservation actions, and engage the public in climate change science. We illustrate this approach with two international networks of botanical gardens. Second, scientists are using historical databases of plant phenology and abundance combined with modern observations to determine how climate change has already affected plants. As these historical data sets become available online, scientists are using powerful analytical tools to understand how climate change responses vary around the world, improving forecasts of future global changes. Third, millions of herbarium specimens and photographs of plants are being digitized, allowing researchers to study flowering and leafing out times at unprecedented geographic, temporal, and taxonomic scales. We present an example of how trees and wildflowers are responding to climate change across Europe, Eastern North America, and East Asia. Fourth, community and citizen science programs, such as iNaturalist and the National Phenology Network (USA), have greatly expanded, increasing the data available to researchers and engaging the public in climate change research. Researchers are now challenged to develop methods to combine these diverse data sources in ways that take advantage of the special characteristics of each source, as illustrated with examples from

Denmark and Massachusetts. The insights gained from such research could greatly advance our understanding of the effects of past climate change and anticipate the impacts of future climate change on plants and ecosystems around the world.



## Bauhin's 400-year-old herbarium specimens reveal a mixed origin of early European tomatoes

Thomas Grubinger<sup>1</sup>, Guelfirde Akguel<sup>2</sup>, Alessia Guggisberg<sup>3</sup>, Reto Nyffeler<sup>4</sup>, Jurriaan M. de Vos<sup>5</sup>, Verena Schuenemann<sup>2,6</sup>, **Simon Aeschbacher**<sup>1</sup>

- <sup>1</sup> Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich, Switzerland, [simon.aeschbacher@ieu.uzh.ch](mailto:simon.aeschbacher@ieu.uzh.ch)
- <sup>2</sup> Institute of Evolutionary Medicine, University of Zurich, Zurich, Switzerland
- <sup>3</sup> Department of Environmental Systems Science, ETH Zurich, Zurich, Switzerland
- <sup>4</sup> Department of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland
- <sup>5</sup> Department of Environmental Sciences, University of Basel, Basel, Switzerland
- <sup>6</sup> Department of Evolutionary Anthropology, University of Vienna, Vienna, Austria

The tomato (*Solanum lycopersicum*) was brought to Europe in the 16th century after the Spanish and Portuguese conquest of the Americas. Historical sources suggest that the earliest European tomatoes appeared fully domesticated and displayed a large variation in fruit morphology. However, the geographic origin and genomic ancestry of these tomatoes remain largely unknown. Names assigned to the tomato in the historical literature are compatible with both a Mexican and a Peruvian origin. The genome of a single 16th-century herbarium specimen sequenced previously at low coverage grouped with both Mexican and South American cherry tomatoes, and thus remained inconclusive about the geographic origin. To shed further light on the ancestry of European tomatoes, we sequenced 21 herbarium genomes collected between 1596 and 1915. Mean alignment depths at filtered SNPs ranged from 8.7 to 21.4. Including published sequences from 166 modern accessions, we found that the historical specimens split into one group associated with Mexican cherry tomatoes, and one with Mexican large-fruited tomatoes. However, the latter group was found to share substantial genomic ancestry with Peruvian cherry tomatoes. We observed that the evolutionary relationship among modern and historical tomatoes varies along the genome and correlates with recombination rate and gene density.

Both groups of historical tomatoes we identified were already represented among our oldest four specimens, which were all collected or curated by Caspar Bauhin around 1600. Our results support historical sources pointing to a Mexican origin of European tomatoes and previous findings of genetic admixture between South American and Mexican tomatoes.

## The significance of taxonomic publications to understand biodiversity in the digital world

**Donat Agosti**<sup>1</sup>, Laurence Bénéichou<sup>2</sup> and Lyubomir Penev<sup>3</sup>

- <sup>1</sup> Plazi, Bern, Switzerland; [agosti@amnh.org](mailto:agosti@amnh.org)
- <sup>2</sup> Laurence Bénéichou, Muséum national d'Histoire Naturelle, Paris, and CETAF publishing group
- <sup>3</sup> Pensoft Ltd, Sofia, Bulgaria

Bauhin's pioneering Flora of Basel „Catalogus Plantarum circa Basileam sponte nascentium“ published exactly 400 years ago is a precursor to the artificially identified beginning of taxonomic publishing with Linnaeus Systema plantarum ... 1753. Indeed, botanical publishing existed far before Linnaeus', however his contribution has not only been the Latin Binomen, but the highly structured way he published the taxonomic treatments for each species, and to cite previous works. In the digital age, this kind of structuring of the information and the existing implicit citation links allows building the biodiversity knowledge graph, opening up the entire corpus of taxonomic treatments imprisoned in publications by providing it in a format that can be found and reused, cited and linked to data referenced in the publications. This provides access to all the published data about a specimen in a natural history collection, to trace back the history of a taxonomic name or the traits used to describe and delimit the species. The Swiss based Biodiversity Literature Repository and Treatment-Bank provide access to over 750,000 taxonomic treatments, over 1M material citations and are the largest data set provider to the Global Biodiversity Information Facility (GBIF). This highly automated workflow has and continues to liberate data from over 70,000 publications, which are further converted to RDF and structured into Linked Open Data via the OpenBiodiv Biodiversity Knowledge Graph. At the same time new ways to structure publications so that their resident data can immediately be reused upon publication are being developed in collaboration with Pensoft

publishers, the Muséum d'histoire naturelle, Paris and the CETAF publishing group. The Swiss NGO Plazi, Zenodo at CERN and SIBiLS at the Swiss Institute of Bioinformatics are involved in the EU Horizon 2020 project BiCIKL and the Swissuniversities funded project eBioDiv to develop ways to link data in publications to specimens, taxonomic names and genes and vice versa. This lecture will explain the concept and state of the art in taxonomic publishing, access and reuse of its data.



## A large phylo-floristic study reveals evolutionary constraints on the past, present, and future assembly of a unique regional flora in North America

Kenneth M. Cameron

Department of Botany, University of Wisconsin-Madison, USA, [kmcameron@wisc.edu](mailto:kmcameron@wisc.edu)

With 1.4 million specimens the Wisconsin State Herbarium (WIS) is one of the largest in the Americas and Wisconsin offers botanists a unique opportunity to study species representing a confluence of global biomes: boreal conifer forests, eastern deciduous forest, savannas, and grasslands. The state harbors at least 2,640 species of vascular plants, of which 1,873 are native and 767 are introduced. We have sequenced the two-gene plant DNA barcode (rbcL+matK) and reconstructed a complete community phylogeny for the Wisconsin flora with genomic DNA extracted almost exclusively from herbarium specimens. At the same time >300,000 georeferenced specimens from the state were used together with bioclimatic and soil data to produce species distribution models for the flora, which were subsequently aggregated in order to determine patterns of species richness and phylogenetic diversity across the state. In order to predict future phylofloristic change, a supermatrix of all Eastern North American vascular plants (ca. 2,300 spp) was studied under models that account for climate change. Among the many surprising results we uncovered are predictions that whereas species richness will increase as ca. 850 southern taxa move northward into the state, ca. 242 species will become extirpated by 2070. Unfortunately, these are not random, but instead represent 15 % of monocots, 28 % of ferns/lycophods, and 30 % of orchids. Furthermore, our models suggest that Wisconsin's projected climate will be unsuitable for most species to be able to retain their present distributions; only 65 % will be able to retain more than half of their current distributions.

## Documenting, understanding and opening the botanical collections of Hans Sloane (1660–1753)

Mark Carine

Algae, Fungi and Plants Division, The Natural History Museum, Cromwell Road, London, UK, [m.carine@nhm.ac.uk](mailto:m.carine@nhm.ac.uk)

The death of Sir Hans Sloane in 1753 led to the creation of Britain's first national collection. Bought by the British state on behalf of the nation, Sloane's collection was made freely available for "all curious and interested persons" through a new institution, the British Museum (BM). Sloane's vast collection included natural history specimens, books, manuscripts, prints, drawings, coins and other objects from across the world. The surviving botanical collections alone comprise an estimated 120,000 herbarium specimens and 8,500 'vegetables and vegetable substances' from over 70 countries and territories worldwide. Assembled from c.1680, in part financed by profits from the transatlantic slave trade, Sloane's vast botanical collection was made as Britain became a global trading and imperial power. In this talk I discuss ongoing work that aims to better document Sloane's botanical collections and to better understand their provenance and how Sloane valued and catalogued them. I also introduce the SloaneLab project. Anyone wanting to interrogate Sloane's collection today is hampered by its distribution across three different institutions (the Natural History Museum (NHM), the British Library (BL), and BM). The collection is split broadly (but imperfectly) along disciplinary lines and it is recorded in multiple cataloguing systems that reflect the needs of different disciplines and institutional histories. The SloaneLab project aims to digitally reunite Sloane's original collection catalogues and surviving specimens and objects from across the NHM, BM and BL and support different ways to search those collections for any "curious or interested person".



## Impossible to press? – Succulents in Renaissance herbaria: The history of the struggle to prepare succulent plants for the herbarium

Urs Eggli<sup>1</sup>, Reto Nyffeler<sup>2</sup> and Felix Merklinger<sup>1</sup>

<sup>1</sup> Sukkulanten-Sammlung Zürich / Grün Stadt Zürich, Zürich, Switzerland,  
urs.eggli@zuerich.ch

<sup>2</sup> Department of Systematic and Evolutionary Botany (ISEB), University of Zürich, Zürich, Switzerland

Several Renaissance herbaria, including the Bauhin herbarium, contain preserved specimens of various succulent plants such as cacti, stonecrops, palm lilies or aloes. In view of the difficulties experienced even today when preparing succulents for the herbarium, the efforts of the Renaissance botanists to tackle the challenge is really remarkable. The view that succulents by definition are unsuitable for pressing for the herbaria, as e.g. expressed by Richard Bradley in his 1716-book, prevails to these days. Combining selected early specimens from several plant families with published and unpublished illustrations allows us to trace the history of introduction of these exotics into European science.

## The herbarium of Swiss naturalist Jean-Frédéric Chaillet (1747–1839) meticulously records the plants and fungi of the Neuchâtel region of the Swiss Jura

Jason Grant, Mathias Vust, Edouard Di Maio and Eva Riat

Laboratoire de génétique évolutive, Institut de biologie, Université de Neuchâtel, Switzerland,  
Jason.grant@unine.ch

The extensive herbarium of Jean-Frédéric Chaillet (1747–1839) conserved at the Institute of Biology, University of Neuchâtel, Switzerland catalogues the flowering plants, bryophytes, algae, lichens, and fungi of the Neuchâtel region of the Swiss Jura. However, since he published very little, his significance has been obscured since the time of his death despite being well-known during his lifetime. Our recent study of his plant and fungal specimens, catalogues, manuscripts, library, and extensive correspondence has demonstrated Chaillets' unquestioned importance as a compiler of knowledge of 18th-century European organismal biology, especially mycology. To understand his methodology, Chaillet's herbarium and associated material kept at the University of Neuchâtel (NEU) and his personal botanical library at the Public and University Library of Neuchâtel (BPUN) have been databased, cross-referenced, and subjected to detailed analysis. Chaillet's collections of bryophytes, lichens, and fungi in bound volumes are nearly unique in science and constitute some of the oldest known cryptogam collections. His technique demonstrates a passion and meticulousness rarely seen in herbaria, leading us to a study of the history of the object itself. Chaillet's discoveries, especially over 150 new species of fungi, were published during his lifetime by others, notably Alphonse Pyramus de Candolle (1806–1893) in Geneva, the founding father of systematic mycology, Christian Hendrik Persoon (1761–1836) in Paris, and Elias Magnus Fries (1794–1878) in Uppsala. Therefore, we

compare the botanical practices of Chaillet with that of these 'professional' Swiss and European 18th-century botanists and mycologists as well as other 'amateurs'.



