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Phylogeny and biogeography of Hispaniolan palms

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The Caribbean is a biodiversity hotspot and harbours 2% of the Earth’s plant diversity. The region is comprised of more than 700 islands, one of the largest of which is Hispaniola. Hispaniola is home to two nations, Haiti and the Dominican Republic, and harbours approximately 38 palm species distributed among 16 genera. The impressive Caribbean palm diversity is poorly known, particularly on Hispaniola. Previous work on Caribbean palms will be reviewed to identify knowledge gaps and contextualize our work on the colonization history of Hispaniola. Using a dated phylogeny and historical biogeographic analysis, we discuss island diversification. From this, palm species delimitation and conservation action will be discussed, with a focus on *Coccothrinax*. Recent monographic work on *Coccothrinax* will be summarized in a preliminary phylogenetic framework. A multispecies coalescent inference with multiple samples for nearly all populations present on Hispaniola supports novelties in the genus, species limits, and conservation needs on the island.

Keywords: Areaceae, *Coccothrinax*, palm, phylogeny, species tree, taxonomy.

Island settings determine assembly of rattan palm diversity in the Asian tropics

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Distributed across two continents and thousands of islands, the Asian tropics are among the most species-rich regions in the world. Understanding the assembly of their extant biodiversity, however, has been hindered by their geographic complexity and the scarcity of genetic data for resident lineages. Here, by leveraging species-level phylogenomic data and two new fossils of the most species-rich Asian palm lineage, the rattans and relatives (Calamoideae), we show that their extant biodiversity was mainly generated in Borneo, Indochina, New Guinea and Sulawesi, whereas other areas mostly consist of immigrants. These regional differences in biotic assembly can be explained by simple biogeographic rules involving region size and isolation, suggesting that the unique island-dominated setting of the Asian tropics is the key factor driving their outstanding biodiversity.

Keywords: biodiversity, biogeography, biotic assembly, Calamoideae, phylogenomics.

Does relatedness explain diversification interactions between rainforests and surrounding areas?

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Rainforests are characterized by extremely high species richness, likely due to climatic stability that results in low extinction rates through time. Non-rainforest areas, despite having lower species richness, have higher speciation rates than rainforests. However, these higher speciation rates are coupled with higher extinction rates, so non-rainforest areas do not accumulate species to the same extent as rainforests. Furthermore, species migrate to surrounding areas from rainforests more frequently than the opposite. This suggests that lineages persist and accumulate over time in the rainforest, and then disperse to surrounding areas, where they speciate and go extinct at elevated levels compared to their rainforest sister taxa. We aim to disentangle the relative effects of diversification and migration in rainforest and non-rainforest areas of the Neotropics using novel phylogenies for monophyletic clades of neotropical palms (Arecaceae). Palms are characteristic of the tropics and an excellent system for studying neotropical evolution. We use Net Relatedness Index (NRI) to test for phylogenetic over- or underdispersion of neotropical palm species. Net primary productivity (NPP) across the Neotropics is used as a continuous variable to represent rainforest and non-rainforest areas, where rainforests have higher NPP. We will test for a potential correlation between NRI and NPP through a regression between the two variables. Our hypothesis is that frequent migration from the rainforests to non-rainforest areas coupled with high speciation and high extinction has led to random phylogenetic structure, or overdispersion, in non-rainforest areas relative a neotropical sampling pool. Because species infrequently migrate into rainforests, relatedness should be high and therefore underdispersed compared to the Neotropics sampling pool. Therefore, we expect to find a positive correlation between NRI and NPP in neotropical palms. Understanding how rainforest biodiversity may contribute to the diversity of surrounding areas is fundamental to understanding how global biodiversity arises and is maintained.

Keywords: Arecaceae, Neotropics, Phylogenomics, Biogeography, Relatedness.

Palms in space and time: Progress towards a genomic species-level phylogeny

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Evolutionary and ecological studies rely on phylogenies to shed light on the patterns and processes that have shaped biodiversity through space and time. However, our understanding is often fragmented due to incomplete phylogenetic sampling. In Palms, a species-level phylogeny was completed under a total evidence approach, yet many uncertainties about the genera and species relationships remain. Here, we are moving towards having a complete overview of palm evolution based on target enrichment sequencing data. Bioinformatic analyses are based on a “divide and conquer” approach where each palm subfamily is analyzed separately to minimize the effects of paralogous genes. Then, subfamilies are clustered to understand their relationships and to reconstruct the backbone. Our sequencing database includes all 183 genera and 2,027 species (81% accepted species, being the family plant with the largest taxonomic sampling in the next-generation sequencing era). The astonishing taxonomic sampling could only be achieved due to a massive joint effort of 41 researchers of the Palm Phylogeny Working Group (PPWG). Our phylogenetic tree includes five subfamilies (Calamoideae, Nypoideae, Coryphoideae, Arecoideae, and Ceroxyloideae) and resolves enigmatic clades with high support on nodes. The phylogeny tree was dated using the most recent revision of fossils available for the family and will be used as a framework to understand its historical biogeographic patterns through space and time, diversification, and biome evolution.

