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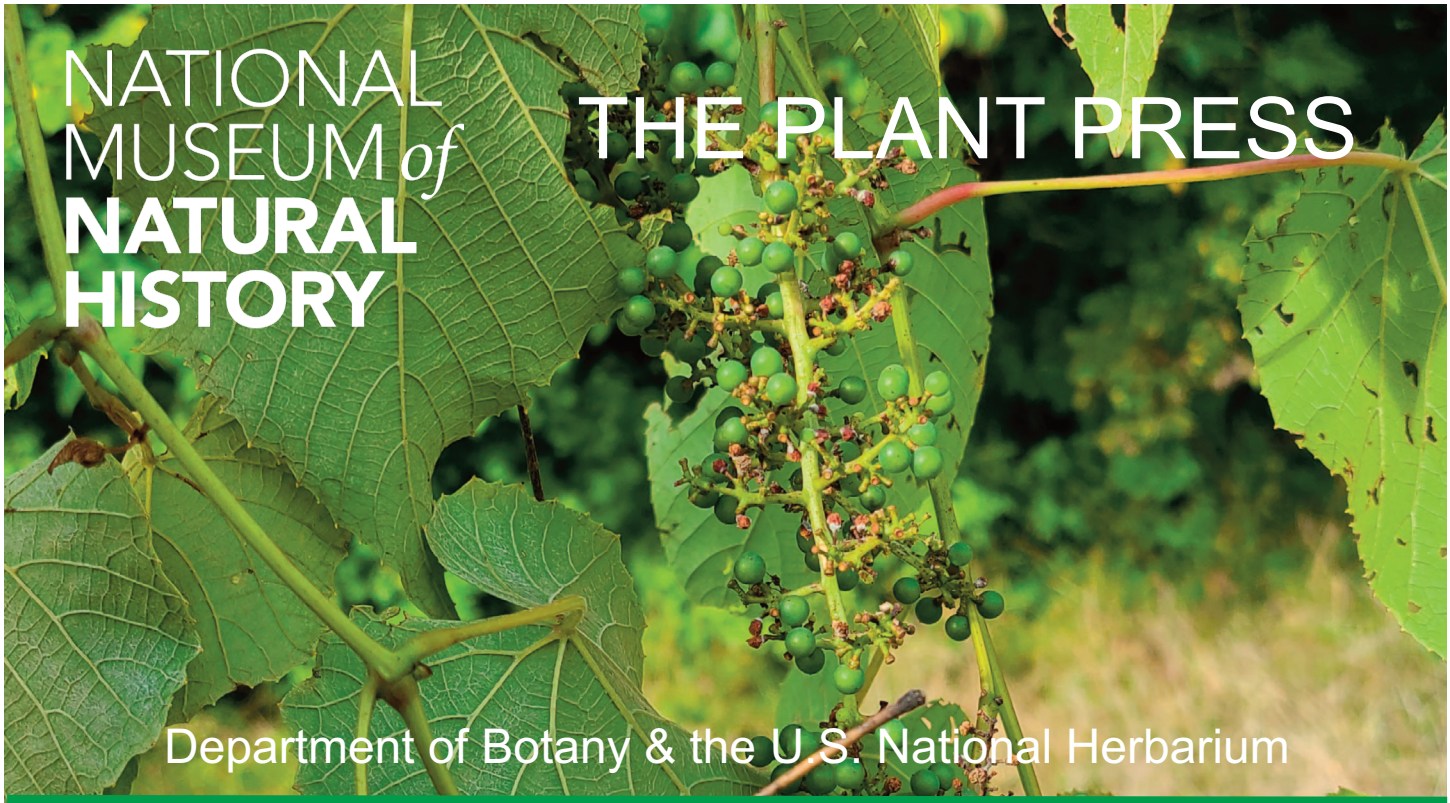

Department of Botany & the U.S. National Herbarium

New Series - Vol. 25 - No. 4 October-December 2022

Grape escapes and beyond:

A summer of botanical adventures in southern US and Mexico

By Jun Wen, Alicia Talavera and Greg Stull

Curator Jun Wen and her collaborators have been conducting extensive field work on the grape family Vitaceae, especially the grape genus *Vitis*. This summer Wen traveled throughout the southern US in early July with postdoctoral fellow Alicia Talavera, and to Mexico throughout August with Research Collaborator Greg Stull to collect Vitaceae and specimens of other plant groups significant for biogeographic studies of the Northern Hemisphere. The two trips in the USA and Mexico resulted in approximately 800 specimens representing one of the most important sets of Vitaceae collections from North America (including Mexico), many specimens of Northern Hemisphere intercontinental disjunct plants, and also economically important wild relatives of food and drug plants.

Grape hunting in the southern US: North America is one of the two major centers of diversity for the grape genus *Vitis*. It is home to approximately 30 of the 75 species in the genus. The wine grape *Vitis vinifera* is one of the earliest domesticated crops and is considered the most economically important fruit crop in the world. Despite the economic and evolutionary interests, the taxonomy of the grape genus remains controversial, largely due to extremely complex histories of hybridizations and morphological plasticity. Studies in the Wen lab incorporating evidence from the field, herbarium, and genome sequences are ongoing to unravel the complex evolutionary history of *Vitis*, especially several species complexes in North America, e.g., the *Vitis cinerea* complex, and the *Vitis aestivalis* complex. Talavera's postdoctoral research focuses on clarifying the taxonomy and evolutionary diversification of North American *Vitis* and exploring phylogeographic patterns in

Continued on page 2

The two trips in the USA and Mexico resulted in approximately 800 specimens representing one of the most important sets of Vitaceae collections from North America to Mexico.

Grapes

Continued from page 1

this region. In order to expand the population sampling for Talavera's postdoctoral research, Wen and Talavera conducted a field trip to the southern US, covering Virginia, North Carolina, Tennessee, Alabama, Florida, Mississippi, Louisiana, Arkansas, Missouri, Kentucky, Indiana, Ohio, and West Virginia.

Wen and Talavera collected approximately 300 specimens of *Vitis*, and many other taxa (e.g., *Angelica*, *Ampelopsis*, *Arundinaria, Carya, Clematis, Cyrilla, Halesia, Juglans, Magnolia, Nekemias, Nyssa, Parthenocissus*, *Polymnia, Prunus, Sagittaria, Sabatia, Trepocarpus,* and *Wisteria*). This southern US field trip was critical for Talavera's *Vitis* studies and provided the opportunity for her to gain a broad understanding of species variations in natural populations. They collected in diverse types of habitats across the eastern deciduous forests in North America, including the mesophytic forests in the Appalachians, the southern mixed oak-pine forests, the coastal cypress-tupelo swamp forests, the Mississippi alluvial plain forests, and the rich oak-hickory forests in the Ozarks.

