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Population genetics and phylogeography of the tropical African tree *Staudtia kamerunensis* using newly developed microsatellite markers.

Samuel Vanden Abeele¹, Steven Janssens¹, Franck Monthe², Armel Donkpegan², Olivier Hardy²

1. Botanic Garden Meise

2. Université Libre de Bruxelles

Despite the high levels of tree biodiversity in African rainforests, current logging is mainly focused on a selected number of tree species, which causes these species to be under high pressure. To facilitate the conservation and regeneration of these valuable timber species, knowledge on the genetic population structure is extremely valuable. In the current study, the genetic structure of *Staudtia kamerunensis* populations from Central Africa was analyzed with a set of newly developed microsatellite markers. Both variants of the species were included to verify if there is a genetic component underlying the morphological differences. The software QDD v2.1 was used to detect microsatellite loci of interest and to select suitable primers from a microsatellite enriched genomic library of *Staudtia kamerunensis*. Selected primers were then tested with different PCR conditions to ensure DNA amplification and readability after which polymorphic loci were retained and combined in multiplexed reactions using Multiplex Manager 1.2. Multiplexed reactions were carried out on populations from Cameroon, Gabon, Republic of the Congo and Democratic Republic of the Congo. Allele lengths of the different loci were analyzed with Peak Scanner Software 2 and Geneious 9.1.6. Heterozygosity levels, allele frequencies and the number of alleles were then used to assess genetic diversity within and between populations and clustering analyses were carried out with Structure 2.3.4 and the *adegenet* package for the R software. Finally, these results were discussed in a historic climatological and biogeographical context.

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Phylogenomics of the phaseoloid and millettoid legumes using a target enrichment approach

Mohammad Vatanparast¹, Adrian Powell², Sue Sherman-Broyles², Jeff J. Doyle², Ashley N. Egan¹

1. Smithsonian Institution

2. Cornell University

The legume family (Leguminosae) is the third largest family of flowering plants and is the second most important family in economic value. The phaseoloid (ca. 2,070 species in 112 genera) and millettoid (ca. 1,100 species in 56 genera) legumes form a single large clade of the papilionoid subfamily and include various important crops such as soybean, common bean, cowpea, pigeon pea and winged bean. The majority of taxa in this clade correspond to the Phaseoleae sens. lat. and Millettoid sens. stric. subclades; however, in spite of multiple molecular phylogenetic studies, relationships within this clade remain unresolved or with low statistical support, particularly along the backbone. To understand the evolutionary history of these legumes, we used transcriptomes of 24 taxa from this group as well as six outgroup legume genera

to develop thousands of hybridization probes. Our probes include representatives of all subtribes and major, delineated clades determined in previous studies within the millettoid clade. We obtained sequences for hundreds of genes to build a robust phylogenetic tree encompassing phaseoloid and millettoid legumes. Our results reveal robust phylogenetic relationships of multiple clades and subclades within the millettoid clade and provide well-supported phylogenetic evidence useful for the classification within this important legume clade.

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Assembling Brazilian subtropical highland vegetation over space and time

João R. V. Iganci¹, Josimar Kulkamp¹, Cássia Plá¹, Mariane Dornelles¹, Tiina Sarkinen³, Gustavo Heiden²

1. Universidade Federal do Rio Grande do Sul

2. Embrapa Clima Temperado

3. Royal Botanic Garden Edinburgh

A high number of endemic species is being reported for the Brazilian subtropical highland grassland and mixed forest biomes. Both formations occur in highland areas mainly in Southern Brazil, under similar climate and environmental conditions. Bayesian inference on biogeography using multiple lineages have been proving to be a good approach for assembling biomes evolution over space and time. Here we apply this method to assemble both subtropical highland grassland and mixed forest evolution. The subtropical highland grasslands are a species rich formation found over basalt rocky outcrops and peatlands, while the mixed forest is an Ombrophilous Forest dominated by the gymnosperm *Araucaria angustifolia*. Both formations behave as continental vegetation islands, and encompasses tropical and temperate lineages, sharing species with other surrounding biomes. Dominant and endemic species from each formation were mapped and their distribution as communities were modeled to identify the most suitable areas for both grasslands and mixed forests. Specific lineages represented by species rich taxa in each formation were chosen to compose the Bayesian analyses. Each biome represents a complex history of niche evolution represented by lineages reaching new habitats or local speciation events.

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Ployploids on islands: A NGS study of Macaronesian endemic *Lavatera acerifolia* (Malvaceae)

Irene Villa-Machío, Gonzalo Nieto Feliner, Javier Fuertes Aguilar
Real Jardín Botánico

By increasing dramatically the sampling of genomes, Next Generation Sequencing (NGS) techniques opened a wide avenue towards reconstructing species evolutionary histories thus representing a crucial source of information for phylogeography. However, polyploidy --a very common process among vascular plants-- is a major challenge for the NGS techniques due to difficulties in genotyping individuals resulting from the existence of multiple paralogous loci, which is even more complex in plants without a reference genome. In addition, population-base studies require