Keywords: Biome evolution, Diversification, Historical Biogeography, Next-Generation Sequencing.

The phylogeny of palm subfamily Coryphoideae

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The Coryphoideae subfamily of palms comprises *ca.* 500 species, approximately one fifth of all palm diversity. Despite the rich history of research into the subfamily, taxonomic uncertainties still persist, hindering our understanding of the subfamily. Here, we address these uncertainties through a comprehensive species-level phylogeny utilizing high-throughput sequencing and target-capture methods. We aim to elucidate the relationships within the Coryphoideae, especially focusing on the Cryosophileaea, Sabaleae, Phoeniceae and Trachycarpeae (CSPT clade) and the placement of the unplaced Trachycarpeae genera. Our study draws upon extensive sampling from herbaria and botanical gardens, harnessing a custom bioinformatic pipeline to analyze historical and recent collections. By employing target-capture datasets, we can overcome challenges associated with degraded DNA, offering a contrasting view to previous studies. Through our phylogenetic analysis, we also seek to provide insights into sister species relationships within the Coryphoideae, especially of the species which have never before been sampled. Ultimately, our study aims to construct the largest and most comprehensive phylogeny of the coryphoid subfamily to date, offering a valuable resource for further evolutionary studies and comparative investigations.

Keywords: Coryphoideae, Phylogenomics.

The Palm Phylogeny Working Group – where are we, and what comes next?

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The Palm Phylogeny Working Group (PPWG) was founded at the World Palm Symposium 2015 in Quindío, Colombia, at a time when the “phylogenomic revolution” brought both great promise for species-level systematics and a real risk of different labs adopting different approaches and generating data that would never be possible to combine. Seeing the first real opportunity to achieve a comprehensive species-level phylogeny for all palms, the PPWG quickly got behind target sequence capture as their approach of choice, agreeing on a coordinated approach focusing on a set of palm-specific standard loci. This early agreement and persistent collaboration is now coming to fruition. With the first phylogenomic tree of almost all palms (~80% of species) now finished and being prepared for publication, we reflect on the important question: what next? We briefly discuss the weaknesses of the tree, and what the community can do to address them. We then discuss how the tree can be used, focusing on our own plans for 1) using the tree to shed new light on the macroevolution of palms, and by extension tropical rainforests, and 2) updating the classification of palms based on the new phylogenomic evidence. Finally, the full potential of phylogenetic trees can only be unlocked in conjunction with other data, and we introduce a new initiative to gather geographic distribution data for all palm species to complement the phylogenetic tree generated by the PPWG.

Keywords: phylogenomics, phylogenetics, target sequence capture, species distributions.

The Palms of New Guinea – published at last!

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Palms of New Guinea, a monograph of all 250 species of the world's largest tropical island, was published in February 2024, shining a light on the largest remaining gap in our understanding of global palm diversity. The project has taken almost 26 years to complete and is the product of a collaboration between numerous institutions, co-authors and other collaborators. When the project began, New Guinea palm taxonomy was in an advanced state of chaos. To address this, we have explored extensively for palms in the field, collecting 1,100 new specimens. We have published nearly 40 preparatory papers and have described 91 species new to science, 37% of the entire native palm flora. Numerous generic monographs and two field guides have also been delivered. We have tackled systematic problems in the family pertaining to New Guinea genera using DNA-based methods and have described three new genera. Capacity building activities have also been undertaken, including the completion of postgraduate degrees by team members and infrastructural activities at the Manokwari herbarium. We hope that the Palms of New Guinea book will stimulate an entirely new phase of study of the palms of New Guinea, as has happened in Madagascar after the publication of *The Palms of Madagascar* in 1995, and will contribute to the long term forest conservation in New Guinea, home of the richest island flora in the world.

Keywords: Arecaceae, New Guinea, taxonomy, monography, new species, exploration.