Overall, the trip was a great experience for Talavera, who came to the Smithsonian from southern Spain in January 2022. Talavera returned to Washington D.C. with a greater appreciation of the ecological and cultural diversity in the areas where grapes thrive. They look forward to their phylogenomic results from these collections and the insights into the evolutionary diversification history of North American *Vitis* and the drivers that have shaped the species diversity in this region.

Journey into tropical Mexico: Tropical Mexico remains the key to understanding the diversity and evolutionary diversification of Central American Vitaceae. This is particularly true for the taxonomically difficult genera *Vitis* and *Cissus*, which are in need of detailed study to clarify species boundaries and species numbers in the Americas. Tropical Mexico also represents one of the keys to better understanding the biogeographic history of the Northern Hemisphere, including the fragmentation of mesic forests across the North American continent during episodes of aridification and glaciation over the past 10 million years. With these research problems in mind, Wen and Stull conducted a major field trip to Mexico, in collaboration with Dr. Marcelo Pace from the Universidad Nacional Autónoma de México (UNAM). Joining them was one of Pace's graduate students, Angelica Quintanar, who is starting her doctoral dissertation research on Vitaceae wood anatomy and the evolutionary adaptation of the wood characters. Quintanar's collecting goal aligned perfectly with that of the others: to collect as many Vitaceae specimens as possible, including extra collections of stem and wood samples for subsequent anatomical work.

Jun Wen and Alicia Talavera collecting *Vitis cinerea* var. *floridana* in central Virginia. (photo by Alicia Talavera)

Prior to going to the field, Wen and Stull spent a few days working in the National Herbarium MEXU in UNAM, and were kindly welcomed by Dr. Susana Magallón Puebla, the director of the UNAM Institute of Biology, and by Dr. Gerardo Salazar, the director of MEXU. The MEXU herbarium is truly a gem and is the largest herbarium in Latin America. Recently it has been fully digitized, making more than 1.3 million specimens at MEXU online to the scientific community and the public. While at UNAM, Wen gave a well-received seminar on "Collections-based systematics in the age of genomics and informatics" in the Institute of Biology. Salazar and Dr. Lidia Cabrera also gave Wen and Stull a terrific tour of the National Biodiversity Pavilion, a new museum that was recently opened to showcase Mexico's mega-biodiversity using collections, the tree-of-life theme, stories of scientists connecting with the public, and the behind-the-scenes labs (still under construction). The creation of the museum was inspired in part by visits to the Smithsonian's Natural History Museum by Carlos Slim, the Mexican philanthropist who funded the Biodiversity Pavilion project.

Over the course of about 20 days in the field, the team made over 500 plant collections mostly emphasizing the entire southern half of Mexico and also in central to northeastern Mexico, driving approximately 3,800 miles across the states of Puebla, San Luis Potosi, Tamaulipas, Veracruz, Campeche, Tabasco, Yucatan, Chiapas, Oaxaca, Morelos, and Mexico. In distance this is roughly equivalent to taking the long route between Key West, Florida, and Vancouver, British Columbia. The resulting collections included about 150 accessions of Vitaceae and 350 accessions of plants that are important for further understanding Northern Hemisphere biogeography.

Wen and Stull both have research interests in studying Northern Hemisphere biogeography. Wen has a long history of

studying disjuncts across the Northern Hemisphere, particularly genera disjunct between North America and Asia, and a number of the specimens collected are relevant for this pattern (e.g., *Bocconia*, *Dendropanax*, *Saurauia*). Stull is especially interested in exploring the evolutionary patterns and processes of plant disjunctions between the eastern United States and the montane zones in Mexico, an underexplored biogeographic pattern that includes more than 90 species or closely related species disjunct between these regions. One of the most iconic examples of this disjunction, *Liquidambar styraciflua*, was collected at several locations in Puebla and Veracruz. Other noteworthy collections include the root parasite *Bdallophytum* (Cytinaceae), the liana genus *Dichapetalum* (Dichapetalaceae), and *Petenaea*, a previously unplaced genus now treated as its own family, Petenaeaceae. The latter collection was made by graduate student Quintanar, who started her first botanical collection number of her career during this trip.

Reflecting on the field trips to Mexico, it was well noted that the lowland habitats across southern Mexico have changed drastically with the loss of primary forests in the last 35 years. The team had a difficult time relocating populations of the Mexican *Ampelocissus* (Vitaceae) along the Gulf coast. The New World *Ampelocissus* is a small lineage of 5-6 species that often occur in primary seasonally dry tropical forests. This lineage of *Ampelocissus* is sister to the economically important genus *Vitis*, and the locals in Puebla have been making wine from the fruits. We had a taste of the *Ampelocissus* wine bought from a small village store in Puebla at our farewell party with our UNAM friends on the eve of our departure; it was sweet, tasting like the muscadine wine from southeastern US. We hope that the rapid economic growth in Mexico will also go along with serious conservation efforts and strong public education programs about the tropical forests and the natural treasures in these vulnerable forests.

Work is now underway to sequence and morphologically examine the collected Vitaceae specimens, facilitating phylogenomic and taxonomic studies that should lead to the recognition of several new species of *Vitis* and *Cissus* and clarify the early diversification of the grape genus. The disjuncts collected also lay an important foundation for future work by Stull and Wen, in collaboration with botanists at UNAM, that will unravel one of the last major puzzles in Northern Hemisphere biogeography: what is the evolutionary history behind the eastern US-Mesoamerican cloud forest floristic disjunction?

Left: Jun Wen, Marcelo Pace and Angelica Quintanar collecting *Ampelocissus erdvenbergiana* near Valladolid, Yucatán. (photo by Greg Stull)
Right: Greg Stull pressing specimens near Jalcomulco, Veracruz. (photo by Angelica Quintanar)

Stem cross-section of the liana, *Cissus erosa*, northeast of Ciudad Valles, San Luis Potosí. Angelica Quintanar and Marcelo Pace are studying wood anatomy of Vitaceae so a large collection of Vitaceae wood was made during the trip. (photo by Jun Wen)

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On the cover: An odd grape specimen of the *Vitis cinerea* complex in Alabama, likely a hybrid between *V. cinerea* var. *baileyana* and *V. cinerea* var. *cinerea*. (photo by Jun Wen)

