

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 saprophilous 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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