## Herbarium specimens reveal inter-continental migration tracks, phylogeography and taxonomic boundaries of a widespread tropical tree

Elizabeth M. Joyce<sup>1</sup>, Caroline M. Pannell<sup>2,3,4</sup>, Maurizio Rossetto<sup>5</sup>, J.-Y. Samantha Yap<sup>5</sup>, Kevin R. Thiele<sup>6</sup>, Darren M. Crayn<sup>7</sup>

<sup>1</sup> Faculty of Biology, Ludwig-Maximilians-Universität München, München, Germany, E.Joyce@lmu.de

<sup>2</sup> Department of Plant Sciences, Oxford University, Oxford, UK

<sup>3</sup> Queen's University Belfast, Marine Laboratory, Portaferry, UK

<sup>4</sup> Royal Botanic Gardens, Kew, Richmond, Surrey, UK

<sup>5</sup> Research Centre for Ecosystem Resilience, Australian Institute of Botanical Science, Royal Botanic Garden Sydney, Sydney, New South Wales, Australia

<sup>6</sup> School of Biological Sciences, The University of Western Australia, Crawley WA, Australia

<sup>7</sup> Australian Tropical Herbarium, James Cook University, Cairns, Queensland, Australia

Biotic exchange between Australia and South-east Asia has had a substantial impact on the evolution of Australia's northern tropical flora, with important ramifications for its conservation and biosecurity. Despite this, floristic migration tracks between northern Australia and South-east Asia remain poorly characterised. We used 135 herbarium and 6 field-collected samples of the widespread tropical monsoonal tree *Aglaia elaeagnoidea* (Meliaceae) to identify migration tracks between Australia and Southeast Asia. DArTseq of samples from across the range of *A. elaeagnoidea* yielded 176,331 single nucleotide polymorphisms across 90,456 loci that were analysed using multivariate, population genetic and coalescent methods to characterise phylogeographic and phylogenetic patterns. These analyses were considered in the context of environmental niche modelling for the last glacial maximum. *Aglaia elaeagnoidea* was found to comprise three distinct species that are consistent with morphological and ecological differences, and we recircumscribed the taxonomy of the species complex. Two migration tracks of *A. elaeagnoidea* s.s. into Australia were identified: one from New Guinea to Cape York Peninsula in north-east Australia, and a second from Timor to the Kimberley Plateau of north-west Australia. The Cape York Peninsula track is contemporary with ongoing genetic exchange,

whereas the Kimberley Plateau track is historic, facilitated by multiple past exposures of the Arafura Shelf during the Pleistocene. We suggest that phylogeographic patterns of *A. elaeagnoidea* s.s. have resulted from a combination of repeated range expansion and contraction cycles concurrent with Quaternary climate fluctuations and stochastic dispersal events.

## The stable isotopes composition of herbarium specimens reveal physiological responses of plants to environmental change

Ansgar Kahmen, Daniel Nelson, Jurriaan de Vos, Cristina Moreno Gutierrez, David Basler

Dept of Environmental Sciences, Basel University, Switzerland, ans gar.kahmen@unibas.ch

The isotope analysis of archived plant material offers the opportunity to reconstruct the physiological responses of plants to environmental change. Specifically, the carbon isotope composition of plants can be used as proxy of leaf-level intrinsic water use efficiency (which is the ratio of net photosynthesis over stomatal conductance), and the oxygen isotope composition can provide time-integrated information on leaf stomatal conductance. In combination, the stable isotope analysis of carbon and oxygen thus allows to explicitly determine values for net photosynthesis and stomatal conductance from archived plant material. In my presentation, I will show carbon and oxygen isotope data of 3000 herbarium specimen from the Herbaria Basel, that have been collected across Switzerland over the past century for more than 70 different plant species. The analysis shows that plants from all taxa and irrespective of their growing conditions improved their water use efficiency over the past century and that the contribution of net photosynthesis or stomatal conductance to changes in intrinsic water use efficiency dramatically different among different plant functions groups. Our study demonstrates that the stable isotope analysis of herbarium specimen is a valuable approach to determine how the carbon and water relations of plants are responding to long-term changes in the environment.



## Using herbarium specimens to study biogeography and response to global change in *Arabidopsis thaliana*

Lua Lopez<sup>1</sup>, Victoria L. DeLeo<sup>2</sup>, Christina Yim<sup>2</sup>, Patricia Lang<sup>3</sup>, Stephanie Marciniak<sup>2</sup>, Emily S. Bellis<sup>4</sup>, Logan Kistler<sup>5</sup>, Sergio Latorre<sup>6</sup>, Asnake Haile<sup>7</sup>, Diana Gamba<sup>2</sup>, Patrick Woods<sup>8</sup>, Mistire Ysfiru<sup>7</sup>, Jeffrey Kerby<sup>9</sup>, Duncan N. L. Menge<sup>10</sup>, Tigest Wondimu<sup>7</sup>, Collins Bulafu<sup>11</sup>, John K. McKay<sup>8</sup>, Jon Ågren<sup>12</sup>, George Perry<sup>2</sup>, Robert Muscarella<sup>12</sup>, Hernan Burbano<sup>6</sup>, Thomas E. Juenger<sup>13</sup>, Ephraim M. Hanks<sup>2</sup>, **Jesse R. Lasky**<sup>2</sup>

<sup>1</sup> California State University – San Bernardino, San Bernardino, USA

<sup>2</sup> Pennsylvania State University, University Park, USA, lasky@psu.edu

<sup>3</sup> Carnegie Institute of Science, Stanford, USA

<sup>4</sup> Arkansas State University, Jonesboro, USA

<sup>5</sup> Smithsonian Institution, Washington, USA

<sup>6</sup> University College London, London, UK

<sup>7</sup> Addis Ababa University, Addis Ababa, Ethiopia

<sup>8</sup> Colorado State University, Ft. Collins, USA

<sup>9</sup> Aarhus Institute of Advanced Studies, Aarhus, Denmark

<sup>10</sup> Columbia University, New York, USA

<sup>11</sup> Makerere University, Kampala, Uganda

<sup>12</sup> Uppsala University, Uppsala, Sweden

<sup>13</sup> University of Texas at Austin, Austin, USA

Biologists have many questions and hypotheses about ecological and evolutionary patterns and processes at large spatial scales. However, these hypotheses often remain untested by information on individuals across entire species' ranges, despite the importance of these hypotheses for global change biology. For many widespread species, herbaria represent a large repository of individual information. Here we collect data on genotype, phenotype, and performance from herbarium specimens of the model plant *Arabidopsis thaliana*. We use these data to test hypotheses about mechanisms of range margins and response to global environmental changes. We found that individual *Arabidopsis* decline in size as environments are predicted to become less suitable near range margins. We found turnover through time in population genomic composition across the species range, though geographic patterns in population structure were generally consistent through time. We also found major shifts in phenology and physiology

over time, potentially indicating a shift to a rapid cycling life history in Eastern Europe. Overall, our research shows how climate constrains the distribution of *Arabidopsis* through space and time. Population genotypes and phenotypes are dynamic through time, potentially as adaptive responses to changing environments.

## Machines can be taught to identify phenological anomalies described on herbarium labels

Austin Mast<sup>1</sup>, Shubo Tian<sup>2</sup>, Zhe He<sup>3</sup>, Erica Krimmel<sup>3</sup>, Fritz Pichardo-Marciano<sup>1</sup>, Buckley Mikayla<sup>1</sup>, Sophia Gomez<sup>1</sup>, Ashley Hennessey<sup>1</sup>, Allyson Horn, Olivia Howell<sup>1</sup>

<sup>1</sup> Department of Biological Science, Florida State University, Tallahassee FL, USA, amast@fsu.edu

<sup>2</sup> Department of Statistics, Florida State University, Tallahassee FL, USA

<sup>3</sup> College of Communication and Information, Florida State University, Tallahassee FL, USA

Biodiversity specimen collectors are on the front lines of observing biotic anomalies, some of which herald early stages of significant changes (e.g., the arrival of a new disease or the emergence of phenological mismatches). However, the mechanisms by which those valuable observations reach stakeholders who would use the information have been idiosyncratic. Here, we explore the use of machine learning to identify all of one type of anomaly (phenological; related to the timing of life history events) amongst the world's biodiversity specimen records. As a first step, we classified every occasion of six focal words that seemed likely to be used in most descriptions of phenological anomalies (early, earlier, earliest, late, later, latest; e.g., "flowering earlier than I've ever seen") in a promising data field (occurrenceRemarks) from the 130 million+ records aggregated by iDigBio. This resulted in a subset of 59,420 records, and our classification of them found that only about 3 % of those records contained a description of a phenological anomaly. The remaining 97 % of examined records used the focal words in ways not suggesting anomalies (e.g., "collected in early morning"). This initial discovery highlights the value of identifying features of anomaly descriptions that can be used to find them in this large and ever-expanding recordset. As a second step, we implemented a machine learning algorithm that classified >97 % of a test dataset accurately. We will discuss the implications of that work for understanding and identifying anomaly descriptions made on the world's herbarium labels stretching back centuries.



## An integrated approach to studying tropical plant diversity: botanical monographs, herbarium specimens and sweet potato

Pablo Muñoz-Rodríguez, John R.I. Wood and Robert W. Scotland

Department of Plant Sciences, University of Oxford, UK, pablo.munoz@plants.ox.ac.uk

Recent decades have witnessed a massive increase in data accumulation, but our knowledge of the world's biodiversity is still fragmentary. This is partly because data accumulation has not been matched by a parallel taxonomic effort: on the contrary, taxonomic studies are in decline, and many groups of organisms have never been comprehensively studied. Lack of comprehensive taxonomic studies has resulted in widespread identification errors, with estimates of 50 % of tropical plant specimens in herbaria (and associated data in global databases) having an incorrect name. In addition, we now know it takes decades to accumulate a minimum number of correctly identified specimens of a species to enable subsequent research. Accelerating biodiversity studies and species discovery requires a good taxonomic and phylogenetic framework, which is missing for most groups of tropical plants.

In this talk, I will present the results of a monographic study of the megadiverse genus *Ipomoea* based on the analysis of c. 25,000 herbarium collections. I will present a pipeline, developed as part of our work, that integrates specimen based morphological studies and techniques of phylogenetic and genomic analysis to develop more robust species delimitation hypotheses and accelerate biodiversity studies.

Beyond taxonomy, the results of our study have implications for other disciplines such as archaeology or food security. I will specifically show how this integrated approach using herbarium specimens enabled several important discoveries on the origin and evolution of sweet potato (*Ipomoea batatas* (L.) Lam.), one of the most important food crops worldwide.

## Spatiotemporal monitoring of the rare Northern dragonhead, *Dracocephalum ruyschiana* (Lamiaceae) — SNP genotyping and environmental niche modelling herbarium specimens

Malene Nygaard<sup>1,2</sup>; Alexander Kopatz<sup>3</sup>, James M.D. Speed<sup>1</sup>, Michael D. Martin<sup>1</sup>, Tommy Prestø<sup>1</sup>, Oddmund Kleven<sup>3\*</sup>, Mika Bendiksby<sup>1,4\*</sup>

<sup>1</sup> NTNU University Museum, Norwegian University of Science and Technology, Trondheim, Norway, malene.o.nygard@uia.no

<sup>2</sup> Natural History Museum and Botanical Garden, University of Agder, Kristiansand, Norway

<sup>3</sup> Norwegian Institute for Nature Research, Trondheim, Norway

<sup>4</sup> Natural History Museum, University of Oslo, Norway

\* Co-senior authors

Data from different time points is key for understanding how populations behave under various conditions. In this regard, herbarium specimens are an invaluable source of information from the past. We have studied change in genetic structure and diversity through time in the Northern dragonhead (*Dracocephalum ruyschiana*, Lamiaceae), a plant species that has experienced a drastic population decline and habitat loss in Europe. A microfluidic array consisting of 96 SNP markers was applied on 130 herbarium specimens collected from 1820 to 2008, mainly from Norway but also beyond. Obtained genotype data were compared with data from modern samples to assess genetic structure and diversity across space and through time. Finally, we used sample metadata and observational records to model the species' environmental niche and potential distribution in Norway. Despite reduction in population size in recent times, the Norwegian historical-modern comparison revealed similar genetic structure in space and limited change of genetic diversity through time. The regional populations in Norway have remained genetically divergent, both from each other and more so from populations outside of Norway, rendering continued protection of all existing populations of the species in Norway relevant. The ecological niche modelling suggests that dragonhead has

not fully achieved its potential distribution in Norway, which is anchored in warmer and drier regions. The SNP array successfully genotyped all included herbarium specimens, but the captured genetic diversity was negatively correlated with distance from Norway. This negative correlation is likely due to ascertainment bias of the SNP array; solvable with appropriate design procedures.



## Ancient DNA analysis of medieval German grape seeds: How archaeological plant remains can contribute to the understanding of plant domestication

Verena Schünemann<sup>1,2</sup>, Xuzhen Li<sup>3</sup>, Donike Sejdiu<sup>1</sup>, Susanne Jodoin<sup>4</sup>, Judith Neukamm<sup>1,4</sup>, Johannes Krause<sup>5</sup>, Christoph Breitwieser<sup>6</sup>, Elyashiv Drori<sup>7</sup>, Wei Chen<sup>3</sup>

<sup>1</sup> University of Vienna, Austria

<sup>2</sup> University of Zurich, Switzerland, verena.schuenemann@iem.uzh.ch

<sup>3</sup> Yunnan Agriculture University, Yunnan, China

<sup>4</sup> University of Tübingen, Germany

<sup>5</sup> Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany

<sup>6</sup> Stadtkultur Museum Bensheim, Germany

<sup>7</sup> Ariel University, Israel

In the last decade, improvements in ancient DNA research combined with simultaneous advances in sequencing technologies have revolutionized our understanding of the evolution of many species. Now we can directly look at evolution in action, via the analysis of genomes recovered from individuals who lived in the distant past. However, regarding plant species the field is only taking its first steps. Here, we will present an example of three medieval grape-vine seeds from Bensheim, Germany, to showcase the importance of archaeological plant remains for the understanding of plant domestication. DNA extraction and direct sequencing resulted in the recovery of up to 8131 SNPs per seed, which were compared to a diversity panel of 2448 modern and 28 ancient grape varieties. The three samples fall together with previously published ancient samples from France as well as contain genetic components of modern Muscat grapes and Central European and Iberian grapes in the admixture analysis. Overall, our results point to the use of grape varieties in medieval Germany, which show genetic similarities to modern varieties cultivated in Europe today.

