

distinguish among species, whereas there is an important overlap in the spectra of flowers. Results showed differences in floral color patterns considering the spectral analysis versus that one perceived by the pollinators, suggesting different ecological and evolutionary processes underlying the observed variation of each group of data sets: the adaptive component of color would be primarily associated with pollinators assemblage which seems to be species-specific, suggesting an isolation mediated by pollinators among *Monttea* species, while the spectral variation of color, would be associated with other factors, like climatic and/or neutral processes.

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Flower morphology and its relationship with the pollination system in the southern South American genus *Jaborosa* (Solanaceae)

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Flower morphology has been considered an important factor in species isolation because of its dual impact on the attraction and mechanical fit with pollinators. In the present work we quantified the variation in floral shape amongst twelve species of the genus *Jaborosa* Juss. (Solanaceae) to assess whether this variation is spurred by pollinator shifts or is explained by their phylogenetic history. Floral morphology (i.e. corolla limb shape and disposition of stamen and pistil within the corolla) was studied using traditional and geometric morphometrics. Flower shape and pollinator guild were mapped onto a molecular phylogeny of the genus and ancestral states were reconstructed. Two major clades were recovered, one grouping species that clearly exhibit a sphingophilous syndrome and the second one grouping the species pollinated either by saphrophilous flies or moths. Sphingophilous species showed salverform flowers with dissected petals whereas the clade grouping the remaining myophilous and phalaenophilous species showed a greater variation in flower morphology from rotate to urceolate and tubular flowers. Flower architecture determined that pollen was carried in the proboscis of long-tongued hawkmoths and moths and in a nototribic or pterotribic position by carrion flies. These results suggest that pollinator shifts either than phylogenetic ancestry would be responsible of the diversification of flower shapes and patterns of pollen removal/deposition within the genus *Jaborosa*.

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Pollination by *Hemimepsis* wasps: A newly described South African guild with an analysis of trait convergence between guild members

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Pollination syndromes are based on the premise of convergence in floral traits of plants that share a common pollinator. Although syndromes are widely used as a conceptual framework for studies of floral evolution, pollinator-mediated convergence in floral traits has seldom been examined in the context of syndromes. In this study, we describe a guild of plants that are pollinated by *Hemimepsis* wasps, and examine levels of floral trait convergence in this newly recognized pollination system. The *Hemimepsis*-wasp pollination

guild includes 23 plant species from three families (Apocynaceae, Orchidaceae and Asparagaceae) which are pollinated by between one and four species of *Hemimepsis* wasp (Pompilidae: Pepsinae). Of the known guild members, 18 are pollinated exclusively by these wasps. The guild is distributed throughout the grasslands of eastern South Africa. Guild members share several qualitative traits, including dull greenish- or brownish-white flowers, often with purple blotches, mid-summer flowering, sweet spicy scent and exposed nectar. To explore levels of floral trait convergence within the guild we compared the floral traits of guild members to those of congeneric plant species pollinated by other vectors. We found limited evidence of convergence in the nectar properties (volume and concentration) and floral scents of guild members. However, we found evidence of convergence in the floral colours of guild members and loci for the spectral reflectance of guild members were more tightly clustered in the hymenopteran colour hexagon than those of non-wasp-pollinated congeners. Our results firmly establish the existence of a specialized system of pollination by *Hemimepsis* spider-hunting wasps and suggest that some traits do not necessarily evolve during shifts between pollinators.

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RAPD and SSR genetic diversity analysis of *Moringa oleifera*

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Moringa oleifera is potentially an economically important tree species. It has gained interest globally for its multipurpose uses, in particular as a source of nutrition and oil as well as various medicinal properties. *Moringa* is native to India, Malaysia and the Middle East, but have been introduced to many countries throughout Africa ranging from Niger to South Africa. There is however limited knowledge regarding the genetic variation of both native and introduced populations of *Moringa*, although phenotypic observations suggests the presence of significant genetic diversity. In this study we aim to determine the level of genetic variation found between different populations of *Moringa* from locations including India, South Africa, and Hawaii. Molecular marker such as Random Amplified Polymorphic DNA (RAPD) and Simple Sequence Repeats (SSR), will be used to analyse the genetic diversity based on their success in other tropical tree population studies. Their low capability for SSR conservation, make them ideal for the application at the intra-specific level. Various RAPD primers and 17 SSR primer pairs will be used to generate amplification profiles that can be used in a diversity analysis. Initial screening has identified markers that show significant genetic diversity amongst the populations. Furthermore the study will try to identify markers related to quantitative traits such as seed oil content and yield that could potentially be useful in future selection and breeding programs aimed at tree improvement.

