

was almost entirely due to an increase in grass biomass; in the process forbs were overtopped and shaded out such that a significant decline in species richness was recorded. In contrast, herbivore exclusion did not significantly impact nitrogen mineralization, perhaps due to the short period of herbivore exclusion (3 years in 2005). However, the moist riparian and wetland zones supported a high nitrogen mineralization rate, while the potential denitrification rate was also significantly higher than other topographic positions. Thus, it is clear that large herbivores are essential agents for disturbance in the riparian zone, acting to maintain species richness by keeping grass biomass low.

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Phylogeny of the South African centred plant genus *Cotula* (Asteraceae)

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The genus *Cotula* comprises about 55 species, most of them endemic to South Africa, two occur in Australia, two in Asia, two on the Tristan da Cunha Islands in the South Atlantic Ocean, and one each in North Africa, East Africa, and Mexico. The sister group of *Cotula* is the genus *Leptinella* from Australia and New Zealand, formerly treated as a subgenus of *Cotula*. Most *Cotula* species are disciform (lacking ray florets), but some South African species like *C. turbinata*, *C. duckittiae*, and *C. macroglossa* are radiate. A nuclear sequence (ITS) and a plastid sequence (trnC-D) have been used to build a molecular phylogeny of the genus. In the analyses *Cotula* forms a well supported clade, with the exception of *C. cinerea* from North Africa which is more closely related to *Tanacetum* and *Chrysanthemum*. The results suggest a basal split into two clades: one comprising *C. coronopifolia*, its sister species *C. pusilla*, and *C. bipinnata*; the other consisting of the remainder of the genus. Secondary ray florets apparently evolved separately in *C. turbinata/duckittiae* and *C. macroglossa*. The endemic species of Tristan da Cunha, *C. moseleyi* and *C. goughensis*, are sisters to the South African species *C. turbinata* and *C. duckittiae*.

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Seed bank strategies in a Kalahari ecosystem in relation to habitat and grazing

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Few studies have been conducted on soil seed banks in arid summer rainfall regions of South Africa. Seed banks form an important part of the vegetation in arid regions as seeds can be the most prevalent or only viable form of many plant species for several years. Therefore, the complete description of a plant community should include the buried viable seeds because they are as much a part of the species composition of the vegetation as the aboveground components. Five habitat types within the southwestern Kalahari duneveld were selected to investigate seed bank composition and dynamics. The habitats include Dune crests, Dune slopes, Dune streets, Calcrete outcrops and a Riverbed. Soil samples were collected over four seasons and were analysed using the seedling emergence method to determine the seasonally-germinable seed bank in each of the four seasons. The seed-extraction method was avoided as it is best used for seed bank studies in areas where large-seeded species predominate. Comparisons are made between the species composition of the aboveground vegetation and the species composition of its corresponding soil seed bank. Changes in seed bank size and composition over the four seasons are investigated. By comparing the proportion of annual dicotyledons, perennial dicotyledons, annual grasses and perennial grasses occurring in a habitat; a possible response of the vegetation to grazing can be hypothesized.

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Genetic variation and pollination biology in the threatened *Gerbera aurantiaca* (Asteraceae)

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Gerbera aurantiaca is a long-lived endemic daisy confined to a few small populations in the mist belt grasslands of KwaZulu-Natal and Mpumalanga as a result of severe habitat destruction and fragmentation over the last century. The species exhibits two geographically isolated colour morphs along its distributional range, an undescribed yellow-flowered subspecies and the typical red-flowered subspecies. This presentation reports on the results of an investigation into some aspects of the population biology of the species. A preliminary study of genetic variation in three representative populations using allozyme electrophoresis has indicated