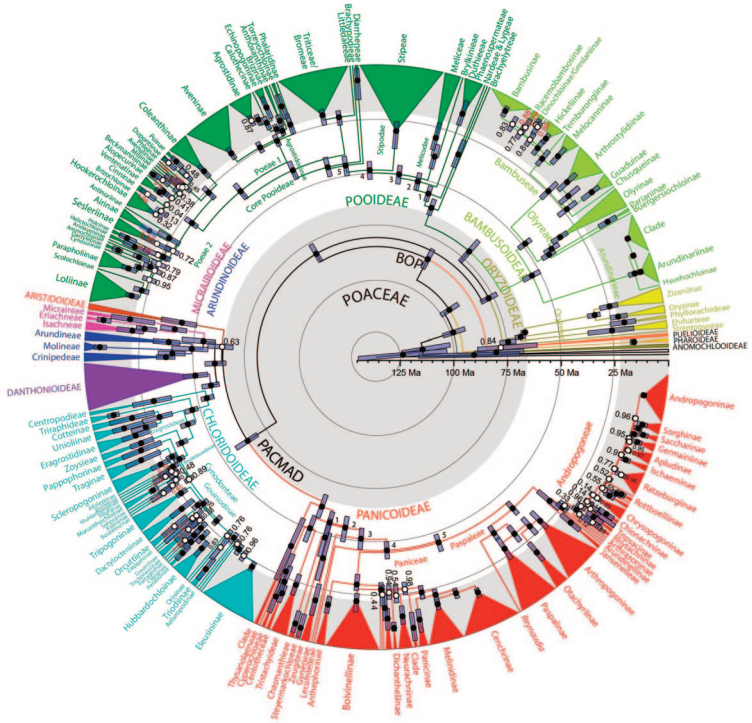
New issue of the *Journal of Systematics and Evolution* investigates the biogeography and phylogenetics within the grasses

Paul Peterson and **Robert Soreng** organized and published (with help from **Konstantin Romaschenko**) a complete issue of the *Journal of Systematics and Evolution* [60(3): 473-712; 2022 https://doi.org/10.1111/jse.12776] investigating the biogeography and phylogenetics within the grasses. Using the fossil record to aid in dating their phylogenetic trees and combining molecular sequence studies of DNA, they reconstructed ancestral states to infer the origin of major clades; i.e., subfamilies, tribes, supersubtribes, subtribes, and selected genera in the grasses. For this special issue, Peterson and Soreng invited a broadly trained group of 35 scientists to collaborate and present their most recent advances culminating in 10 publications.

Four of the manuscripts in the issue include new dated biogeographical analyses (Gallaher et al., 2022; Peterson et al., 2022b; Soreng et al., 2022a; Zhou et al., 2022); three comprise new phylogenetic analyses with novelties (Da Silva et al., 2022; Peterson et al., 2022a, 2022c), one is an ecological study investigating functional traits in a clade of savanna/wetland grasses (Arthan et al., 2022), one looked at the current distribution of the grasses over the Australian continent to determine migration directionality (Bryceson & Morgan, 2022), and one is an updated classification of the family primarily based on molecular phylogenetic studies (Soreng et al., 2022b).

The Poaceae began to diversify in the early–late Cretaceous (crown age of 98.54 Ma) on West Gondwana before the complete split between Africa and South America, and Africa clearly served as the center of origin for much of the early diversification of the lineages within the family (Gallaher et al., 2022). The plastid analysis included 700 taxa. In addition, Gallaher et al. (2022) includes an extensive review of the extant diversity and distribution of species, molecular and morphological evidence supporting the current classification scheme, and a biogeographical history of most lineages.

Soreng et al. (2022a) found that the ancestral area of the PPAM clade of tribe Poeae, including ca 870 species in 43 genera (42 in the DNA analysis) in 12 subtribes (Alopecurinae, Avenulinae, Beckmanniinae, Brizochloinae, Cinninae, Coleanthinae, Dupontiinae, Hookerochloinae, Miliinae, Phleinae, and Poinae, Ventenatinae), was in the high mountains of southwestern Asia (including the Caucasus), originating in the early Miocene (crown mean of 21.81 mya).



Phylogenetic reconstruction and timetree of the Poaceae and close relatives (*Joinvillea*, *Ecdeiocleа*, and *Flagellaria*) based on chloroplast DNA sequence from 700 samples, as seen in Gallaher, et al. (2022). The branches are color-coded by subfamily and collapsed at the subtribal level. Nodes with posterior probabilities below 0.99 are marked with a white node symbol and the posterior probability is shown. Node bars represent the 95% highest posterior density of node age estimates.

Muhlenbergia Schreb. (183 species), of the C4 subfamily Chloridoideae, apparently originated 9.3 mya in the Sierra Madre (Occidental and Oriental) in Mexico before splitting into six lineages, of which one (*M.* subg. *Muhlenbergia*) via long distance dispersal, colonized Central Asia 1.6–1 mya (Peterson et al., 2022b).

The tribe Bambuseae subtribe Melocanninae (nine genera) originated in the East Himalaya to northern Myanmar in the early Miocene (crown mean of 19.68 mya), and three routes were revealed in forming its present biogeographic pattern: in situ diversification on the Asian mainland, dispersing southwest to Sri Lanka and to the Western Ghats in South India, and spreading southeast to Malesia and Oceania via the Indo-China Peninsula (Zhou et al., 2022).

Peterson et al. (2022a), in a molecular study of nine Eleusininae genera (Chloridoideae), found *Coelachyrum* Hochst. & Nees polyphyletic and *Schoenefeldia* Kunth to be paraphyletic, subsequently describing a new genus, *Schoenefeldiella* P.M. Peterson with a single species and transferring *Apochiton burttii* C.E. Hubb. to *Coelachyrum*.

In another molecular study of tribe Poeae, this of supersubtribe Agrostidodinae, Peterson et al. (2022c) investigated *Calamagrostis* Adans. (Agrostidinae), hypothesizing the phylogenetic and biogeographical history of seven major species groups and proposing a new genus, *Condilorachia* P.M. Peterson, Romasch. & Soreng, while subsuming *Dichelachne* Endl. and more *Calamagrostis* into *Pentapogon* R.Br. (Echinopogoninae) and further narrowing *Calamagrostis* (including *Deyeuxia* s.s.) to 130 species.

Articles in the special issue of the *Journal of Systematics and Evolution* [60(3): 473-712; 2022 https://doi.org/10.1111/jse.12776]:

Arthan, W., V. Morales-Fierro, M.S. Vorontsova, E.A. Kellogg, J. Mitchley, and C.E.R. Lehmann. 2022. *Heteropogon-Themeda* grasses evolve to occupy either tropical grassland or wetland biomes. *J. Syst. Evol.* 60: 653-674.

Bryceson, S.R. and J.W. Morgan. 2022. The Australasian grass flora in a global context. *J. Syst. Evol.* 60: 675-690.

