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Abstracts

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1862), while the SRR species were last revised by Gillett (1958). Decades of herbarium research by Schrire identified about 100 undescribed species from South Africa, laying the foundation for this multidisciplinary study. The past five years have included fieldwork in both regions, resulting in the collection of roughly 90% of *Indigofera* species in South Africa, which has further expanded our knowledge on new species and the role of habitat specificity that have resulted in the high species diversity. Taxonomic work in the GCFR is nearing completion, with three taxonomic revisions already published, and several more in preparation, resulting in the description of about 58 new species. A biogeographical study of the genus found that *Indigofera* originated in Africa, with multiple “Out-of-Africa” dispersal events during the Miocene leading to the colonization of all continents except Europe and Antarctica. New high-throughput phylogenomic sequencing has allowed for a detailed study of habitat preference and localized biogeography of GCFR *Indigofera*, and will play a crucial role going forward in understanding the evolutionary drivers that led to the radiation of the genus in South Africa and beyond.

The systematics of *Nemesia* (Scrophulariaceae)

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The genus *Nemesia* Vent. (Scrophulariaceae) comprises about 77 species, the majority of which are endemic to South Africa. *Nemesia* has garnered significant horticultural interest due to its diverse floral shapes, vibrant colours and ease of hybridization and cultivation. The genus was last revised in 1904 by Hiern and the only molecular phylogeny for *Nemesia* was published in 2008 by Datson and others. Datson *et al*'s phylogeny grouped the 23 included species into five distinct clades highlighting evolutionary relationships and potential adaptive traits. Their ancestral state reconstruction suggested that multiple transitions occurred between a perennial life history in species occurring in the summer rainfall areas to an annual life form in species adapting to winter rainfall or seasonally dry conditions in the Cape Floristic Region and parts of the Karoo. It was hypothesised that *Nemesia*'s diversification may have been driven by climate change in the Cape Region during the Miocene and Pliocene. Our research aimed to generate a more comprehensive phylogeny incorporating as many *Nemesia* species as possible, to deepen understanding of the genus's evolutionary history. This phylogeny was generated from gene regions ITS, ETS and trnL-intron, representing 48 species. The phylogeny is divided into two main clades, with five subclades that show significant geographic affiliations among species within clades. In this paper we review the phylogeographic patterns and morphological variation within the five clades of *Nemesia*. The phylogeny also contains several newly discovered, but as yet, undescribed species and their relationships to known species are explored.

New additions to the *Nemesia* lineage from the Succulent Karoo

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The genus *Nemesia* (Scrophulariaceae) is one of the most diverse in the Hemimerideae tribe, comprising approximately 77 species, with nearly all endemic to southern Africa. Three species have been recorded in Zimbabwe, but none are endemic to that country. Eleven species occur in Namibia, of which at least five are endemic or near-endemic. South Africa is home to most *Nemesia* species, with their centre of diversity located in the Cape Floristic Region (CFR) and Succulent Karoo. Between 1994 and 2010 Steiner published

several new species, the majority primarily endemic to the winter rainfall region of South Africa. In his contribution to *Strelitzia* 30, Steiner published several brief, informal descriptions of new *Nemesia* species, the majority of which have never been formally described or named. During a taxonomic revision and phylogenetic analysis of *Nemesia* it became clear that the winter rainfall region of South Africa is likely to produce yet more new species of this genus. Here we review the morphology and phylogenetic relationships of *Nemesia* sp. E, as described by Steiner, and compare it to already known and putative new species from the Succulent Karoo.

Genetic diversity and population structure of *Strychnos madagascariensis*: Insights for conservation and sustainable utilization

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Strychnos madagascariensis Poir. is a highly valued indigenous fruit tree in South Africa with potential for domestication and commercialization. However, no study has reported the molecular diversity of *S. madagascariensis* morphotypes. This study assessed the genetic diversity among *S. madagascariensis* morphotypes using simple sequence repeat (SSR) markers. Newly sprouted leaves from 27 *S. madagascariensis* morphotypes were used for DNA extraction. Genotyping was performed using 17 SSR markers, followed by polymerase chain reaction (PCR) amplification and capillary electrophoresis for allele size determination. Genetic diversity and population structure were analyzed using PowerMarker, Cervus, STRUCTURE, GenAlEx, and XLSTAT software, revealing genetic variation and relationships among morphotypes. Seventeen amplified SSR markers produced 144 alleles, with a mean of 4.28 per locus. The polymorphic information content (PIC) values ranged from 0.00 to 0.72. The population structure had the highest delta value $K = 2$, thus dividing morphotypes into two subpopulations based on a Bayesian approach. Morphotypes were clustered according to genetic distance and phylogenetic relationship in the principal coordinate analysis where eight distinct sub-clusters were formed. The dendrogram based on genetic distance classified the morphotypes into two major clusters, where Cluster II was further subdivided into two sub-clusters. This study is the first to report on SSR marker development and their successful use for genetic diversity and population structure studies of *Strychnos madagascariensis*. These findings offer practical insights and understanding of the genetic diversity among various *S. madagascariensis* morphotypes, which could be beneficial for breeding programs and conservation efforts on behalf of this valuable species.

Lineage diversification and long-term preservation in the Greater Cape Floristic Region

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The Greater Cape Floristic Region (GCFR) is a globally recognized biodiversity hotspot, distinguished by its extraordinary species richness and fine-scale beta diversity. This unique flora has intrigued scientists for centuries, with numerous studies investigating the processes driving lineage diversification. Key mechanisms shaping this diversity include environmental heterogeneity, periodic fire, pollinator-driven divergence, range-limited dispersal, and phenological shifts. Another potentially significant yet underexplored driver is the impact of sea-level fluctuations during the Pleistocene (2.5 Ma – 11.7 ka) which likely played a crucial role in recent divergence of coastal specialist taxa endemic to coastal calcareous substrates. During glacial periods, lower sea levels expanded the GCFR's land area, exposing vast areas of calcareous substrata along the Palaeo-Agulhas Plain. Contemporary sea levels are approximately 130 m higher than at the Last Glacial Maximum, leaving modern coastal substrates spatially fragmented and