Monographing *Hydriastele* and *Heterospathe* (Areceae) for the Palms of New Guinea

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In preparation of the recently published, comprehensive monograph the Palms of New Guinea, separate taxonomic accounts were published including monographs of the arecoid palm genera *Hydriastele* and *Heterospathe* (Areceae). The accounts of both genera are presented in monographic form that include chapters on taxonomic history and phylogeny, identification keys and taxonomic treatments with the detailed description of new as well as known species, scientific illustrations, distribution maps, preliminary IUCN red list assessments, and notes on uses, identification, synonymisation and typification. Prior to revision 34 species of *Hydriastele* were accepted from New Guinea, but describing 7 new species, and placing 17 species in synonymy, the number of accepted species was narrowed down to 24. Prior to revision 20 species of *Heterospathe* were accepted from New Guinea, but synonymising six species this number was reduced to 14 accepted species. Pivotal to the preparation of the generic accounts were the recent bout of intense collecting for the Palms of New Guinea project in addition to specimen loans, access to taxonomic literature and sharing of taxonomic expertise.

Keywords: Arecaceae, Areceae, monography, New Guinea, revision, taxonomy, new species.

Introgressive hybridization plays an essential role in peripheral, founding, and expanding populations of wax palms (genus *Ceroxylon*)

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Wax palms, genus *Ceroxylon* (Arecaceae: Ceroxyloideae), form a group of 13 species endemic to the Tropical Andean region. They live in isolated populations, in extreme, high-elevation environments for palms. Despite their patchy distributions, species can overlap in some localities, coexisting as morphologically unique, syntopic entities. Three of these species were shown to share a main pollinator by flowering at different times of the year, suggesting they are reproductively isolated. However, the demographic history of these species also revealed historical interspecific gene flow. Through hybrid capture, we sequenced ca. 4,000 nuclear regions in populations of six species of wax palms, five of which form a monophyletic group. Our work shows that peripheral populations are backcrosses of other species. Also, introgressed regions do not seem to be under positive selection and their retention in a population is likely the result of inefficient reproductive barriers and drift. The magnitude of introgressive hybridization is likely determined by demographic factors, such as population size and interspecific pollen availability. This points to the species likely functioning as an ‘evolutionary syngameon’ where expanding, peripheral, small, and isolated populations maintain diversity by crossing with individuals of other available wax palms. In mountain contexts, species can benefit from the enhancement of population sizes and genetic diversity by recreating an interspecific common genetic pool. In general, introgressive hybridization is not geographically widespread and can play an essential role in the evolutionary history of founding and expanding populations.

Keywords: ABBA-BABBA statistics, admixed, Andes, demography, syngameon, Tropical.

Nipa – the lone traveler from the past

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The Nipa palm, *Nypa fruticans* Wurm, constitutes a monospecific lineage that diverged early in the evolution of palms. The presentation will provide an overview of research projects on Nipa completed over the last two decades in collaboration with thesis project students. I will compare the results obtained from our study sites in southern Thailand with those of similar investigations throughout the distributional range of this enigmatic species. I will argue for its uniqueness of the Nipa palm, not only morphologically, but also in its ecology.

Keywords: mangrove, pollination mechanisms, population ecology, clonality, southern Thailand.

Acaulescent palms are highly resilient to disturbances

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Natural or human-induced disturbances affect aerial biomass and select distinct resilience strategies for plants. The resprouting ability is considered one of the primary response traits in post-disturbance recovery. Cerrado (the world’s most species-rich tropical savanna) is experiencing a loss of its native vegetation mainly due to monoculture cultivation for agricultural expansion purposes. In this study, we investigated if long-term pine cultivation affects two native acaulescent palms: *Allagoptera campestris* (with a single saxophone-axis rhizome) and *Syagrus loefgrenii* (that forms clusters of ramified rhizomes). We assessed and compared the morphological features of plants from areas with different disturbance histories. Then, we tested the resprouting ability by removing the aboveground biomass of the species. We also created the first database of disturbance types and outcomes that acaulescent palms undergo, the global distribution of these plants, and classified the belowground systems of all acaulescent palm species found. The results suggest that acaulescent palms are highly resilient to disturbances. The species altered the morphological features to deal with the environmental changes caused by pine cultivation. Plants from disturbed areas can regenerate properly since the individuals from all study areas recovered the pre-cutting state after one year of aerial biomass removal. In addition, we found that almost 10% of palm species are geoxyle and their distribution is concentrated in the tropics. By classifying the belowground systems, we highlight that there is a wide field of investigation possibilities with this large and diverse group of species that have several morphological responses to environmental disturbances.

Keywords: Ramified rhizome; Arecaceae; Resprouting; Vegetative propagation; Meta- analysis; Geoxyle palms; Bud bank.