Da Silva, L.N., J.M. Saarela, L. Essi, and T.T. de Souza-Chies. 2022. [2021]. A comprehensive species sampling sheds light on the molecular phylogenetics of Calothecinae (Poaceae, Pooideae, Poeae): Evidence for a new subtribe and multiple genera within the *Chascolytrum* clade. *J. Syst. Evol.* 60: 691-712.

Gallaher, T.J., **P.M. Peterson**, **R.J. Soreng**, F.O. Zuloaga, D.Z. Li, L.G. Clark, C.D. Tyrrell, C.A.D. Welker, E.A. Kellogg, and J.K. Teisher. 2022. Grasses through space and time: An overview of the biogeographical and macroevolutionary history of Poaceae. *J. Syst. Evol.* 60: 522-569.

Peterson, P.M., **K. Romaschenko**, Y. Herrera Arrieta, and M.S. Vorontsova. 2022a. [2021]. Phylogeny, classification, and biogeography of *Afrotrichloris, Apochiton, Coelachyrum, Dinebra, Eleusine, Leptochloa, Schoenefeldia,* and a new genus, *Schoenefeldiella* (Poaceae: Chloridoideae: Cynodonteae: Eleusininae). *J. Syst. Evol.* 60: 630-639.

Peterson, P.M., C. Roquet, **K. Romaschenko**, Y. Herrera Arrieta, and A. Susanna. 2022b. [2021]. A biogeographical analysis of *Muhlenbergi*a (Poaceae: Chloridoideae: Cynodonteae: Muhlenbergiinae). *J. Syst. Evol.* 60: 621-629.

Peterson, P.M. and **R.J. Soreng**. 2022. The biogeography of grasses (Poaceae). *J. Syst. Evol.* 60: 473-475.

Peterson, P.M., **R.J. Soreng, K. Romaschenko**, P. Barberá, A. Quintanar, C. Aedo, and J.M. Saarela. 2022c. Phylogeny and biogeography of *Calamagrostis (*Poaceae: Pooideae: Poeae: Agrostidinae), description of a new genus, *Condilorachia* (Calothecinae), and expansion of *Greeneochloa* and *Pentapogon* (Echinopogoninae). *J. Syst. Evol.* 60: 570-590.

Soreng, R.J., L.J. Gillespie, E.A. Boudko, and E. Cabi. 2022a. Biogeography, timing, and life-history traits in the PPAM clade: Coleanthinae (syn. Puccinelliinae), Poinae, Alopecurinae superclade, Miliinae, and Avenulinae and Phleinae (Poaceae, Pooideae, Poeae). *J. Syst. Evol.* 60: 591-620.

Soreng, R.J., **P.M. Peterson**, F.O. Zuloaga, **K. Romaschenko**, L.G. Clark, J.K. Teisher, L.J. Gillespie, P. Barberá, C.A.D. Welker, E.A. Kellogg, D.Z. Li, and G. Davidse. 2022b. A worldwide phylogenetic classification of the Poaceae (Gramineae) III: An update. *J. Syst. Evol.* 60: 476-521.

Zhou, M.Y., J.X. Liu, P.F. Ma, J.B. Yang, and D.Z. Li. 2022. Plastid phylogenomics shed light on intergeneric relationships and spatiotemporal evolutionary history of Melocanninae (Poaceae: Bambusoideae). *J. Syst. Evol.* 60: 640-652.

Nature editorial connects the dots between forests, models, and funding

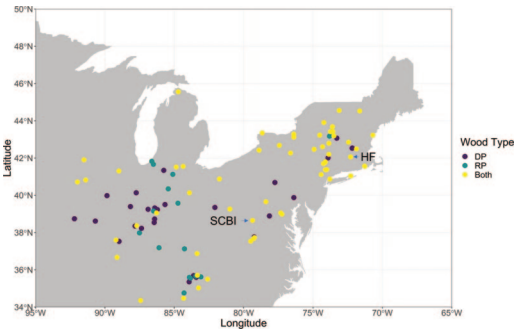
A *Nature* editorial (608: 449; 2022 https://doi.org/10.1038/d41586-022-02182-0) contends that it is well-past time to fund forest science like our future depends on it, stating, "Forests are our life-support system, and we should be more serious about taking their pulse."

Forest systems store about half of the world's carbon. They also take up 25% of all new anthropogenic carbon emissions; but can we expect them to continue doing so as climate change intensifies? Dynamic global vegetation models are our best way of anticipating the answer. They are also incredibly difficult to create due to the complexity of forest systems and the limits of drawing upon studies that were conducted at single forest sites.

A new *Nature* paper by Dow, et al. (608: 552-557; 2022 https://doi.org/10.1038/s41586-022-05092-3) uses dendrometer data from Harvard Forest and Smithsonian Conservation Biology Institute Forest Dynamics Plots, plus tree-ring records from 108 forests across the eastern US to examine the impact of warmer springs on carbon sequestration capacities of forests. Contrary to the expectations of many vegetation models, the data from Dow, et al. indicates that warmer springs do not lead to increased wood growth. Consequently, current vegetation models are overestimating the capacity of forests to mitigate climate change. This paper was lead-authored by Cameron Dow who began this manuscript with colleagues during his internship in Kristina Anderson-Teixeira's ForestGEO Ecosystems & Climate Lab.

The *Nature* editorial highlights the connections between complex forests, complex models, and complex funding systems. To reflect forest dynamics accurately, modelers need access to long-term data sets. Increasingly, though, long-term funding is unavailable, the current philanthropic landscape favoring three-to-five-year funding cycles. Commenting on the repercussions of these short funding cycles, ForestGEO Director, **Stuart Davies**, notes, "We have trained people and then lost them due to job insecurity." Short-term funding fails to provide job stability to the skilled technicians whose labor makes the data possible.

Dynamic global vegetation models inform policy decisions, but their accuracy is hindered when the assumptions they are built with do not reflect the more complicated reality. In short: We need forests; we need data; we need funding.



Map from Dow, et al. (2022) depicting sampling locations of tree-ring chronologies analyzed in the study. Sites are colored by the xylem porosity type of species sampled: ring porous (RP), diffuse porous (DP), or both.

Hawaii Rare Plant Genetics Workshop advances conservation research

By Warren Wagner & Gary Krupnick

The National Museum of Natural History (NMNH) co-hosted a Hawaii Rare Plant Genetics Workshop from October 2021 to March 2022, featuring 32 speakers over the course of 10 virtual sessions. From those recorded sessions, 19 presentations are now publicly available for viewing as a playlist on NMNH's Natural History for Scientists' YouTube channel <https://www.youtube.com/playlist?list=PLQmxS2U3B6KYo441UojIVJmNBpAu974v1>.