## Herbarium DNA traces *Phytophthora infestans* strain that caused Irish Famine into 20th-century Europe

Donikë Sejdiu<sup>1,2</sup>, Jurriaan M de Vos<sup>3</sup>, Reinhard Berndt<sup>4</sup>, Simon Aeschbacher<sup>2</sup>, Verena J. Schünemann<sup>1</sup>

<sup>1</sup> Institute of Evolutionary Medicine, University of Zurich, Switzerland, donike.sejdiu@iem.uzh.ch

<sup>2</sup> Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland

<sup>3</sup> Department of Environmental Sciences, University of Basel, Switzerland

<sup>4</sup> Department of Environmental Systems Science, Eidgenössische Technische Hochschule Zurich, Switzerland

Plant pathogens may have a strong impact on human societies as they reduce harvests and cause economic losses. *Phytophthora infestans* is one of those pathogens with potentially devastating consequences. The pathogen was introduced to Europe in the 1840s and expanded rapidly over the whole continent, where it caused severe epidemic outbreaks, including the Irish Potato Famine. Studies that included historical *P. infestans* DNA from herbarium records of the 19th century identified HERB-1 as the lineage responsible for the Irish Potato Famine. It was hypothesized that HERB-1 was globally replaced by other lineages in the 20th century. However, a recent study identified samples belonging to HERB-1 in modern populations from Mexico and South America. When exactly, if at all, HERB-1 went fully extinct in Europe remained open. To answer this question, we extracted *P. infestans* DNA from 27 herbarium specimens of potato and tomato collected in Europe across the 20th century. We sequenced two full mitochondrial genomes at 35- and 37-fold mean coverage, combined them with 73 published historical and modern mitochondrial genomes, and performed phylogenetic analyses. We found that HERB-1 still existed in our two potato specimens collected in Switzerland in 1982 and 1987. Our results thus challenge the belief that HERB-1 went extinct after the 19th-century famine. Our study demonstrates the value of herbarium genomics in informing biogeographic analyses of plant-pathogen systems.



## Digitization efforts of the phanerogamic Geneva herbarium (G, G-DC, G-BOIS, G-PREL): from 2004 to present

**Fred Stauffer**, Laurent Gautier, Nathalie Rasolofo, Raoul Palese

Herbier de Phanerogamie, Conservatoire et Jardin botaniques de la Ville de Genève, Chambésy, Suisse, Fred.stauffer@ville-ge.ch

Major collections such as the ones kept in the Geneva herbaria have played a major role for botanical sciences as the specimens therein included have been cited since more than two centuries in taxonomic literature. Nowadays, the existence of botanical data and their availability has increasing implications for research and education and public service beyond what was originally envisioned in the past. Likewise, the importance of digitization of natural history collections and its critical role in making available images of biological samples for a much broader public than the one traditionally visiting repository institutions has been highlighted by several authors. The present contribution aims to provide a rough overview of the digitization efforts undertaken by the phanerogams department of the herbarium of Geneva. Special emphasis is given to the projects undertaken in the past 13 years, in particular to the ones framed by the Global Plant Initiative (GPI), and further efforts funded by the Global Biodiversity Information Facility (GBIF) Swiss node and the Franklinia Foundation. The main objectives, complexities and achievements of these initiatives are described and the workflows and associated means that enabled this non-stop effort are discussed. We present also the current projects on historical collections (G-DC, G-BOIS and G-PREL) and the future perspectives on the digitization of the Geneva phanerogamy herbarium.

## Combining 16th-century botanical history and genomics to understand the complex taxonomy of the wild tulip, *Tulipa sylvestris*, in Europe

**Anastasia Stefanaki**<sup>1,2</sup>, Floris C. Breman<sup>1</sup>, Federico Barbier<sup>1</sup>, Tilmann Walter<sup>3</sup>, M. Eric Schranz<sup>1</sup>, Freek T. Bakker<sup>1</sup>, Tinde van Andel<sup>1,2,4</sup>

<sup>1</sup> Biosystematics, Wageningen University & Research, Wageningen, The Netherlands, anastasia.stefanaki@wur.nl

<sup>2</sup> Naturalis Biodiversity Center, Leiden, The Netherlands

<sup>3</sup> Institute of the History of Medicine, Julius-Maximilians-Universität Würzburg, Würzburg, Germany

<sup>4</sup> Clusius chair History of botany and gardens, Leiden University, Leiden, The Netherlands

Taxonomy of naturalized plants with a past of introduction can be complex and its understanding requires an interdisciplinary perspective. Combining botanical history and genomics we assess the taxonomy of *Tulipa sylvestris*, commonly called the “wild tulip”. This small, yellow-flowered species was introduced to northern Europe from the Mediterranean in the 16th century. Unlike tulips that came from the Ottoman empire and gave birth to modern garden cultivars, *T. sylvestris* became a garden escapee that successfully naturalized across Europe. Its taxonomy is complex due to morphological diversity, polyploidy and naturalization of cultivated plants. Two subspecies, sometimes treated as distinct species, are tentatively accepted in Europe: naturalized plants are suggested to belong to the tetraploid subsp. *sylvestris*, while native Mediterranean plants to the diploid subsp. *australis*. By screening 16th-century literature, herbaria and illustrations we reconstructed the 16th-century history of introduction of *T. sylvestris*. The first bulbs came from Montpellier (S. France) and Bologna (N. Italy) in ca. 1550–1580. Famous botanists were involved in their introduction, including Gessner, Aldrovandi, de Lobel and Clusius. Our historical findings showed that both subspecies were introduced in northern Europe and therefore do not agree with the currently accepted subspecific classification. Using genomic repeat profiling we

attempt to elucidate the species’ controversial taxonomy, using both fresh and historic (up to ca. 500-year-old) herbarium vouchers from historical gardens and wild localities around Europe. Preliminary results show that the two subspecies can be distinguished based on their repeat profile and that they do not seem to merit species recognition.



## Parasitic flowering plant collections embody the extended specimen

Luiza Teixeira-Costa<sup>1</sup>, J. Mason Heberling<sup>2</sup>, Carol A. Wilson<sup>3</sup>, Charles C. Davis<sup>4</sup>

<sup>1</sup> Vrije Universiteit Brussel, Brussels, Belgium, luiza.teixeira-costa@vub.be

<sup>2</sup> Carnegie Museum of Natural History, Pittsburgh, PA, USA

<sup>3</sup> University of California, Berkeley, CA, USA

<sup>4</sup> Harvard University Herbaria, Cambridge MA, USA

Widespread digitization of natural history collections, combined with novel tools and approaches is revolutionizing biodiversity science. The 'extended specimen' concept advocates a holistic approach in which a specimen is framed as a diverse stream of interconnected data.

Herbarium specimens that capture multispecies relationships, such as certain parasites, fungi and lichens, hold great potential to provide a broader and more integrative view of the ecology and evolution of symbiotic interactions. The potential is even greater in the case of species that act as keystone players in natural and disturbed ecosystems, such as most parasitic flowering plants. To achieve the full potential of parasitic plant collections and help motivate the next generation of collections-based research, we assessed the representation of these peculiar plants in herbarium collections worldwide. Nearly 1.02 million records housed in 950 institutions were gathered from the Global Biodiversity Facility. Over 40 % of the freely available records were observed to include images and geographical coordinates. Although apparently low, this percentage is well above the general proportion reported for animal parasite collections, highlighting that parasitic plant specimens are primed for further exploration. We also discuss how data and metadata obtained from parasitic plant specimens can inform analyses of co-distribution patterns, functional traits, changes in species plasticity, chemical ecology of tripartite interactions, and molecular data critical for species conservation. This presentation will also explore how the historic nature and sheer size

of global herbarium collections can provide the spatiotemporal breadth essential for investigating organismal response to global change using parasitic plant specimens.

## Harnessing herbaria to assess geographic extent and genetic consequences of habitat loss

Gabriel F. Ulrich, Enrique Rayo, Alessia Guggisberg, Simone Fior, Martin C. Fischer, Alex Widmer

Institute of Integrative Biology (IBZ), ETH Zurich, Switzerland, gabriel.ulrich@usys.ethz.ch

Genetic diversity is one of three levels of biodiversity and the raw material for evolution to act on. Population size reduction via loss of habitat and connectivity can lead to loss of neutral and adaptive genetic diversity. The Hare's tail cottongrass (*Eriophorum vaginatum*) is strongly associated with peat bogs and has undergone major habitat loss in Switzerland, especially in the Central Plateau, over the last two centuries as a consequence of wetland drainage and peat extraction. Assessing herbarium-based georeferencing data and observation records indicates a reduced occurrence of *E. vaginatum*, especially under relatively warm and dry climates. This raises the question of whether habitat loss has caused a reduction in genetic diversity in general and of variants adaptive under warm conditions in particular. We selected 226 herbarium specimens, collected between 1804 and 1949, from seven Swiss herbaria for whole genome re-sequencing. Where possible, we additionally collected contemporary samples from the same or a nearby location. By comparing the genetic diversity of historical and contemporary samples, we will examine whether an overall loss of genetic diversity has occurred in *E. vaginatum* across Switzerland. We will assess historical genotype-climate associations in order to test whether genetic variants associated with warm climatic conditions occur at reduced frequency in the contemporary gene pool. With this project, which is part of a pilot study for monitoring genetic diversity in Switzerland, we hope to contribute to a better understanding of the genomic consequences of habitat loss by making use of specimens and metadata stored in herbaria.



## How did 16th century tomatoes look like?

Tinde van Andel<sup>1</sup>, Anastasia Stefanaki<sup>2</sup>

<sup>1</sup> Naturalis Biodiversity Center, Leiden, The Netherlands, [tinde.vanandel@naturalis.nl](mailto:tinde.vanandel@naturalis.nl)

<sup>2</sup> Biosystematics group, Wageningen University, Wageningen, The Netherlands

Soon after the Spanish conquest of the Americas, tomatoes were presented as curiosities to the European elite and drew the attention of sixteenth-century naturalists, but their exact origin was unknown. The discovery of a tomato specimen in the sixteenth-century 'En Tibi' herbarium at Leiden led to claims that its DNA would reveal the 'original' taste and pest resistance of early tomatoes. We provide an overview sixteenth-century tomato specimens, early descriptions and 13 illustrations. Several were never published before, revealing what these tomatoes looked like, who saw them, and where they came from. Our survey shows that the earliest tomatoes in Europe came in a much wider variety of colors, shapes and sizes than previously thought. Recent molecular research on the ancient nuclear and chloroplast DNA of the 'En Tibi' specimen clearly shows that it was a fully domesticated tomato, and genetically close to three Mexican landraces and two Peruvian specimens that probably also had a Mesoamerican origin. Molecular research on the other sixteenth-century tomato specimens may reveal other patterns of genetic similarity, past selection processes, and geographic origin. Clues on the 'historic' taste and pest resistance of the sixteenth-century tomatoes will be difficult to predict from their degraded DNA, but should be rather sought in those landraces in Central and South America that are genetically close to them. The indigenous farmers growing these traditional varieties should be supported to conserve these heirloom varieties *in-situ*.