Assessing genetic structure and functional connectivity of *Butia yatay* (Mart.) Becc. (Arecaceae) in northeastern Argentina

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Expansion of the agricultural-livestock frontier in northeastern Argentina has led to the degradation and in some places the disappearance of the savannas where *Butia yatay* palms thrive. Since landscape heterogeneity influence the genetic structure and functional connectivity of populations, our study aimed to assess the genetic structure of *B. yatay* in relation to environmental patterns and land-use/land-cover using double restriction site-associated DNA sequencing (ddRADseq) and geographic information systems (GIS). We found significant genetic structure among *B. yatay* populations, as evidenced by F_{ST} value (0.10). Multivariate and Bayesian analysis support this result, grouping individuals into three clusters ($K=3$). Utilizing Circuitscape and least-cost path approaches, we identified increased gene flow among nearby individuals and we propose a potential corridor for *B. yatay* populations. We identified four putative barriers to gene flow, which coincided with geographical features and anthropogenic constructions. This is the first investigation of the functional connectivity of plant populations in northeastern Argentina and shed light on the relationship between the genetic variability in palm species and the landscape characteristics of Argentina.

Keywords: Landscape genetics, LULC, fragmentation, Arecaceae.

Did pre-Columbian humans leave their fingerprints in the genetics of a key tropical plant lineage?

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The narrow vision of the pristine forests prevented scientists in many areas, such as ecology, anthropology and etnoarchaeology to think of plants as co-evolving elements in human civilizations. The domestication of plants as well as animals, is well documented for some of the most important crops today, but not for wild plants. How early humans interacted with wild plants as they arrived in the Neotropics? In the Amazon, there are evidence for manipulation of abundance of resourceful trees and palm species, but carrying seeds around as dispersers, or even intentionally planting them along migration routes would not impact as significantly as the notion of choosing plants with specific attributes to harness their potential. Would early humans have that notion? Would they manipulate plants in such a way? Here I used an widespread, iconic and economically crucial plant group of the tropical regions, the palms, to ask questions whether early human-plant interaction left a fingerprint in the palms DNA, and if this mark could be distinguished from natural selection.

Keywords: Arecaceae, Attaleinae, *Butia* spp., domestication of plants, genomics.

Grafting as a tool for functional studies in palms with the potential to improve the performance of cultivated species

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The grafting of cultivated plants has been practiced since antiquity, particularly for fruit trees. Until very recently, this technique was thought to be impossible to achieve with monocotyledons, due to their lack of a vascular cambium and scattered distribution of vascular bundles within the stem, preventing the establishment of functional connections between the scion (above-ground) and rootstock (below-ground) portions of the plant.

However, in a study by Reeves *et al.* (2022), it was shown that the undifferentiated tissues present within the hypocotyl region of monocot embryos possessed the capacity to form grafts, which were successfully obtained for each of the three main monocot clades (commelinids, lilioids and alismatids). For Arecaceae, the technique was successfully applied to oil palm (*Elaeis guineensis*) and date palm (*Phoenix dactylifera*). In this context, we recently initiated experiments in Montpellier using *E. guineensis* and *Chamaedorea* species, with a view to studying how interactions between the scion and rootstock portions of plants may influence plant architecture. Initial observations and progress will be described.

Keywords: Grafting, Arecaceae, Embryo, Architecture.

Palms in a Novel Biosphere

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Palms often play important or even foundation species roles in their native ecosystems. Now anthropogenic changes to the biosphere favor the expansion of at least some species of palms, notably climatic warming and globalization. In this presentation, I discuss conceptual and new empirical work on how these dynamics may play out, the potential ecosystem consequences, and what might be appropriate management responses.

Palm species distributions drivers and human use footprints in Amazonia

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Palms are iconic elements of Neotropical forests and have been managed by Amazonian peoples for millennia. To better understand the complex interplay of ecological, historical, and societal factors that shape distributions of palms in Western Amazonia, we used data from 430 palm inventories and information on the human uses of each species. We used a set of environmental predictor and applied Hierarchical Modelling of Species Communities (HMSC) framework. We found a higher proportion of used species and higher diversity of uses in floodplains, closer to rivers and in nutrient-rich soils, even though the regional species pool is naturally lower in rich soil areas. We conclude that environmental conditions directly shape species distribution according to their natural niche preferences but also have an indirect effect in palm species distribution, by regulating human settlement patterns and human-palm relationships.

Keywords: Tropical forest, soils, Arecaceae, ecology.