The goals of the 10-day workshop were to better understand how the latest molecular research, especially in the field of genomics, can benefit the ongoing challenges in plant conservation in Hawaii, and to determine when and how to incorporate molecular techniques into species recovery and management. Discussions centered around identifying particular techniques and methods most appropriate for a variety of questions and challenges regularly faced by field biologists in preventing species extinctions. One outcome of the workshop is that the workshop organizers are developing a decision tree for when and how best to utilize molecular techniques in plant conservation practices in Hawaii, and are creating a prioritization scheme that will allow field biologists to prioritize resources in funding and carrying out the highest priority research.

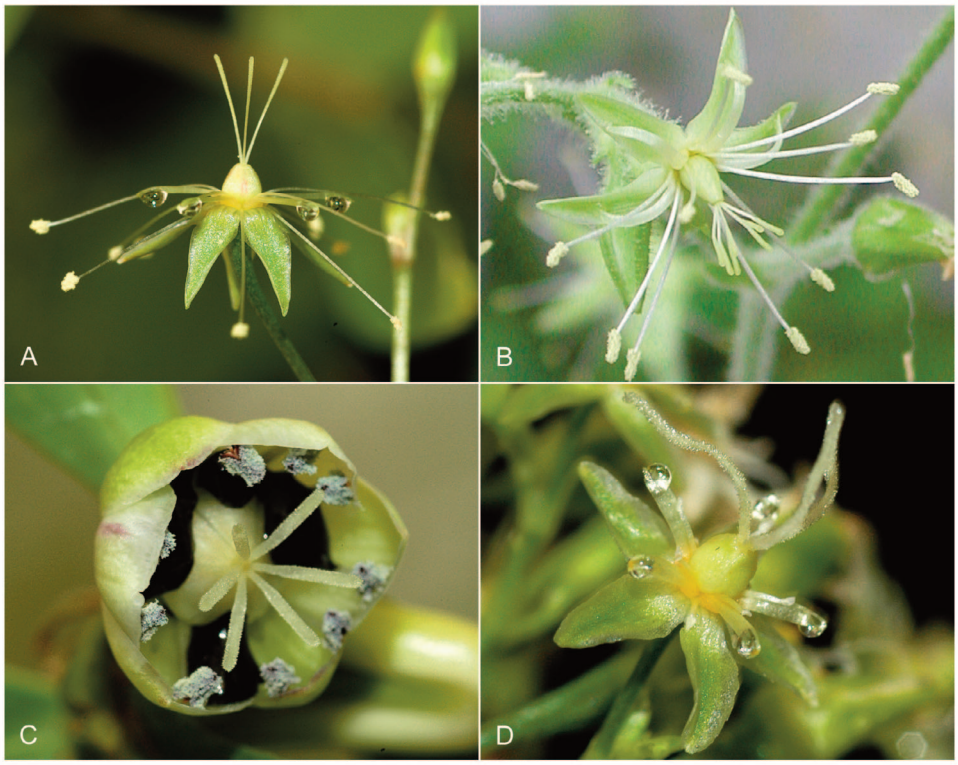
The workshop was part of a National Science Foundation (NSF)-funded collaborative project headed by Ann Sakai and Steve Weller (University of California, Irvine), Michael Moore (Oberlin College), Norm Wickett (Chicago Botanic Garden), and **Warren Wagner** (NMNH via National Tropical Botanical Garden) to capitalize on recent advances in molecular methods for the study of evolution and to allow for considerable enhanced detail of the evolution and conservation of *Schiedea*, one of the largest Hawaiian endemic lineages in the carnation family, Caryophyllaceae.

The central research goal of the funded proposal is to resolve the evolution of breeding systems in *Schiedea*, an extraordinarily diverse Hawaiian endemic lineage that serves as a natural laboratory of plant reproductive evolution, using a variety of field- and sequencing-based techniques. *Schiedea* is one of the most spectacularly diverse clades in any island plant group with respect to pollination and breeding systems, varying from insect to wind-pollinated species, hermaphroditic to dioecious breeding systems, and outcrossing to selfing mating systems.

Since the entire *Schiedea* lineage is of high conservation concern the funded grant included a conference to be held in Honolulu, Hawaii to cover topics in Hawaiian conservation and to infuse the best modern methods using molecular tools to enhance the outcomes of conservation and restoration work.

Originally the project organizers scheduled a venue in Honolulu for a 150-person conservation tools workshop and symposium for June 2020, but the Covid-19 pandemic forced its cancelation in 2020 and again in 2021. A new reformatted approach moved the conference to a virtual setting consisting of ten 2- to 4-hour Zoom sessions spanning a six-month period. **Gary Krupnick** (NMNH) joined the team as Technical Producer and hosted all 10 sessions.

Additional collaborators included



Flowers of *Schiedea* have evolved a variety of ways to present nectar. *Schiedea* is the focal genus of an NSF-funded project employing a suite of high-throughput sequencing tools to better resolve the phylogeny and enhance understanding of trait evolution, especially related to breeding system diversity, which is among the highest exhibited in any island plant lineage. *Schiedea* has a unique nectary structure where each one has a shaft-like tubular extension that develops to varying extents. This nectary shaft is thin and translucent. Nectar fills the shaft and is extruded from the tip as a drop in species with elongate nectar shafts (A, *S. lydgatei*) or it forms in a pool on the surface of the sepal in species with recurved nectaries (B, *S. verticillata*). In the species likely bird pollinated the nectary is enlarged forming a nearly contiguous ring of nectariferous tissue. The abaxial margin of each nectary has a flap-like extension rather than a shaft. The black nectar produced in these species is usually copious and hexose-rich (C, *S. obovata*). Nectaries tend to be reduced in size in wind-pollinated species (D, *S. adamantis*). Figure reproduced from Wagner, et al. (2005). Images taken in the greenhouse of the University of California at Irvine; A, C, and D taken by Nobumitsu Kawakubo; B taken by W.L. Wagner.

Lauren Weisenberger (US Fish & Wildlife Service) and Matt Keir (Hawaii State Botanist), who distributed a survey to Hawaiian field biologists to determine their interests for the conservation workshop, which was used to develop the workshop agenda. The final agenda included two focused topics: (1) Identifying taxa: Considerations for molecular techniques in classifying taxa in Hawaii, and (2) Managing taxa: Using population genetics to guide *ex situ* collections and reintroduction design.

The 10 sessions were received with tremendous enthusiasm from the 70-120 participants attending each session. The attendees were diverse, including many participants from outside of Hawaiian Islands, but also included many organizations involved in Hawaiian Islands conservation work including the Plant Extinction Prevention Program (PEPP), environmental consultants, Oahu Army Natural Resources (OANRP), The Nature Conservancy (TNC), University of Hawaii (UH), Hawai'i Plant Conservation Network (HPCN), and the National Tropical Botanical Garden.