## Network analysis of the herbarium collection of the Moravian Church from the 18th century

Sarah T. Wagner<sup>1</sup>, Frank Müller<sup>1</sup>, Richard Ehrlacher<sup>1</sup>, Lena Frencke<sup>1</sup>, Christoph Neinhuus<sup>1</sup>, Thomas Ruhland<sup>2</sup>

<sup>1</sup> Institut für Botanik, Technische Universität Dresden, [sarah.wagner@tu-dresden.de](mailto:sarah.wagner@tu-dresden.de)

<sup>2</sup> Interdisziplinäres Zentrum für Pietismusforschung, Martin-Luther-Universität, Halle-Wittenberg

One of the most valuable collections in the Herbarium Dresdense (DR), Germany, is the historical herbarium collection of the Moravian Church (in German: Herrnhuter Brüdergemeine) from mid to late 18th century. On their mission to spread the Christianity the Moravians settled on many continents and took the advantage of exploring culture and nature of their new home countries. Being excellent observers and documentarists, they left a barely explored corpus of objects and texts of tremendous importance for natural sciences and humanities. A current project analyses the 1259 remaining herbarium samples from the cabinet of natural curiosities in Barby in a network approach combining botanical methods with digital humanities and data digitalisation. We aim to identify the historical contexts of the collection, i.e. through personal correspondence, itineraries, botanical manuscripts, and publications to reconstruct the names of the individual collectors, to clarify their manifold contributions to botany and finally to create an overview of the influence of the Moravians on the development of modern natural sciences. The scientific heritage of the Moravians demonstrates that they were strongly integrated into the scientific community of the 18th century. Letters in the collections of the Linnean Society show, that Friedrich Adam Scholler (1718–1785), one of the most important Moravian botanists, was in close contact with leading scientists, e.g. Carl v. Linné, discussing issues on plant taxonomy, exchanging specimens and presenting own fieldworks like Scholler's *Flora Barbiensis*, published in 1775. First results from the network analysis will be presented in our contribution.



## Plants, Gardens and Herbaria. Physicians as the earliest botanists in Germany

Tilman Walter

Institut für Geschichte der Medizin, Universität Würzburg, Germany, [tilmann.walter@web.de](mailto:tilmann.walter@web.de)

Starting with an overview including references to publications, pictorial material, and the typical academical training paths of the German-speaking physicians who became known as “botanists” in the 16th century, the focus of my presentation will be on the practice of botanizing in the field and in gardens. Well-illustrated books, beginning with Otto Brunfels’ (1488–1534) *Herbarum vivae eicones* (Strasbourg 1530), were essential to help identify plant species. Around 1550, many German-speaking physicians went to study medical botany in Italy (where the first botanical gardens were established around 1545) or in Montpellier, France. In Montpellier, Guillaume Rondelet (1507–1566) taught Kaspar Ratzenberger (1533–1603), Felix Platter (1536–1614) and Leonhard Rauwolf (1535?–1596) how to create their herbaria, which are the oldest preserved in the German-speaking world. Recent studies of the handwritten entries in the Rauwolf herbarium have shown how the identification process took place. Rauwolf was also the first to leave behind a long and very detailed description of his fieldwork, which he undertook on botanical excursions as far away as Syria, Lebanon and Iraq. In Basel, Caspar Bauhin (1560–1624) was to become a particularly influential academic teacher when in 1588 he accepted the newly established chair for anatomy and botany. In Bauhin’s extensive correspondence, letters from his former student Sigismund Schnitzer (d. 1622) about rare as well as specially shaped and colored plants in the Bamberg Court Garden show how precisely a botanically interested scholar came to observe plant individuals at that time.

## Evidence for parapatric speciation in selfing *Arabidopsis* revealed by herbarium specimen

Yvonne Willi<sup>1</sup>, Kay Lucek<sup>1</sup>, Nora Walden<sup>1,2,3</sup>

<sup>1</sup> Dept of Environmental Sciences, Basel University, Switzerland, [yvonne.willi@unibas.ch](mailto:yvonne.willi@unibas.ch)

<sup>2</sup> Dept of Plant Sciences, Wageningen University, The Netherlands

<sup>3</sup> Centre for Organismal Studies, Heidelberg University, Germany

Herbarium specimen of species with remote distributions are important resources to study their ecology and evolution. Based on herbarium samples of the subarctic *Arabidopsis arenicola*, we addressed whether re-colonization after the last glacial maximum was associated with its speciation. The budding of a new species along the expansion route over ecological gradients has so far received little attention. Theory generally questions parapatric speciation because gene flow from the parental species is predicted to prevent reproductive isolation, while assortative mating, and serial bottlenecks during range expansion in particular, increase mutational load. Based on whole-genome sequences of temperate North American *A. lyrata* and *A. arenicola*, we show that the latter speciated during range expansion of the former, after the end of the last Pleistocene glaciation. Briefly before, a shift in mating system to selfing had evolved in the parental species at northwestern Lake Superior, the birthplace of the new species. Probably because of selfing and quasi-clonal selection, mutational load did not increase further even during the vast range expansion of *A. arenicola* to subarctic regions. We conclude that parapatric speciation combined with inbreeding has a good stand in being an important but so far overlooked mode of speciation.



## Herbarium DNA degradation: different ways of falling to pieces

**Freek T. Bakker** & Lia Hemerik

Biosystematics Group and Biometris, Department of Mathematical and Statistical Methods, Wageningen University and Research, The Netherlands, freek.bakker@wur.nl

Herbarium genomics is a promising field mainly driven by recent advances in next-generation sequencing (NGS) technology. Therefore, herbarium collections represent an enormous botanical repository of phenotypic observations and locality data, of sometimes long-extinct taxa. Post-mortem damage in herbarium DNA consists mainly of genome fragmentation (single- and double-stranded breaks), and damage-derived miscoding lesions appear to be highly limited or even negligible. For organelle genomes and other repetitive genomic compartments, genome skimming appears effective in retrieving sequence data from plant herbarium specimens, whereas studies addressing herbarium nuclear-encoded genes and particularly whole genomes are still in minority. Typically, high levels of genomic fragmentation are observed in herbarium DNA and when many short fragments are present this can possibly lead to insert sizes being smaller than Illumina read lengths applied. Using a series of 93 herbarium DNA samples, representing 10 angiosperm families, near-complete plastomes were assembled for 80 % of the specimens, some of which are 146 years old. Overlapping read pairs were found to occur in roughly 80 % of all read pairs obtained. After merging such overlapping pairs, the resulting fragments and their distribution can be considered to reflect the ongoing process of genome fragmentation up to the moment of DNA extraction. Fragment length distributions appear to fit gamma distributions with either many small fragments present or an increasing number of longer fragments having accumulated, with no apparent correlation with specimen age. These distributions appear to differ from usually observed first-order genomic degradation kinetics, possibly due to the nonrepresentative nature of genome skimming samples.

## Simple procedures for obtaining DNA sequences from old herbarium material

**Mika Bendiksbj**, Lisbeth Birgitte Thorbek, Charlotte Sletten Bjorå, Rune Halvorsen

Natural History Museum, University of Oslo, Blindern, Norway, mika.bendiksbj@nhm.uio.no

Because DNA degrades over time, obtaining high-quality DNA is presumed to be more difficult from older than younger plant material. During molecular phylogenetic investigations of the subfamily Lamiioideae (Lamiaceae; the Mint family) and subtaxa, we extracted DNA from 651 herbarium specimens collected between 1826 and 2006 using regular mini-prep procedures. The aim was to obtain DNA of sufficient quality for PCR amplification and DNA sequencing of various plastid and nuclear genetic markers. By using successful rps16 sequence amplification as a measure of DNA quality, logistic regression analysis demonstrates a negative relationship between time since collection and DNA quality of the extract. We successfully sequenced at least one genetic marker for 90 % of the specimens, the oldest being 168 years old. Our results further indicate that the upper age limit for successfully sequencing herbarium specimens is considerably higher. We provide protocols that include minor modifications of the regular mini-prep and PCR procedures that made us succeed with obtaining DNA sequences from old herbarium specimens, including samples that did not amplify using the regular procedures.



## Collections from the cold solving hot questions

Charlotte S. Bjorå, Mika Bendiksby, Bjørn Petter Løfall, Einar Tindal

Natural History Museum, University of Oslo, Blindern, Oslo, Norway, charlotte.bjora@nhm.uio.no

The Arctic has always been an area of focus for the botanical and fungal collections at the Natural History Museum in Oslo. These collections house around 280 000 unique accessions dating back more than two centuries. The Arctic collections have a broad circumpolar representation.

Recent analyses published by the Norwegian Meteorological Institute identified a statistically significant annual warming of up to 2.7 to 4.0 °C per decade in Spitzbergen. This is the highest temperature increase measured in modern time. Important polar expeditions like “Fram II” to Greenland and Canada (1898–1902), “Gjøa” and “Maud”, through the Northwest Passage (1903–1906, and 1918–1925, respectively) deposited accessions in the Oslo herbarium from highly remote areas. These collections is a unique repository for comparisons with today’s vegetation. The temperature has unquestionably increased in the Arctic lately, so also its geopolitical importance. Political tensions has made some areas inaccessible to researchers, however the collections are welcoming all researchers.

A case study of an expedition to the arctic collections demonstrate how the understanding of *Carex saxatilis* changed from one to three taxa through a journey of almost thousand accessions collected over more than 200 years and a span of more than 20 degrees latitude.

## Comparing historic and contemporary phenology of plants in northwest Switzerland in the light of climate change from 1850 to today

Maya Bosshard, Jurriaan M. de Vos

University of Basel, Department of Environmental Sciences – Botany, Basel, maya.bosshard@unibas.ch

Long-term historical records allow to study the responses of ecosystems to climate change such as shifts in flowering phenology. Though widely predicted, only few studies worldwide document such changes since the 19th century, and, to our knowledge, no such study exists for Switzerland. In this study, we transcribed historic flowering phenology data for Basel-Landschaft for 116 herb and shrub species based on an unpublished manuscript “Flora Raurica” (1837–1877s) by doctor and botanist Franz Eduard Fries. In addition, we used peak flowering observations from the Swiss Phenological Network (1980s to today) and in 2021 we observed the onset of flowering in the field in two regions in NW Switzerland, Sissach and Diegten. Fries’ notes were judged reliable and accurate, and revealed that species began to flower 5 days earlier and peak-flowered 13.7 days earlier in 2021 compared to the 1860s. As hypothesized, they showed an overall sensitivity to temperature, flowering earlier when mean temperatures of the preceding months were warmer (overall trends: beginning of flowering 3.3 days per K, peak flowering 4.6 days per K). Temperature sensitivities were highly species-specific, with some phylogenetic component. Moreover, there was a t. This study highlights the importance and utility of rare historic phenology data for addressing important questions about the effects of changing temperatures on phenology and demonstrates the challenge to characterise the variation in sensitivities between species.

## A 150-year-old herbarium exemplifies the change of a regional flora

Michèle Büttner<sup>1</sup>, Urs Weibel<sup>1</sup>, Michael Jutzi<sup>2</sup>, Ariel Bergamini<sup>3</sup>, Rolf Holderegger<sup>3,4</sup>

<sup>1</sup> Museum zu Allerheiligen, Schaffhausen, Switzerland, michele.buettner@stsh.ch

<sup>2</sup> Info Flora, Berne, Switzerland

<sup>3</sup> WSL Swiss Federal Research Institute, Birmensdorf, Switzerland

<sup>4</sup> ETH Zürich, Department of Environmental Systems Science, Zurich, Switzerland

The pharmacist Johann Conrad Laffon had the aim to collect all wild plant species in the Swiss canton of Schaffhausen. Today, his herbarium (1820–1847) is kept at the Museum zu Allerheiligen in Schaffhausen. Laffon’s herbarium, gathered within a clearly defined study area, proves to be a lucky stroke: It originates from a time period when few historical data are available and industrialisation just began. We compiled a list of the plant species in the herbarium of Laffon (as well as from a commented species list by Laffon) and compared it with present-day flora of the canton of Schaffhausen ( $\geq 2000$ ). We then studied whether the flora of the canton of Schaffhausen had changed during the last 150 years (i.e. 1847–2000), whether floral change was particularly strong in certain habitat types and whether the environmental requirements of extinct species differed from those of extant species. 154 of the 987 species listed by Laffon are no longer found in the canton of Schaffhausen, which translates into an extinction rate of one species/year. Wetland, pioneer and ruderal species as well as agricultural weeds and light-demanding species showed highest extinction rates. In contrast, forest species had a low extinction rate, and species from fertilized meadows showed no decline. Therefore, the extinction of plant species in the canton of Schaffhausen was exceptionally strong in habitats affected by drainage, intensified agriculture and river management. Our results inform nature conservation about particularly endangered habitats and possible drivers of species decline.

## Emerging methods for non-destructive sampling of wood collections: microCT and fluorescence

Alana R.O. Chin

Department of Environmental Systems Science, ETH Zürich, Switzerland, alana.chin@usys.ethz.ch

Collections of tree trunk cores and wood blocks are held by universities and agencies worldwide, but are used primarily for dendrochronology and climatology research. Furthermore, the fragile nature of wood cores, especially old ones, a desire to preserve these collections, limits anatomical research and our understanding of wood properties. With limitations on destructive sampling, we cannot form links between ecological factors such as climate, elevation, and stand density, and structural and physiological parameters like hydraulic risk, wood density, and heartwood deposition. Fortunately, emerging technologies such as multi-spectrum fluorescent imaging and synchrotron-based X-ray microtomography have the potential to enable non-destructive sampling of wood collections. I demonstrate the feasibility of anatomically targeted wood-density analysis, tracheid, ray and pit measurements, and quantification of heartwood deposits in three-dimensional wood scans. I will additionally present options for autofluorescent imaging for use in visualizing tiny rings and assessing their relative degree of lignification. In addition to the digital preservation of irreplaceable wood collections, these tool hold the potential to merge dendrochronological and dendroclimatic research with contemporary anatomical physiology. The methods discussed have the power to determine the anatomical components of wood density and the drivers of variation in heartwood chemical deposition – two key factors in the carbon-storage potential of forests and their responses to both management practices and climate change.