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Baobab population dynamics - Investigating spatial and temporal patterns in KNP

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The African Baobab (*Adansonia digitata* L.) is a keystone species in the African savanna, providing food for a multitude of organisms whilst its massive structure provides important sites for habitation. Kruger National Park (KNP), South Africa, falls at the southernmost limit of *A. digitata*'s current range in Africa where currently local scientists have reported failed recruitment. Concern is mounting among conservationists over the possible loss of suitable habitat for adult survival and seedling recruitment of *A. digitata*, locally and elsewhere in Africa, due to predicted changes in climate. Failed recruitment in KNP may confirm this predicted range contraction. Alternatively the apparent absence of immature individuals may be consistent with past recruitment events, wherein cohorts of *A. digitata* trees recruited during infrequent windows of favourable conditions. In this case the survival of the population - particularly where conditions are marginal, is reliant on the ability of reproductive trees to outlast periods unfavourable for recruitment ('the storage effect'). Long-term population monitoring is required to better understand the population dynamics of *A. digitata* in KNP. Building on an existing 17-year dataset detailing tree morphometrics and vigour, this project aims to monitor changes in population density and structure of *A. digitata* at various temporal and spatial scales by revisiting ~600 individual trees in northern KNP. By determining those factors limiting adult survival and seedling recruitment, appropriate management actions can be initiated to conserve this species. *A. digitata* populations in KNP persist in marginal conditions at the edge of its southern African range and may prove useful in elucidating the relative roles of short- and long-term climate variability, inter-specific interactions and management on the survival of this iconic species.

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The pollination biology of *Solanum mauritianum*

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Invasive species are a worldwide phenomenon and pose a major threat to local biodiversity and ecosystem functioning. In South Africa, the invasive species *Solanum mauritianum* Scop. (Solanaceae; 'bugweed') is considered to be one of the five most widespread invasive alien species. It is native to South America (northern Argentina, Uruguay, Paraguay and southern Brazil) and was first introduced into South Africa in the mid 19th Century. This category 1 weed commonly invades natural areas and plantations. *S. mauritianum* is believed to be

buzz pollinated in its natural range but observations in Grahamstown, Eastern Cape have shown native honeybees (*Apis mellifera*) may manipulate the poricidal anthers with their heads and mandibles. Pollen loads of collected bees were examined using fuschin gel. Previous studies have shown that *S. mauritianum* is self-compatible and is partially autogamous. To test this, we conducted a breeding system which showed *S. mauritianum* to be autogamous, although the number of seeds per fruit varied between the self- and cross-pollination treatments.

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Are meta-topolins better in the clonal micropropagation of *Pelargonium sidoides*?

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Pelargonium sidoides DC is a geophytic species with high demand in the pharmaceutical and cosmetic industries due to its unique phytochemistry. The high demand has led to overexploitation of *P. sidoides*, hence its conservation status has been characterized as 'declining' in the Red List of South African Plants (2011). The aim of this study was to develop a clonal propagation system for *P. sidoides* using explants from mature plants, with particular emphasis on the regeneration potential of different cytokinins including N⁶-benzyladenine (BA), kinetin (KIN) and meta-topolins. The topolins evaluated in this study were meta-topolin (*mT*), meta-topolin riboside (*mTR*) and meta-methoxytopolin riboside (*MemTR*). Cytokinins had a significant effect on shoot regeneration and *in vitro* plant growth compared to the control. Meta-topolins had significantly higher shoot multiplication and *in vitro* growth indices compared to both BA and KIN. Shoot length increased with increasing indole-acetic acid (IAA) and indole-butyric acid (IBA) concentrations whereas the response for α -naphthalene acetic acid (NAA) increased to an optimum and then decreased. The highest root biomass was achieved on 1.0 μ M IAA. The rooting response observed in control plants may be due to the influence of endogenous auxins. *In vitro*-derived *P. sidoides* plants were successfully acclimatized in the greenhouse. In conclusion, meta-topolins were significantly better than BA and KIN in shoot multiplication and *in vitro* plant growth of *P. sidoides*. The current findings highlight the increasing importance of topolins in micropropagation.

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