Topics in the recorded videos on YouTube include how new species and hybrids are discovered, understanding which molecular techniques may be helpful in describing new species, how species relationships impact conservation efforts, applying population genetics to plant recovery, maximizing effectiveness of *ex situ* collections, and understanding of the genetic considerations in reintroduction planning.

Reflections on the Botany 2022 hybrid conference

The Botany 2022 meeting (July 24-27) was held in person in Anchorage, Alaska, with hundreds of attendees also participating virtually. This was the first time the Botany meeting took on a hybrid format, with both in-person and virtual attendees. In total, there were 1,200 registered botanists representing 38 countries and all 50 U.S. states; more than half of the attendees traveled to Alaska to participate in-person. There were some challenges associated with the hybrid meeting format; Covid-19 was spiking before the meeting and unfortunately some botanists that planned to present in person had to cancel their talks at the last minute because of positive Covid tests.

Several members of the Botany Department participated in the meetings either in-person (**Richie Hodel**, **Jun Wen**) or virtually (**Laurence Skog**, **Warren Wagner**, **Liz Zimmer**). Additionally, other people associated with the National Museum of Natural History, or other Smithsonian Units participated in-person (Jenna Ekwealor and Andy Simpson) or virtually (Logan Kistler).

A symposium in memory of Vicki Funk, "A Botanist at the Extreme: Honoring the great contributions of Dr. Vicki A. Funk," was organized by Jennifer Mandel, Mauricio Bonifacino, Erika Moore, Warren Wagner, and Jun Wen. Seven colleagues including Jennifer Ackerfield, Nicola Bergh, Mauricio Bonifacino, Daniel Jones, Matt Knope, Loren Rieseberg, and Warren Wagner gave presentations covering topics of systematics, biogeography, collections, conservation, development, and genomics. The symposium was co-sponsored by Botanical Society of America (BSA) and International Association for Plant Taxonomy (IAPT) and was a well-attended event. A special issue honoring Funk resulted from this symposium will be published in *International Journal of Plant Sciences*.

Jenna Ekwealor (OCIO Data Science Lab postdoctoral fellow) co-organized a symposium, "Stress-tolerant mosses: adaptations to life on the edge, from genes to ecosystems." Sponsored by the American Bryological and Lichenological Society, the symposium brought together researchers from California, Arizona, Utah, Idaho, and even Peru! Two speakers presented remotely, and the whole symposium was livestreamed so remote attendees were able to see the live presentations and Q&A sessions. The symposium was organized into three topics: dimensions of diversity in *Syntrichia*, ecosystem functions of biological soil crusts (biocrusts), and biocrust restoration. The session toured ecosystems in the Mojave Desert, the Colorado Plateau, the Great Basin, and, appropriately, the Alaskan tundra.

Vicki Funk, shown here in Tahiti in 2012, was the subject of a special symposium in her memory, "A Botanist at the Extreme: Honoring the great contributions of Dr. Vicki A. Funk," at the Botany 2022 meeting in Anchorage, Alaska. The symposium featured presentations covering the systematics, biogeography, collections, conservation, development, and genomics of Compositae (Asteraceae). (photo by Jean-Yves Meyer)

Richie Hodel co-organized a workshop, "Using deep learning with digitized herbarium specimen image data," with Pam Soltis (University of Florida), Sundre Winslow (NHRE summer intern at NMNH), Will Weaver (University of Michigan), and Stefano Fochesatto (University of Alaska-Fairbanks). The workshop took place on Sunday, July 24 before the main conference program began. The workshop helped participants—which ranged from undergraduates to tenured faculty—get over some of the initial hurdles to executing deep learning analyses using digitized herbarium specimen data in their own research.

Next year, the Botany 2023 meetings will be held in Boise, Idaho from July 22-26. Until then, recorded talks from Botany 2022 will be available to watch on-demand for registered participants in the conference.

ForestGEO hosts multi-network tree mortality workshop

The Alliance for Tropical Forest Science (ATFS) convened a workshop July 15-20 in Cartagena, Colombia. During that time, 22 representatives from ten tropical forest networks discussed the pantropical patterns of forest mortality, providing hands-on experience for early-career researchers to participate in international science collaborations that address broad scientific questions.

ATFS <http://www.alliancetropicalforestscience.net> is a collaboration of 11 forest science networks across the tropics (ForestGEO, 2ndFor, AfriTRON, ATDN, DryFlor, GEM, RAINFOR, RBA, SEOSAW, TmFO, and TreeCo) made possible through an AccelNet grant from the United States National Science Foundation. ATFS is dedicated to accelerating the research and capacity-building needed to improve understanding of how tropical forests function and to predict how they will respond to and drive future changes in the Earth System.

José Medina-Vega and **Daniel Zuleta** are ForestGEO postdoctoral fellows based at the National Museum of Natural History who participated in the ATFS workshop. Below, they share about tropical tree mortality and their time in Cartagena.

What forest mortality patterns are consistent across the tropics?

Generally, forests with higher availability of resources (i.e., light, water, and nutrients) tend to be more productive and have higher tree mortality rates than forests with lower availability of resources. It is common in tropical forests for intermediate size trees to die less than both small and large trees and for trees with lower wood density–regardless of tree size–to have a high risk of mortality. These general patterns appear to be consistent across regions. Still, they may differ in intensity in response to biogeographic and/or edaphic factors or be altered due to stochastic events. For example, variations in rooting depth and variations in the capacity of soils to retain (and supply) water may be related to variations in drought-associated mortality. Additionally, random events such as stochastic lightning and/or winds may alter tree mortality rates.

What was a highlight of the workshop?

The workshop provided an excellent opportunity to share ideas among experts in the field. Participants highlighted several important points in the workshop, particularly the need to tackle pantropical-level knowledge gaps by combining large-scale research efforts. Collaboration among networks is critical because individual networks alone do not have enough information to infer large-scale patterns. Many other ideas emerged from the multi-network interactions including protocol and data alignment, statistical biases, and proposals for improving communication between field-based ecologists and modelers.

During the workshop, participants also had the opportunity to receive feedback on their current analysis. We allocated the mornings to mentoring specific Master, PhD, and postdoc projects related to forest dynamics.

ATFS is a collaboration between 11 forest science networks across the tropics. Twenty-two participants collectively representing ten networks attended the Cartagena workshop. (photo by Stuart Davies)

During the field trip, participants from different networks discussed the role of damage as a condition preceding tree mortality. In the above photo there is a tree which is rotted at the trunk's base but looks very healthy if only the crown is evaluated. These discussions clarified the need for a holistic assessment of tree health (not only crown) and highlighted the influence that damage has on both an individual tree's risk for mortality and its biomass stock. (photo by Daniel Zuleta)

What plans are there to continue momentum for the collaboration that began at the workshop?