## Potentials and limits in the genomic uses of a 200 years old herbarium

Camille Christe<sup>1,2</sup>, Carlos G. Boluda<sup>1,2</sup>, Yamama Naciri<sup>1,2</sup>, Mathieu Perret<sup>1,2</sup> and Fred Stauffer<sup>1,2</sup>

- <sup>1</sup> Conservatoire et Jardin botaniques de la Ville de Genève, Chambésy, Geneva, Switzerland  
<sup>2</sup> Laboratoire de Systématique végétale et Biodiversité, Université de Genève, Chambésy, Geneva, Switzerland, camille.christe@ville-ge.ch

Major herbaria, such as the one hosted by the botanical garden of Geneva have played a central role in the development of plant systematics over the last 200 years. Today, advances in high throughput sequencing technologies together with the development of specific and universal capture kit has considerably improved the use of herbaria as a source of genetic data, opening new avenues in the study of plant biodiversity. Our research projects using herbarium specimens from different taxonomical groups, ages, geographical origins and preservation methods showed that herbaria allow 1) the reconstruction of phylogenetic relationships within lineages difficult to collect in the wild, 2) the discovery of species new to science, 3) the filling of taxonomical gaps in the plant tree of life by integrating historical referenced material and extinct species. We found that fragmented DNA does no more represent a limit in using this type of material but the relatively high quantity of DNA that is needed for high throughput sequencing and the destructive nature of the sampling request a wise selection of the samples to be sequenced. We are now ready to explore genetically the herbarium at a higher scale with some prospective applications such as the discovery of undescribed diversity, or the monitoring of regional flora. We foresee that the use of herbaria as source of genetic data will play a central role for the completion of the plant tree of life and the accurate quantification of plant diversity at all taxonomical levels.

## Bioprospecting in Herbaria: The case of Laurent Garcin's Geneva specimens

Alexanda Cook

University of Hong Kong and University of Neuchâtel, cookga@hku.hk

Herbaria offer promising possibilities for prospecting forgotten medicinal plants by analogy with Tu You You's Nobel Prize-winning research in ancient Chinese manuscripts and bioprospecting in sixteenth- and seventeenth-century herbals (Buenz, et al. 2004). Furthermore, many collectors, such as Laurent Garcin (ca. 1681–1751), the subject of this paper, were seeking plants for their curative properties. Given that approximately 40 % of current pharmaceuticals have a plant source, the search for novel plant-source remedies, especially those known in traditional medicine, should be expected to play a key role in developing new treatments for, among others, superbugs, cancer, lifestyle diseases, and malaria, which alone menaces 40 % of the world's population. Operationalizing this thesis is easier said than done, however; in Garcin's case we don't have his list of specimens, conserved at G in the general collection. Nor did he leave notes or labels with his specimens. Yet in the absence of detailed notes, we can reconstruct his motives and some of his findings from publications, correspondence and manuscripts. These lead us to, for example, *Andrographis paniculata* (Burm. f.) Nees, the subject of an entire chapter of World Health Organization monographs on selected medicinal plants. In double-blind control studies *A. paniculata* is effective against dysentery and the common cold. *Salvadora persica* L. is another Garcin discovery with recognized use as a dentifrice.

## Bridging herbaria cultural heritage and digital art: immaterial herbaria

Rhinaixa V. Duque-Thüs<sup>1</sup>, Philipp Schlüter<sup>1</sup>, Helmut Dalitz<sup>1</sup>, María Beatriz Eggl<sup>2</sup>

- <sup>1</sup> Institute of Biology, Herbarium HOH, University of Hohenheim, Stuttgart, Germany, r.duquethues@uni-hohenheim.de  
<sup>2</sup> Tüscherz, Switzerland

The aim of this project is to show the development of "immaterial herbaria" based on the idea of the Swiss-Venezuelan visual artist Beatriz Eggl of creating a work with digitised images of a selection of Orchidaceae specimens from the herbarium. The Images were generated with the help of IRIS Book 5, a lightweight portable scanner and others with a Nikon DF camera, as in her previous works "The Power of Vulnerability" and "Immaterial Forests", while the herbarium specimens were resourced, catalogued and included in the database. The result of this work would create a connection between science and art with the image of resilience of epiphytic Orchidaceae that use their roots as holdfasts and the feeling of an artist who is partaking of the Venezuelan Diaspora, sees her strategy to adapt to new countries and cultures as the one from orchids, able to move elsewhere, carrying her roots for holding herself to a substrate where she will be able to thrive and bloom.

## A museomics approach to study the evolution of disease resistance genes in a crop wild relative of tomato

Edeline Gagnon<sup>1</sup>, Gabriel Renaud<sup>2</sup>, Remco Stam<sup>3</sup>

- <sup>1</sup> Chair of Phytopathology, TUM School of Life Sciences, Technical University of Munich, Freising, Germany, edeline.gagnon@tum.de  
<sup>2</sup> Department of Health Technology, Section for Bioinformatics, Technical University of Denmark (DTU), Copenhagen, Denmark  
<sup>3</sup> Institute of Phytopathology, Christian-Albrecht University (CAU), Kiel, Germany

Unlocking the genetic diversity of Crop Wild Relatives (CWRs) is crucial to improving crop resistance to abiotic and biotic stress, but CWRs are at the risk of losing genetic diversity due to anthropogenic pressures and climate change. Recent advances in high throughput sequencing now facilitate sequencing of CWR herbarium collections, which are more widely distributed than germplasm collections and contain historical specimens from extinct populations. Through target enrichment capture, they represent a quick way to screen species and populations for large numbers of loci, such as polygenic disease resistance genes. Sequencing historical herbarium and germplasm collections of CWRs can be used to develop time-series analyses, to gain a more direct and realistic understanding of how these genes evolve in the face of habitat loss. Using *Solanum chilense*, a well-studied CWR of tomato in germplasm collections, I propose to apply previously designed baits for population genomics and the study of disease resistance genes to answer the following questions: (1) Are germplasm collections representative of the genomic diversity present in the entire population of *S. chilense*? (2) Are there signs of loss of genetic diversity in populations of *S. chilense* in the past 70 years due to habitat loss? This will be achieved by studying contemporary field-collected samples alongside historical collections from both herbarium and germplasm collections. This research will inform how potential loss of genetic diversity caused by anthropogenic pressures is affecting disease resistance in natural populations, a subject of interest to both the agricultural sector and environmental conservation.



## Using herbarium collections to investigate cold and altitudinal adaptations in crustose lichen species

Julia Gerasimova<sup>1,2</sup> and Andreas Beck<sup>1,2</sup>

- <sup>1</sup> Systematics, Biodiversity and Evolution of Plants, LMU Munich, Munich, Germany, jgerasimova@lmu.de  
<sup>2</sup> Botanische Staatssammlung München, SNSB–BSM, Munich, Germany

Lichens are a fascinating example of an obligate symbiosis. It comprises a fungal and one or more photosynthetic partners (either a green alga and/or cyanobacterium), forming a new entity, the lichen thallus. Many lichens have developed numerous adaptations to optimize their survival under harsh environmental stresses and thus colonize different substrates, taking advantage of the symbiotic lifestyle. Detailed knowledge of habitat requirements of lichens is essential for their use as bioindicators and for understanding how lichens might be affected by a changing climate.

*Toniniopsis subincompta* is a common species in the Alpine Mountain region and North Caucasus. It is used as an indicator for old-growth forests and is included in indices for determining the conservation importance of forest areas. It has been found in a range of woodlands from sea level to an altitude of about 3000 m in Eurasia, Macaronesia, Africa and North America. Our results clearly demonstrated the presence of two distinct species, *Toniniopsis separabilis* and *T. dissimilis*. Based on the material examined, *T. separabilis* is a more common taxon and has a wider distribution range, while *T. dissimilis* is less frequent. However, the latter species seems to be more adapted to cold as we have only seen specimens collected above 1000 m or in high latitudes. This finding demonstrates the great potential to investigate cold and altitudinal adaptations in relation to global climate change in this species pair. These questions shall be addressed by using large herbarium collections stored in Eurasia and North America and genomic work.

## In the footsteps of Sarasin & Christ: digitizing fern specimens at the herbaria in Basel and Zurich

Aurélié Grall<sup>1</sup>, Jurriaan de Vos<sup>1</sup>, Reto Nyffeler<sup>2</sup> and Alessia Guggisberg<sup>3</sup>

- <sup>1</sup> Dept of Environmental Sciences, University of Basel, Switzerland, aurelie.grall@unibas.ch  
<sup>2</sup> Department of Systematic and Evolutionary Botany (ISEB), University of Zürich, Switzerland  
<sup>3</sup> Institute of Integrative Biology, ETH Zurich, Switzerland

Many of the first descriptions of plants were based on material stemming from adventurous collection expeditions and remarkable personalities, such as the famous Sarasin cousins (Fritz & Paul, 1850s–1940s) from Basel, who profoundly impacted cultural and natural history and conservation. Sadly, their botanical collections, many from southeast Asia, were neglected compared to their famous zoological and ethnographic collections, even though they are critically important for taxonomy. For instance, Hermann Christ (1833–1933) described many new fern species from these collections. Yet, historic neglect and lack of digitalization renders them inaccessible to present-day science.

In this project, we unlock the botanical treasure trove of the Sarasin cousins by conditioning, taxonomic updating, and digitizing thousands of Sarasin specimens in the Herbaria Basel and the United Herbaria Zurich. By expanding our digitization efforts to additional fern specimens in our herbaria, we will make 60'000 digital specimens publicly available for science and society.

## Diaspore morphospace disparity among Australasian *Atriplex* L. during adaptive radiation

Dominique Groffman<sup>1,2</sup>, Anze Žerdoner Čalasan<sup>2</sup>, Gudrun Kadereit<sup>2</sup>

- <sup>1</sup> Erasmus Mundus Master Programme in Evolutionary Biology; Uppsala, Sweden, djg2181@columbia.edu  
<sup>2</sup> Systematics, Biodiversity and Evolution of Plants, LMU; Munich, Germany

Diaspores serve essential roles during plant range expansion and establishment as mediators of dispersal, dormancy and germination. For taxa *Atriplex* arid landscapes with unpredictable water availability, successful dispersal and germination in favorable conditions is especially crucial. The desert and steppe interior of Australia is the site of ongoing adaptive radiation of the dominant chenopod shrubland genus *Atriplex*, a complex of ~70 taxa varying in sexual system, adult life span and growth habit. The rapid diversification of *Atriplex* in a context of niche availability is supported by our findings of vast among-species fruiting bract morphological variation examined from herbarium material of 59 taxa, including several rare and restricted taxa. Morphogroups and structuring trait variables were identified through multivariate and hierarchical clustering analysis of fruit traits visible from the preserved material. Three fruiting bract syndromes were identified: (1) an entirely spongy syndrome with winged appendages and fully united bracts, (2) a fan-shaped and robust tube syndrome without appendages, and (3) an oval-triangular syndrome with herbaceous bracts united at the base and having spongy appendages. The remaining taxa have complex sets of diaspore trait associations and are not well-differentiated from one another on the basis of fruiting bract morphology. Instead, Australasian *Atriplex* occupies a wide diaspore morphospace, deploying many fruiting bract morphological strategies, as well as a wide climatic space. Most fruiting bract traits are not explained by coarse environmental variables, and diaspore morphology was not found to predict range extent, indicative of obscure interactions between diaspore morphology and environment.

## Historical tomato genomes shed light on the evolution of fruit morphology and flavour

Thomas Grubinger<sup>1</sup>, Gülfirde Akgül<sup>2</sup>, Alessia Guggisberg<sup>3</sup>, Reto Nyffeler<sup>4</sup>, Jurriaan M. de Vos<sup>5</sup>, Verena J. Schuenemann<sup>2</sup> and Simon Aeschbacher<sup>1</sup>

- <sup>1</sup> Inst of Evol Biology and Environmental Studies, Univ Zürich, Switzerland, thomas.grubinger@ieu.uzh.ch  
<sup>2</sup> Inst of Evolutionary Medicine, Univ of Zürich, Switzerland  
<sup>3</sup> Dept of Environmental Systems Science, ETH, Zürich  
<sup>4</sup> Department of Systematic and Evolutionary Botany, University of Zürich, Switzerland  
<sup>5</sup> Department of Environmental Sciences – Botany, University of Basel, Switzerland

Tomato flavour affects consumer liking but has deteriorated as a side-effect of breeding for yield. Modern tomatoes show reduced allelic diversity and a high prevalence of non-favourable alleles at flavour-related genes. Sugar content is negatively correlated with fruit weight due to genetic constraints. To explore the evolution of the size-flavour trade-off in tomato, we sourced whole-genome ancient DNA from 21 herbarium specimens collected in Europe between 1596 and 1915. Incorporating modern sequences from 166 wild, semi-domesticated, and landrace accessions, we examined sequence variation at 125 genes associated with fruit morphology and flavour. We found haplotypes private to (subsets of) historical specimens at 13.3 % of the loci underlying flavour, but only 5.7 % of those underlying morphology. At candidate causal variants underlying fruit morphology and flavour, genotype frequencies in the historical tomatoes matched those in the respective modern groups at most genes including LIN5, which encodes an invertase converting sucrose to glucose and fructose. However, at the malate transporter gene *ALMT9*, we found a much higher frequency of a derived non-synonymous mutation in historical than modern large-fruited tomatoes. The mutation reduces fruit malic acid levels and might thus have caused a unique sugar-acid profile in historical tomatoes. Across all candidate variants, proportions of putatively preferred alleles at size- vs. flavour-related genes in historical tomatoes were similar to those in their modern counterparts. Our findings suggest that the major deterioration in tomato flavour occurred before the introduction to Europe, but subtle differences in flavour profiles remain to be further explored.



## Towards a “reasoned” digitisation of herbaria for research

Alessia Guggisberg<sup>1</sup> and Guilhem Mansion<sup>2</sup>

- <sup>1</sup> Institute of Integrative Biology, ETH Zurich, Switzerland, alessia.guggisberg@usys.ethz.ch
- <sup>2</sup> Institute of Biology, University of Neuchâtel, Switzerland

Within the United Herbaria Zurich (Z+ZT), a recent project aimed at digitising the whole Gentianaceae family showed the importance of taxonomic revisions prior to any digitisation process. Preliminary results revealed a number of spurious information – wrong identification, outdated nomenclature, false geolocation – whose short-term impact can be detrimental to the management of the collections. Indeed, these common sources of error not only affect the scientific quality of the digitised data, but also the process of specimens mounting (herbarium sheets with several species) and the physical reclassification across the storage shelves (outdated taxonomic delimitation), overall requiring the rearrangement of several cubic metres of incorrectly placed samples. A “reasoned digitisation” of the revised and reclassified collections, correct from a taxonomic and nomenclatural point of view, also offers the possibility of rediscovering important specimens (nomenclatural types, historical herbaria) and allows the sharing of valuable data including high-resolution pictures in searchable, aggregated databases like GBIF. With the “revival” of biological collections and their uncritical use by non-specialists, high-quality herbarium data must be guaranteed by involving experts in the digitisation process. This reminds us of the importance of training new generations of taxonomists, without whom biological collections would otherwise become useless in the very near future.

## Using herbaria to reconstruct Japanese knotweed invasion history and eco-evolutionary dynamics

Ramona-Elena Irimia<sup>1</sup>, Farah Badreldin<sup>1</sup>, Uta Grünert<sup>1</sup>, Christina Richards<sup>1,2</sup>, Oliver Bosssdorf<sup>1</sup>

- <sup>1</sup> Plant Evolutionary Ecology, Institute of Evolution & Ecology, University of Tübingen, Tübingen, Germany
- <sup>2</sup> University of South Florida, Department of Integrative Biology, Tampa, Florida, USA

Herbarium records offer an excellent opportunity to examine the temporal and spatial characteristics of plant invasions since many of these introductions occurred during the past two or three centuries and are well documented in herbarium collections. Herbarium specimens preserve important morphological and developmental plant traits that can provide insights into the environmental and anthropogenic changes. In addition, herbarium specimens can be also used as a source of DNA to explore the spatiotemporal dynamics and genomic processes that contribute to species colonization, range expansion and invasion success. Nonetheless, this has been explored in very few species. To understand evolutionary changes associated with biological invasions we will generate historical DNA sequence information from preserved specimens of Japanese knotweed (*Reynoutria*) from the past 180 years spanning the species temporal spread and distribution in its introduced range of Europe and the US and in the native range of SE Asia (Japan) by using a targeted sequencing DNA approach. We will use the time series SNP data generated to determine the genetic make-up of *Reynoutria* populations, changes in allele frequencies and the contribution of novel mutations over time. Furthermore, we will also test for phenotypic changes in two structural plant traits including specific leaf area (SLA) and stomatal size and density and test for association with climate and latitude. The knowledge gained will be critical in understanding how these organisms spread and proliferate allowing stakeholders and land managers to focus their effort and identify appropriate strategies for preventing and managing biological invasions.

## Using herbarium specimens for studying climate change

Thea Kull<sup>1,2</sup>, Kätlin Langerpaur<sup>1</sup> and Tiit Kull<sup>1</sup>

- <sup>1</sup> Institute of Agricultural and Environmental Sciences, University of Life Sciences, Tartu, Estonia
- <sup>2</sup> Herbarium (TAA) of the Institute of Agricultural and Environmental Sciences, thea.kull@emu.ee

Climate change is nowadays an inevitable process. Phenology is a well-accepted indicator for studying climate change. The majority of studies which look at changes in phenological traits are based on observations. In the current study, herbarium material was used. Flowering is particularly sensitive to temperature changes, therefore, the flowering of species from the family Ranunculaceae was investigated. The study material originates from four largest Estonian herbaria (TAA, TAM, TALL, TU) and was collected within the territory of Estonia during 1901–2020. Temperature data was used to explain trends. As a result it was found that during the last 100 years the flowering time has shifted 16 days earlier and the trend has intensified in recent decades. In addition, spring-flowering species had a greater response to increasing air temperature than summer-flowering species. The results based on herbarium data were similar to the earlier results based on observational data, which means that herbarium material can also be used in climate research.

## Can we identify where geneflow between crops and their wild relatives might be more likely to occur based on herbaria and GBIF records?

Beatrice Landoni<sup>1</sup> and Rocio Perez-Barrales<sup>2</sup>

- <sup>1</sup> School of Biological Sciences, University of Portsmouth, UK; up869307@myport.ac.uk
- <sup>2</sup> Department of Botany, Universidad de Granada, Spain

Online repositories and herbaria are commonly employed to understand patterns of variation, especially in relation to phenology, across the distribution of wild plant species. Crop wild relatives (CWR) are wild plant species closely related to cultivated species. The conservation of CWRs is important for both biodiversity and food security. Different studies have assessed the worldwide distribution of CWRs and what are the species and areas to prioritize for CWR conservation. Such global effort, on the other hand, often neglects interactions between species. CWRs can grow in proximity to their cultivated counterparts. If the reproductive phenologies of a crop and its wild relative overlap, geneflow between the two might be more likely. Geneflow from crops to wild relatives can be of concern because it has the potential to introduce resistances to pesticides or other undesired traits in wild populations, but also erode their diversity. Online databases such as GBIF could be harnessed to identify areas where geneflow is more likely to occur between crops and their wild relatives based on overlaps in species occurrence and their reproductive phenology (GBIF record dates). The validity of GBIF record dates as proxies for reproductive phenology could then be validated using herbaria collections and image repositories such as Pl@ntNet. Here, we start to explore this idea using *Linum* species closely related to the crop *Linum usitatissimum* L. growing across the Mediterranean Basin and Europe.



## Following Podlech's legacy: Unleashing the potential of the Munich Herbarium collection for phylogenetic analyses of the largest genus of flowering plants

Diego F. Morales-Briones and Gudrun Kadereit

Princess Therese von Bayern chair of Systematics, Biodiversity and Evolution of Plants, Ludwig-Maximilians-Universität München, Munich, Germany, d.morales@lmu.de

*Astragalus* L. (Fabaceae), with around 2900 species distributed in both Old World (ca. 2400 spp.) and New World (ca. 500 spp.), is the most species-rich genus of flowering plants. The genus has undergone extensive diversifications during the last few million years and is an example of an adaptive radiation on a global scale. Species in *Astragalus* vary from short-living annual herbs to perennial rhizomatous or hemicryptophytic herbs and cushion-forming spiny shrubs. Given its immense species diversity and widespread distribution, it is not surprising that no comprehensive phylogenetic studies covering all its lineages and distribution areas have been done. To start tackling this issue, we have the ambitious project to follow Professor Dr. Dieter Podlech's research legacy on *Astragalus* at the Munich Herbarium (Botanische Staatssammlung München, M). We will use the vast and unique collection (thousands of species and vouchers) of Old World *Astragalus*, curated and maintained by Podlech for over 50 years, as the primary source of DNA to start a compressive phylogenetic analysis of the genus. To this end, we have already selected a set of Astragelean clade-specific 686 orthologous genes (819 exons) to be used for target enrichment or deep genome skimming. In-silico hybridization of this set of genes using publicly available genome skimming libraries of 89 Astragelean species showed great potential by producing a well-supported phylogeny of *Astragalus* at the subgenus and sectional levels.

## Challenges with georeferencing herbarium specimens: a case study derived from the Flora of the Canton Zürich project

Reto Nyffeler

Department of Systematic and Evolutionary Botany (ISEB), University of Zürich, Switzerland, reto.nyffeler@systbot.uzh.ch

More than 18'000 historical occurrence records for some 600 species of vascular plants have been extracted by georeferencing herbarium specimens filed at the United Herbaria Zurich (Z and ZT). This dataset of polygons for assumed collecting areas was collocated by volunteers for the Flora of the Canton Zürich project via a digital online platform. Combined with extant mapping activities, this effort built the foundation for quantifying the change and consistency of individual species from different habitat types in the Canton during the past 150 years. Some 30 % species distinctly diminished their distribution or are locally extinct, while some 17 % of the species increased their presence or have newly arrived in the area. We provided repetitive georeferencing tasks to the different contributors in order to estimate the range of variation in area for the polygons. The distance between centers of the polygons from different contributors are lower than 1000 m in 90 % of the estimates, and lower than 1400 m in 95 % of the estimates. We implemented an interactive portal to select datasets of georeferenced historical records from herbarium specimens and unpublished manuscripts based on different parameters, including area of polygons as estimates of confidence for reconstructed collecting sites.

## Aspects of the organisation of an early 18th century garden revealed by newly studied and discovered specimens from Herman Boerhaave (1668–1738)

Aleida Offerhaus<sup>1</sup>, Anastasia Stefanaki<sup>2</sup>, Tinde van Andel<sup>2</sup>

<sup>1</sup> Naturalis Biodiversity Center, Leiden University, Leiden, The Netherlands, aleida.offerhaus@naturalis.nl

<sup>2</sup> Naturalis Biodiversity Center, Leiden University, Leiden, The Netherlands and Wageningen University, Wageningen, The Netherlands

Due to the digitization of historic herbarium collections, we are now able to study them without risk of damaging the often fragile documents. By studying them we obtain valuable insights in past botanic networks and the development of botany as a science. A prominent 18th-century botanist was Herman Boerhaave (1668–1738), professor of botany and chemistry and prefect of the Leiden Hortus botanicus. From his vast network of correspondents, he regularly received seeds from botanical gardens all over Europe. These seeds, some of which came from as far as Izmir in Turkey, were thereafter sown in the Leiden Garden. Boerhaave meticulously registered everything concerning these seeds in his register of sown seeds, the *Index Seminum Satorum*, of which the Leiden University Library possesses books covering the years 1712–1727. He recorded who sent the seeds, when he sowed them, if they germinated or flowered, what the actual plants looked like and if plants were still present after a certain number of years. Several herbaria were erroneously attributed to Boerhaave, but here we focus on 87 specimens from the collection of Naturalis, that we established to have been part of his true "herbarium". By studying the specimens, that were registered in the Index, we were able to reconstruct the process from reception, registering and sowing of the seeds, picking, mounting and decorating the specimens to adding the labels. Our contribution will contain the presentation of one or more Boerhaave specimens to illustrate how this process evolved.

## Ampelographic collection in 230-year-old Herbarium Wolnyanum

Michelle J. Price

Conservatory and Botanical Garden of Geneva, Michelle.Price@ville-ge.ch

Natural history collections exist because of human curiosity, fueled by our desire to understand the living world. Each collection is unique, in link with how it was composed, who composed it and where the specimens originated from, geographically and historically. Unlocking the patrimonial treasures and scientific data held in collections is one of the key activities of museums and botanical gardens. Access to collections and the innovative scientific use of collections opens up many possibilities in research. Fundamental research, that is more usually associated with natural history collections (species discovery, documentation, description), fitted into an evolutionary context, provides the building blocks (species and species concepts leading to names) for many other fields in biology as well as for ecology and habitat or species conservation. The collections themselves also provide data sources that can be used to establish evolutionary relationships and explore evolutionary questions. Examples of fundamental taxonomy in mosses, using the Johannes Hedwig collection that is linked to the 1801 starting point of moss nomenclature (excepting *Sphagnum*) show the importance of collections as a crucial biological reference resource. Examples of the use of collections to explore evolution in mosses show how modern techniques reveal enormous amounts of information from preserved specimens. Collection-based institutions, in the light of the current biodiversity crisis, should collectively step up and claim their rightful place as key players in ongoing efforts to describe, document and understand the natural world and their importance in providing a reliable and trusted source of information on species themselves.