The Cartagena workshop was the first step to establish ongoing collaboration between networks that study tropical forests. Going forward, each network representative will extend the discussion carried out in Cartagena within their respective network, sharing the defined objectives and working plans. Working plans were divided into core groups (e.g., communication and code development, among others), and group leaders will subsequently be identified for each of those core groups. Virtual and physical (when possible) meetings will be maintained among networks at every step, where every network representative will participate actively (i.e., learn, code, and write) to develop products/outputs.

SPECIMEN SPOTLIGHT

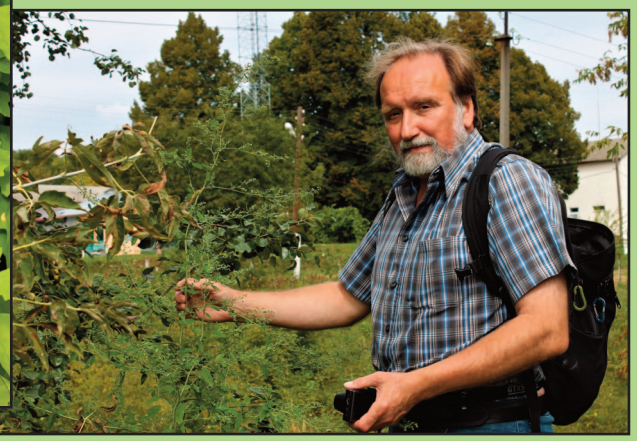
The isotype of *Chenopodium ucrainicum* (Amaranthaceae) was recently processed by the U.S. National Herbarium and was received during the Covid-19 shutdown. Collected in Kyiv, Ukraine on October 2, 2019, the specimen was brought to the herbarium by **Konstantyn Romashchenko**, Research Associate in the Department of Botany.

The specimen was collected by Sergei Mosyakin, Director of the Kholodny Institute of Botany, National Academy of Sciences of Ukraine. He collected it in the Tatarka historical neighborhood of Kyiv. Described in 2020 by Mosyakin and Bohumil Mándak (Prague, Czech Republic) (*Ukrayins'k. Bot. Zhurn.* 77: 237–248; https://doi.org/10.15407/ukrbotj77.04.237), it was initially reliably known from just several localities in Ukraine, but now dozens of new sites in central Ukraine are known, which means that it is probably more widespread in Eastern Europe. Its native versus alien status in Europe remains problematic. A late-flowering and late-fruiting species, the new taxon is well isolated from gene flow and hybridization with closely related species that flower earlier in the year.

The isotype of *Chenopodium ucrainicum*

Chenopodium ucrainicum is an overlooked B-genome diploid related to *C. suecicum* and *C. ficifolium*, meaning that it is a "basic" species that contributed to the recent speciation in the polyploid complex of *C. album* and its relatives, such as noxious weeds like hexaploid *C. album* (in a wide sense) and crops like tetraploid *C. quinoa*. The newly described species will help in understanding the evolution of the group and might prove to be useful for genetic improvement of quinoa crops because of its late development and resistance to cold.

***Chenopodium ucrainicum* in the southern part of Kyiv Region. (photo by Sergei Mosyakin)**



Sergei Mosyakin with *Chenopodium ucrainicum*. (photo by Andrew Mosyakin)

TRAVEL

Pedro Acevedo traveled to Costa Rica (7/1 – 7/11) to participate as an instructor in the Spanish version of the Tropical Plant Taxonomy course and to present several talks and workshops on Sapindaceae and other Sapindales and on the taxonomy and diversity of neotropical lianas and climbing plants.

Rose Gulledge traveled to Gloucester, Virginia (9/7 – 9/9) to visit a graduate student at SMS/VIMS (School of Marine Science/Virginia Institute of Marine Science), to discuss research projects on harmful algal blooms, to tour the lab, to outline possible outreach projects at NMNH, and to deliver duplicates of dinoflagellate reprints and images.

Richie Hodel traveled to Anchorage, Alaska (7/22 – 7/28) to attend the Botany 2022 meeting and to present a workshop on deep learning with digitized herbarium specimen image data.

Gary Krupnick traveled to Reno, Nevada (7/16 – 7/21) to participate in the 2022 North American Congress for Conservation Biology.

Jun Wen traveled throughout the southeastern US (6/29 – 7/10) with **Alicia Talavera** to conduct fieldwork and collect Vitaceae specimens; to Anchorage, Alaska (7/22 – 7/28) to attend the Botany 2022 meeting, participate in the symposium honoring Vicki Funk, and present a talk on North American *Vitis* evolution; and to Mexico (8/1 – 8/26) with **Greg Stull** to conduct fieldwork on Vitaceae and collect specimens of many plant groups significant for biogeographic studies of the Northern Hemisphere.

STAFF ACTIVITIES

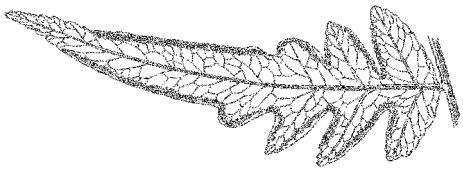
On September 7, **John Kress** gave an invited presentation, "Biodiversity exploration, species discovery, and new technologies: Plant humanities in a rapidly changing world," at the Plant Humanities Conference at Dumbarton Oaks in Washington, DC. The conference explored the deep, complex, and asymmetrical relationship between plants and people. Plants are indispensable to our bodily needs—food, shelter, clothing, medicine—and weave themselves into our experience through ritual, religion, and art. Yet anthropogenic change threatens two out of five plant species with extinction. These pressing environmental challenges make an urgent call for a new dialogue between the humanities and science to point us to vital future directions for scholarship and action. Kress' presentation was one of three during a panel on the environment and biodiversity. The 3-day event was open to the public and livestreamed.

On August 22, 2022, **Alice Tangerini** gave a lecture, "Botanical Illustration, Then and Now," to the Nantucket Conservation Foundation of Massachusetts. She covered a brief history of botanical illustration leading up to present and showing images from the collection of the NMNH Department of Botany. She presented a summary of collecting plants for the herbarium and the drawing process. The audience included gardeners, artists, and architects. After Tangerini explained the use of architectural tools in scientific illustration, one of the architects in attendance offered Tangerini her tools of the trade since she had retired and was looking for an interested party to take them. The next day the architect bicycled to the home where Tangerini was staying and delivered a bag of a variety of leads and holders which Tangerini very much appreciated.