## Ampelographic collection in 230-year-old Herbarium Wolnyanum

Milica Rat

University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia, milica.rat@dbe.uns.ac.rs

Herbarium collections in South-Eastern Europe were founded in 19th century or later. However, the oldest collection dates to the 18th century, and is kept at the place of origin in Sremski Karlovci Gymnasium (Republic of Serbia). The founder was Andreas Wolny, who systematically collected plants and organized them according to their practical value. Herbarium was used as a handbook for different subjects, with an emphasized focus on plant systematics, pharmacy, and agriculture. The collection was closed for more than 100 years, and it has been legally protected by the Republic of Serbia as a cultural monument. With the beginning of modern research in 2017, the first goal was to review the material, re-list it and prepare it for further investigation. As the process of revision began, many interesting discoveries were unveiled. Among them, the discovery of an ampelographic collection of grape varieties grown in the Mt. Fruška Gora at the beginning of the 19th century, in the pre-*Phylloxera* era. Of the 122 herbarium sheets, 75 have been preserved to this day. Each of them contains vine leaf(s) along with pressed bunches. The list of grape varieties includes old, autochthonous grape varieties, which were cultivated in the area for centuries, many of which are not known today, organized as “white grapes” and “red grapes”. First scientific result provides the list of grape varieties, while further research, including molecular analysis of aDNA, will significantly contribute to the identification confirmation and knowledge of the development of viticulture in the Balkans and Pannonia.

The author acknowledges financial support of the Ministry of Education, Science and Technological Development of the Republic of Serbia (Grant No. 451-03-68/2022-14/200125)

## Time Capsule of Renaissance Botanical Illustration: “Plant Images Related to Caspar Bauhin and his Herbarium”

Karen Reeds

Princeton Research Forum and National Coalition of Independent Scholars, karenmreeds@princetonresearchforum.org

The rich holdings of manuscripts associated with Caspar Bauhin (1560–1624) in the Universitätsbibliothek Basel include a remarkable miscellany of botanical pictures: *Pflanzenbilder mit Beziehung zu Caspar Bauhin und seinem Herbar* (UBB Shelfmark K IV 3, A-D, described briefly in Werner Sackmann’s 1991 catalogue of Basel scientific manuscripts). The watercolors, pen and ink line drawings, and copperplate engravings – drawn by least a dozen unnamed artists – portray 29 different European and exotic plants. Many sheets are annotated in contemporary hands. Several came from three correspondents whom Bauhin thanked in his books: Joannes Francus, MD, of Bautzen, Leonardus Doldius, MD, of Nürnberg, and Joannes Pona, pharmacist of Verona. All but one of the pictures are rendered naturalistically; the exception is “Sidereon Serpentina,” a highly stylized image, akin to earlier “alchemical” herbals. Notably, the collection includes at least five New World plants: “*Sassafras*” [*Sassafras albidum* (Nutt.) Nees]; Castor Bean, “*Ricinus Americanus*” [*Ricinus communis* L.]; pineapple, “*Ananas Indorum*,” [*Ananas* Mill]; milkweed, “*Wisauk*,” [*Asclepias syriaca* L.], derived from John White’s 1585 drawing in “Virginia,” and the potato, “*Solanum tuberosum esculentus*,” [*Solanum tuberosum* L.].

How did Bauhin come by these pictures? Who drew them? Where did the plants grow? How did Bauhin and his colleagues use these images? This talk will present the collection in the context of botany in Bauhin’s time. I will argue that these pictures give us, in effect, a precious time capsule of late Renaissance botanical illustration and networking.

## Shifting plant distribution driven by climate change?

Jessica Wang, Markus Fischer, Stefan Eggenberg, Katja Rembold

Botanical Garden of the University of Berne, Bern, Switzerland, katja.rembold@boga.unibe.ch

Herbarium specimens provide an irreplaceable source of historical plant distribution data and therefore allow us to detect and analyse changes in plant distribution across centuries. The majority of available studies on plant distribution shifts only date back a few decades and focus on rare species, often along elevational gradients. Here, we selected 30 character plant species from five habitats mainly in the lowlands of Switzerland (six species per habitat). In the Herbarium of the Botanical Garden of the University of Bern, we studied about 2,000 historical herbarium specimens of the selected species, reaching back to the year 1768 and covering all Swiss cantons. All label data were transcribed and georeferenced (if possible). These historical data were then combined with current data from the Info Flora database (Swiss national plant database), resulting in about 170,000 plant records across more than 250 years. The botanical data were combined with climatic data covering the time period (temperature and precipitation), that were provided by the Institute of Geography of the University of Bern. This comprehensive dataset allows us to investigate the impact of climate change on the distribution of the selected plant species and if distributions shifts affect certain species or entire plant communities. The historical data from the herbarium specimens are provided for the Info Flora database.

## Within-species variation poorly reflects species diversification along elevational gradients in *Saxifraga*

Seraina E. Rodewald<sup>1,2</sup>, Jurriaan M. de Vos<sup>1</sup>

<sup>1</sup> Department of Environmental Sciences – Botany, Basel University

<sup>2</sup> Dept Biology 1 – Systematics, Biodiversity and Evolution of Plants, LMU Munich, Germany, Seraina.Rodewald@lmu.de

Plants display radically different phenotypes across elevational belts, as a response to changing environmental conditions. Convergent adaptation to high elevation environments is indeed well-known across plant groups. Such elevation-associated variation among species (resulting from macroevolution) should be reflected in patterns within species (resulting from microevolution and plasticity), because selective pressure exerted by environmental gradients should structure variation at all hierarchical levels. However, this hypothesis remains poorly tested in plants. We thus analysed variation in 16 morphological traits within and among nine *Saxifraga* species, using georeferenced herbarium specimens from the herbaria Basel (BAS/BASBG) and associated climate data. Contrary to our hypothesis, we demonstrate that within species variation poorly reflects among species variation. Specifically, effect sizes of environmental variables on morphological variables among species greatly exceed those within species. Within species, traits were barely structured by the macroclimatic environmental variables, independent of whether traits were variable within species or not. In the context of alpine plants, our results suggest that the relative invariability of the branching pattern within species may constitute an important and overlooked limit to a species’ environmental breadth, because elaborately branching inflorescences may require more time for development than the short alpine summer season permits. More broadly, our results imply that within-species variation holds some, but not all information to predict environmental adaptation, implying that macroevolution entails more than an extrapolation from microevolution.



## Resurrecting a heterotypic synonym and validly describing a nomen nudum based on herbarium specimens

R. R. Rubite<sup>1</sup>, D. B. H. Ubaldo<sup>1</sup>, J. C. Salcedo<sup>1</sup>, K.-F. Chung<sup>2</sup>, L. T. Evangelista<sup>3</sup>, D. N. Tandang<sup>3,4</sup> & M. Hughes<sup>5</sup>

- <sup>1</sup> University of the Philippines Manila, Department of Biology, College of Arts and Sciences, Padre Faura, Ermita, Manila, Philippines, rrrubite@up.edu.ph
- <sup>2</sup> Research Museum and Herbarium, Biodiversity Research Center, Academia Sinica, Taipei, Taiwan
- <sup>3</sup> Philippine National Herbarium, Botany Division, National Museum, Manila, Philippines
- <sup>4</sup> Biodiversity Program, Taiwan International Graduate Program, Academia Sinica and National Taiwan Normal University; Department of Life Science, National Taiwan Normal University; Biodiversity Research Center, Academia Sinica, Taipei, Taiwan
- <sup>5</sup> Royal Botanic Garden Edinburgh, United Kingdom

The nomen nudum *Begonia hemicardia* Elmer ex Merr. (*B. sect. Petermannia*) was coined by A.D.E. Elmer in 1915. He annotated one of his collections (14366 from Mt. Bulusan, Luzon) in the PNH herbarium with the name, but did not formally publish it. E.D. Merrill in 1923 recognized the name as a synonym of *B. binuangensis* Merr. After thorough studies of the herbarium specimens and literature we found *B. hemicardia* to be different from *B. binuangensis*. *Begonia hemicardia* is allied to a group of climbing *Begonia* in the Philippines with axillary inflorescences and numerous, sub-symmetric, ovate to lanceolate-ovate leaves, i.e. *B. megacarpa* Merr., *B. aequata* A.Gray, *B. binuangensis* Merr., *B. edanoi* Merr., *B. gracilipes* Merr., *B. lagunensis* Elmer, *B. sarmentosa* L.B.Sm. & Wassh. and *B. wenzelii* Merr. However, a combination of characters such as the long internodes, large persistent stipules, serrate leaf margins and the long inflorescence with staminate flowers borne on a jointed rachis readily distinguish *B. hemicardia* from them, and we validly describe the new species.

## Plant Exchange Networks in the 19th Century

Christof N. Schröder

German University of Administrative Sciences Speyer, and Justus-Liebig-University Giessen, and CNSflora Edingen, Germany, cns@cnsflora.de

Herbarium specimens are not only documents of biodiversity, but also historical sources as they demonstrate at least one historical event, the gathering of the preserved plant in the wild. In many cases they contain data on further events: e.g. exchange between plant collectors, exchange through clubs, revision, accession at a collection or databasing. Herbarium specimens are made to be preserved for a long time, in contrast to daily correspondences, which are preserved only if the sender or recipient was an important historical person, e.g. Linnaeus. As herbarium specimens were collected by various people, from a day labourer to a judge at High Court, they reveal social networks hardly visible in correspondences. In this study plant exchange networks are studied by two approaches: Firstly by exchange activities – revealed by specimens in numerous herbaria-related to the rare central European endemic *Saxifraga rosacea* subsp. *sponhemica* (C.C.Gmel) D.A.Webb, which was discovered at the end of the 18th century by Carl Christian Gmelin (1762–1837) from Karlsruhe, and secondly by searching for exchange partners in the private herbarium of Wilhelm Christoph Bochkoltz (1810–1877), chemical engineer and amateur botanist from Trier, who discovered several new populations of the Sponhemian *Saxifraga* and collected large numbers of specimens. These two approaches led to the identification of about 100 plant exchange organizations in Europe and more than 700 individuals who collected, exchanged or revised herbarium specimens in the given context.

## Herbarium phylogenomics, taxonomy and evolution of complex reproductive systems in Connaraceae

Serafin J. R. Streiff, Jurriaan M. de Vos

Department of Environmental Sciences – Botany, University of Basel, Switzerland, serafin.streiff@unibas.ch

Connaraceae is a poorly studied, pantropical angiosperm family that is particularly diverse in complex reproductive systems, such as di- and tristily. However, a lack of molecular phylogenetic framework and stable taxonomy especially in the tribe Cnestideae has discouraged research on this family. Here, we leverage recent advances in sequencing herbarium specimens to greatly expand the molecular sampling of Cnestideae using the Angiosperms353 target enrichment approach, and use the phylogeny to revise generic limits within Cnestideae. During a representative survey of specimens in European herbaria (G, K, L, M, P, U, WAG) we scored herbarium specimens for reproductive systems and test hypotheses on their evolutionary trajectory. Based on our well-supported phylogeny, we find Cnestidae is monophyletic, but none of the generic concepts are tenable. In a formal taxonomic revision we propose a new circumscription of *Rourea*, and accept the following genera: *Byrsocarpus*, amended *Rourea*, s.str., *Roureopsis*, *Santaloides* and *Santaloidella*, as well as previously recognised *Agelaea*, *Cnestis* and *Pseudoconnarus*, which are all strongly supported and morphologically characterised. We document that reproductive system evolution is rather labile: nevertheless, we cannot statistically differentiate between a scenario where tristily is ancestral (with multiple parallel losses) or where distily is ancestral, with multiple independent origins of tristily. Based on morphological considerations, we consider multiple losses of tristily more plausible. These results underscore not only the importance of herbarium-based taxonomy and systematics, in particular for logistically challenging study systems, but also offer perspectives in utilising specimens for more applied studies.

## Correspondence of D.F.L. von Schlechtendal in the herbarium of Halle, Germany (HAL)

Natalia Tkach & Martin Röser

Geobotany and Botanical Garden, Institute of Biology, Martin Luther University Halle-Wittenberg, Halle, Germany, natalia.tkach@botanik.uni-halle.de

D.F.L. von Schlechtendal (1794–1866) was one of the most important botanists of the 19th century. He was professor of botany at the University of Halle-Wittenberg from 1833 to 1866, where his plant collection of some 70,000 specimens is still preserved. Schlechtendal described more than 1,600 new taxa, including 78 new genera, mostly from the New World, although he rarely traveled. Schlechtendal's dense network of scientific contacts is documented by his correspondence. It comprises 5,600 letters from about 500 people, including a large number of famous contemporary botanists, natural scientists, travelers, and plant collectors, e.g., A. von Humboldt, A. von Chamisso, also known as a poet, A.H.G. Grisebach, A.L.P.P. de Candolle, R.F. Hohenacker, C.F.P. von Martius, etc. The letters mostly refer to publications and scientific questions concerning the journals 'Linnaea' and 'Botanische Zeitung' edited by Schlechtendal. The authors send him the manuscripts and often the specimens of the new taxa as a gift, which are kept in our herbarium. The letters of scientists dealing with African, Central and South American plants are often used as an important source of information. The letters are written in old German Kurrent script, the ink is fading and the paper is disintegrating. We therefore want to transcribe all letters (54 % are already finished), index them, digitize them and make them available online. Publications have already appeared on some of these letters. This correspondence is of outstanding and supra-regional importance for today's research and scientific study of the flora of these countries of origin.



## Flora of the Canary Islands – Revised Checklist to a Classic Arena of Botany

Anna Walentowitz<sup>1</sup>, Carl Beierkuhnlein<sup>1</sup>, Walter Welss<sup>2</sup>

<sup>1</sup> Chair of Biogeography, University of Bayreuth, Germany, Anna.walentowitz@uni-bayreuth.de

<sup>2</sup> Botanical Garden and Herbarium Erlangense, Friedrich Alexander University Erlangen, Germany

The Canary Islands are a classic site for botanical collections with a series of seminal works including the description and documentation of many endemic plant species in herbaria. Viera y Clavijo, Christ, Webb, Berthelot, Sventenius, Pitard, Kunkel, or Bramwell are just a selection of scientists with important contributions to the flora. Alexander von Humboldt's botanical description of his stay on Tenerife motivated Charles Darwin to explore Tenerife, but he was not allowed to leave the ship because of quarantine. In recent years, data bases emerged with detailed information about plant lists. This legacy supports the expectation of detailed information and far-reaching agreement about the flora of the islands. Here, we document which taxa are agreed upon in current data sources, and which taxa are accepted in global reference systems. Surprisingly, we find a considerable proportion of taxa that are recorded but missing in current floras and data bases. Furthermore, we identified taxa with deviating status e.g. in Plants of the World Online or World Flora Online. We also analyze deficiencies and related fundamental restrictions in databases that are commonly used in ecology and biodiversity research (e.g. TRY, GBIF). And still, new species are detected and described. Despite the fact of being such a classic playground for botanists, the flora of the Canary Islands is still work in progress. Updating such an important data source is a prerequisite for macroecological and biogeographical studies. Our new checklist is just a current update on the state of knowledge and the basis for further amendments.



## List of participants

Family name	First name	Affiliation		City	Country
Aeschbacher	Simon	University of Zurich	Dept of Evolutionary Biology and Environmental Studies	Zurich	CH
Agosti	Donat	Plazi		Bern	CH
Bakker	Freek T.	Wageningen University	Plant Sciences, Biosystematics Group	Wageningen	CH
Bendiksby	Mika	University of Oslo	Natural History Museum	Oslo	NO
Bjørå	Charlotte	University of Oslo	Natural History Museum	Oslo	NO
Boller	Thomas	University of Basel & BBG	Dept Environmental Sciences	Basel	CH
Bosshard	Maya	University of Basel	Dept Environmental Sciences	Basel	CH
Burbano	Hernán	University College London	Dept Genetics, Evolution and Environment	London	GB
Büttner	Michèle	Museum zu Allerheiligen Schaffhausen	Herbarium	Schaffhausen	CH
Cameron	Ken	University of Wisconsin-Madison	Dept of Botany, Wisconsin State Herbarium (WIS)	Madison, WI	US
Carine	Mark	Natural History Museum	Algae, Fungi and Plants Division	London	GB
Chen	Luo	LMU Munich	Systematik, Biodiversität & Evolution der Pflanzen	Munich	DE
Chin	Alana	ETH Zurich	Dept Environmental Systems Science	Zurich	CH
Chinchilla	Delphine	Jurassica Museum	Botanical Garden of Porrentruy	Porrentruy	CH
Christe	Camille	Conservatoire et Jardin botaniques Genève	PhyloLab	Chambésy, GE	CH
Cook	Alexandra	University of Hong Kong	Philosophy	Hong Kong	HK
Dahinden	Manuela	Zurich-Basel Plant Science Center	ETH Zürich	Zürich	CH
de Vos	Jurriaan M.	University of Basel & BBG	Dept Environmental Sciences – Herbaria Basel	Basel	CH
Détraz-Méroz	Jacqueline			Basse-Nendaz, VS	CH
Di Maio	Edouard	Université de Neuchâtel		Neuchâtel	CH
Duque-Thüs	Rhinaixa V.	University of Hohenheim	Institute of Biology	Stuttgart	DE
Eggli	Urs	Grün Stadt Zürich	Sukkulenten-Sammlung	Zürich	CH
Erhardt	Andreas	University of Basel		Basel	CH
Frenzke	Lena	Technische Universität Dresden	Biology	Dresden	DE
Gagnon	Edeline	Technical University of Munich	Chair of Phytopathology	Freising-Weinstephan	DE
Gerasimova	Julia	Ludwig-Maximilians-Universität München	Systematics, Biodiversity and Evolution of Plants	Munich	DE
Grall	Aurélié	University of Basel	Dept Environmental Sciences – Herbaria Basel	Basel	CH
Grant	Jason	Université de Neuchâtel	Laboratoire de génétique évolutive	Neuchâtel	CH
Gremaud	Colette	Jurassica Museum	Botanical Garden of Porrentruy	Porrentruy	CH
Groffman	Dominique	Ludwig-Maximilians-Universität München	Systematics, Biodiversity and Evolution of Plants	Uppsala	SE
Grubinger	Thomas	University of Zurich	Dept of Evolutionary Biology and Environmental Studies	Zurich	CH
Gruenert	Uta	Tuebingen University	Institute of Evolution and Ecology	Tuebingen	DE
Guggisberg	Alessia	ETH Zurich	Dept Environm Systems Science, Inst of Integrative Biology	Zurich	CH
Haas	Jean Nicolas	University of Innsbruck & BBG	Botany	Innsbruck	AT
Harpke	Dörte	Leibniz Institute IPK	Genbank	Seeland	DE
Hille Ris Lambers	Janneke	ETH Zurich	Department of Environmental Systems Science	Zürich	CH
Hoch	Günter	University of Basel	Dept Environmental Sciences	Basel	CH
Holderegger	Rolf	WSL Swiss Federal Research Institute		Birmensdorf	CH
Irimia	Ramona-Elena	Eberhard Karls Universität Tübingen	Institute of Evolution & Ecology	Tübingen	DE
Joyce	Elizabeth	Ludwig-Maximilians-Universität München	Faculty of Biology	Munich	DE
Jutzi	Michael	Info Flora	c/o Botanischer Garten	Bern	CH
Kahmen	Ansgar	University of Basel	Dept Environmental Sciences	Basel	CH
Klotz	Stefan	Helmholtz Centre for Environmental Research	Community Ecology	Halle (Saale)	DE



Family name	First name	Affiliation		City	Country
Kocyan	Alexander	University of Zurich	Botanisches Museum, Inst. für Pflanzen- und Mikrobiologie	Zürich	CH
Kozlowski	Gregor	University of Fribourg	Department of Biology	Fribourg	CH
Kull	Thea	Estonian University of Life Sciences	Institute of Agricultural and Environmental Sciences	Tartu	EE
Landoni	Beatrice	University of Portsmouth	School of Biological Sciences	Portsmouth	GB
Lasky	Jesse	Pennsylvania State University	Dept of Biology	University Park, PA	US
Lehnert	Marcus	Martin-Luther-Universität Halle-Wittenberg	Herbarium HAL	Halle	DE
Martinez	Sylvia	University of Basel & BBG	Dept Environmental Sciences	Basel	CH
Mast	Austin	Florida State University	Biological Science	Tallahassee, FL	US
Michel	Thibault	Royal Botanic Garden of Edinburgh	Tropical Diversity	Edinburgh	GB
Morales-Briones	Diego F.	Ludwig-Maximilians-Universität München	Systematics, Biodiversity and Evolution of Plants	Munich	DE
Muñoz-Rodriguez	Pablo	University of Oxford	Plant Sciences	Oxford	GB
Naciri	Yamama	Conservatoire et Jardin botaniques Genève	PhyloLab	Chambésy, GE	CH
Neinhuis	Christoph	Technische Universität Dresden	Institute for Botany	Dresden	DE
Nyffeler	Reto	University of Zurich	United Herbaria	Zurich	CH
Nygaard	Malene	Natural History Museum and Botanical Garden	University of Agder	Kristiansand	NO
Offerhaus	Aleida	Naturalis Biodiversity Center	Tropical Botany	Leiden	NL
Perret	Mathieu	Conservatoire et Jardin botaniques Genève		Chambésy, GE	CH
Price	Michelle	Conservatoire et Jardin botaniques Genève	Herbarium	Chambésy, GE	CH
Primack	Richard	Boston University	Biology Department	Newton, MA	CH
Rat	Milica	University of Novi Sad, Faculty of Sciences	Dept of Biology and Ecology	Novi Sad	RS
Reeds	Karen	Princeton Research Forum		Princeton, NJ, USA	US
Rembold	Katja	Botanical Garden of the University of Bern		Bern	CH
Rodewald	Seraina	Ludwig-Maximilians-Universität München	Systematik, Biodiversität & Evolution der Pflanzen	Munich	DE
Rubite	Rosario	University of the Philippines	Dept of Biology, College of Arts and Sciences	Ermita, Manila	PH
Schoenenberger	Nicola	Conservatoire et Jardin botaniques Genève	Direction	Chambésy, GE	CH
Schreier	Esther	Basler Botanische Gesellschaft BBG		Basel	CH
Schröder	Christof N.	CNSflora		Edingen-Neckarhausen	DE
Schünemann	Verena	University of Zurich	Institute of Evolutionary Medicine	Zurich	CH
Sejdiu	Donikë	University of Zurich	Institute of Evolutionary Medicine	Zurich	CH
Spehn	Eva	Swiss Biodiversity Forum	SCNAT	Bern	CH
Stauffer	Fred	Conservatoire et Jardin botaniques Genève		Chambésy, GE	CH
Stefanaki	Anastasia	Wageningen University	Biosystematics	Wageningen	NL
Stöcklin	Jürg	University of Basel & BBG	Dept Environmental Sciences	Basel	CH
Streiff	Serafin	University of Basel	Dept Environmental Sciences	Basel	CH
Teixeira-Costa	Luiza	Vrije Universiteit Brussel	Sciences and Bioengineering Sciences	Brussels	BE
Tkach	Natalia	Martin Luther University Halle-Wittenberg	Institute of Botany	Halle	DE
Ulrich	Gabriel	ETH Zurich	Dept Environmental Systems Sciences	Zurich	CH
van Andel	Tinde	Naturalis Biodiversity Center	Tropical Botany	Leiden	NL
Vust	Mathias	Université de Neuchâtel	Biologie	Neuchâtel	CH
Wagner	Sarah	Technische Universität Dresden	Institute for Botany	Dresden	DE
Walentowitz	Anna	University of Bayreuth	Biogeography	Bayreuth	DE
Walter	Tilman	Universität Würzburg	Institut für Geschichte der Medizin	Würzburg	DE
Willi	Yvonne	University of Basel	Dept Environmental Sciences	Basel	CH



## Impressum / Imprint

© Herbaria Basel, Dept. of Environmental Sciences, Basel University, Switzerland, September 2022

<https://herbarium.unibas.ch/en/bauhin2022/>

Editor: Sylvia Martinez, Basel University

Graphics, layout, cover image: estherschreier.ch

Print: BSB Medien (Bürgerspital Basel), Basel, Switzerland

Print run: 100 copies

Paper: Navigator FCS 80g/m<sup>2</sup> (pages), Image Impact FSC 160g/m<sup>2</sup> (cover)





**15 & 16 September 2022**  
**University of Basel, Switzerland**  
**Main building, room 120, Petersplatz 1, Basel**

# **400 Years Botanical Collections**

## **Implications for Present-Day Research**

### **International Symposium**

**Bauhin2022.ch**



University  
of Basel

D | Departement  
U | Umweltwissenschaften  
W



Basler  
Botanische Gesellschaft  
botges.ch