SUMMER INTERNS

This summer, **Sundre Winslow**, an intern participating in the Natural History Research Experiences (NHRE), worked on a research project, "Tropical to Temperate Transitions in the Genus *Prunus*" with **Richard Hodel**, **Jun Wen**, and **Elizabeth Zimmer**. Winslow presented her findings at an NHRE symposium in the museum on August 4.

From June 20 to August 12, **Alice Tangerini** supervised summer intern to botany, **Abigail (Abbey) Paradis**. Paradis organized, labeled, and made folders for the hundreds of Cuatrecasas illustrations in the Botanical Art Collection, scanned 40 drawings to fulfill a request from a researcher, scanned 25 other new drawings for the Botanical Art Collection and helped scan and organize Poaceae drawings dating from the 1970s and 1980s. Using Adobe software, Paradis was able to optimize the resolution and improve images of the scans. She used Photoshop to improve digital photos for publications. She also illustrated a living specimen collected by Jason Grant from the SI Botanical Research Greenhouses that had been photographed by **Leslie Brothers** and vouchered but not yet identified. Her drawing, along with images of the specimens, proved it to be *Commelina tuberosa* from Ecuador, and has now been added to the Botanical Art Collection.



VISITORS

Francesco Riga, University of California, Davis; Poaceae (6/1-7/3).

Abigail Paradis, Savannah College of Art and Design; Botanical Art Collection internship (6/21-8/12).

Matt Sewell, US Department of Agriculture, Animal and Plant Health Inspection Service (APHIS); Collaborative projects (7/7).

Ellie Kyungran Heo, Zurich University of the Arts, Switzerland; Film making of botanical illustration (7/12-7/13).

Carlos Parra-Osorio, Herbario Nacional Colombiano, Colombia; Myrtaceae and Trigoniaceae (7/18-7/22).

Kim Garrison Means, Mystery Ranch Research Station, Nevada; East Mojave Desert conservation, botanical illustration (7/28).

Ellie Beklund, Ohio University; *Neptunia* (Fabaceae) (8/8-8/12).

Marcelo Oliveira, Federal University of Rio de Janeiro, Brazil; Eriocaulaceae (8/25-8/26).

Ihsan Al-Shehbaz, Missouri Botanical Garden; Brassicaceae (9/19-9/23).

Guillermo Pino, Universidad Nacional Mayor de San Marcos, Peru; Peruvian succulents, esp. *Peperomia* and *Echeveria* (9/19).

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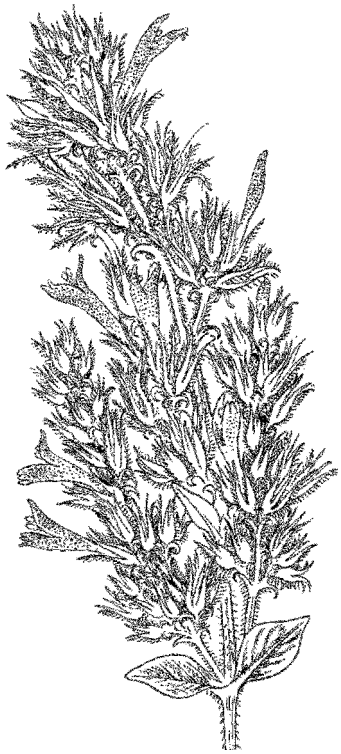
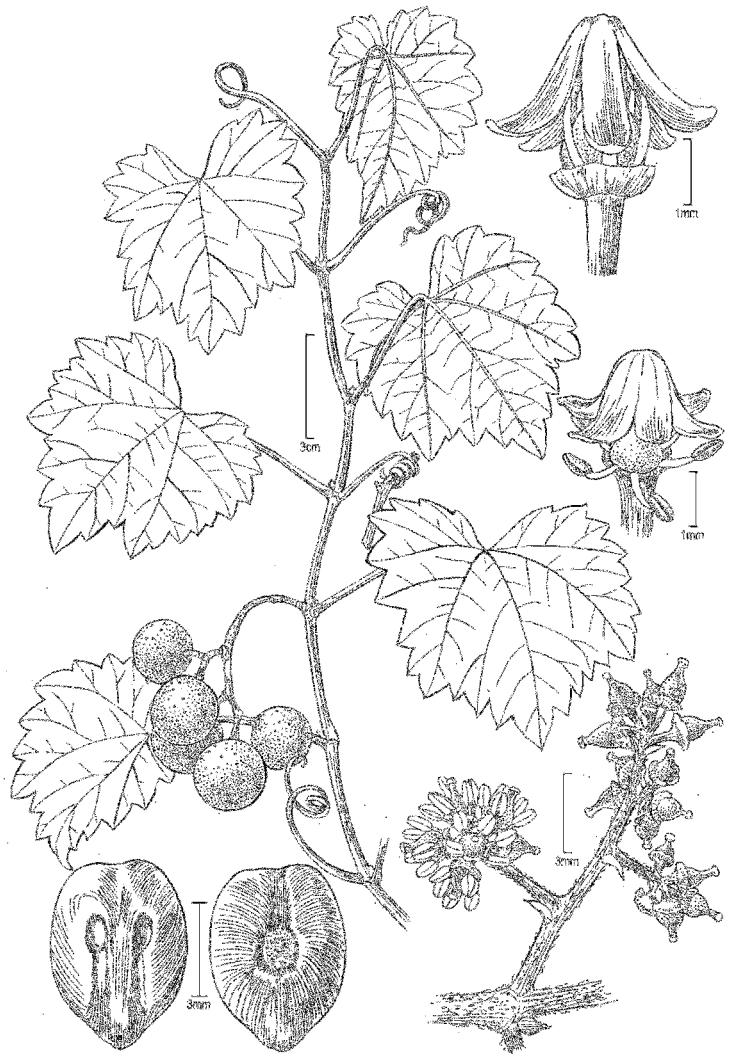


ART BY ALICE TANGERINI

Vitis rotundifolia Michaux

Vitis rotundifolia, or muscadine, is a grape species from the southern USA commonly used as fruits or for cooking and making jelly, juice, and wine. It is a close relative of *Vitis popenoei* from Mexico and adjacent regions. Alice Tangerini used a variety of herbarium specimens for her drawing, taking advantage of many specimens collected by Jun Wen. Images of the living plant and fruit were numerous on the web and were used to convey a more natural appearance of *Vitis* in the drawing. The illustration appears in *The Flora of North America: North of Mexico* (Vol. 12 Magnioliophyta: Vitaceae to Garryaceae). Tangerini was challenged to reduce the drawing to a small size to fit the FNA format. The illustration was also selected for the t-shirt design by the FNA group for Botany 2016.



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