

Cenchrus ciliaris, *Coix lacryma-jobi*, *Cymbopogon* spp, *Cymbopogon validus*, *Eragrostis curvula*, *Imperata cylindrical*, *Penicum maximum*, *Setaria megaphylla*, *Sporobolus africanus*, *Sporobolus pyramidalus* and *Vertiveria zizanoides*. The 11 species were subjected to phytochemical (spectrophotometric/colorimetric method) and biological (antioxidant and antimicrobial) screening. Root methanolic extracts of *Cymbopogon* spp., *Cymbopogon validus* and *Cenchrus ciliaris* contained relatively high levels of total phenolics (27-31 mg GAE/g DW) and flavonoids (4-13 mg CE/g DW). Condensed tannins and total iridoid content was highest in *Cymbopogon validus* (2.3 mg CCE/g DW, 3.2 mg HE/g DW, respectively). The highest ferric reducing power was observed in the whole plant extract of *Cynodon dactylon* (0.085 ± 0.45 ; r^2 0.898). *Cymbopogon* spp. extracts had high phytochemical concentrations and this species was the most frequently used and mentioned during the survey. *Coix lacryma-jobi* and *Setaria megaphylla* had the highest antibacterial activity (0.625 mg/ml) against *Staphylococcus aureus*. *Cymbopogon* spp. root (dichloromethane) extract had moderate activity (1.25 mg/ml) against three bacterial strains (*Staphylococcus aureus*, Multi-drug resistant *Escherichia coli* and *Enterococcus faecalis*). *Sporobolus pyramidalus*, *Sporobolus africanus*, *Cenchrus ciliaris* and *Penicum maximum* were the least active extracts against six selected bacterial strains. Overall, these findings partially validate the use of grasses in traditional medicine and their potential in being sources of secondary metabolites.

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Permanent *Protea* (Proteaceae) monitoring plots and fire frequency in Fynbos

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Fire is an important process in Mediterranean-ecosystem shrublands, and controlled burning is often used to manage these ecosystems. Controlled fire frequencies are based on the rule that at least 50% of the slowest-maturing, obligate seeding *Protea* L. must have flowered for at least three successive seasons. This is guided by permanent *Protea* plots (PPP) that monitor *Protea* age and flowering. Here we test the accuracy, placement and the number of PPP required in one reserve management section. We used the southern slopes of the Potberg mountain of De Hoop Nature Reserve as our case study. We sampled two reseeded *Protea* species at 17 sites along the 12 km management section, and determined age at first flowering and age at 3 times flowering for 480 individuals per species. *Protea repens* (L.) L. starts flowering at 3 years, and all plants have flowered at least once at 12 years. In *P. neriifolia* R.Br. this ranged from 4 - 13 years. Three times flowering for *P. repens* varied from 6 - 17 years and from 7 - 18 years for *P. neriifolia*. There was a significant difference in age at flowering between east and western plots (but not within these areas) for both species. When 50% of *P. repens* and *P. neriifolia* plants on the western side had flowered 3 times, only 25% and 5% respectively have done so on the eastern side. The accuracy, placement and the number of PPP per management section is discussed.

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Invasion of *Acacia mearnsii* stands by natural forest species at Buffeljagsrivier, Swellendam: The process

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Contrary to general belief, invader plant stands facilitate the recovery of natural evergreen forests and their diversity. The Water Research Commission project K5/2081 included a study of how natural forest species from small moist, dry or riparian forest patches of total 3 ha at one end, invaded a 90-ha stand of the invasive Black wattle *Acacia mearnsii* over a distance of 3.1 ha along the Buffeljagsrivier near Swellendam (Western Cape). In total, 329 forest species clusters were recorded across the wattle stand: more large clusters closer to and more smaller clusters further away from natural forest patches. The 28 recorded forest species (of a potential 40 species) included 79% tree and 21% shrub species. The most common tree species in the clusters were *Canthium inerme*, *Celtis africana*, *Gymnosporia buxifolia*, *Rapanea melanophloeos* and *Vepris lanceolata*. Most colonizing forest species had larger fleshy fruit and softer small seeds, dispersed by mostly birds and baboons. Every type of forest, but mostly riparian forest, contributed species to this process. Maturing forest trees within developing clusters in the wattle stand became a source for forest regeneration away from the clusters, showing four expansion patterns. Four sets of fenced-unfenced plots in the wattle stand showed the importance of livestock, antelope, rodents and insects on the successful establishment of regenerating forest species. This study supported the approach to selectively manipulate invader plant stands in the natural forest environment rather than clearing such invasive species stands, to use the natural succession process rather than planting, and to protect developing seedlings against browsing by stacking invader plant debris around establishing forest seedlings.

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Strategies of *Acanthosicyos horridus* (!nara) to exploit alternative atmospheric moisture sources in the hyper-arid Namib Desert

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The Namib Desert is considered hyper-arid due to its low annual precipitation and high potential evaporation rates. However, fog originating offshore sustains life and drives high levels of adaptation in this coastal desert. Organisms may employ different strategies to utilise vital atmospheric moisture. *Acanthosicyos horridus* (Welw. ex Hook. f.), locally known as !nara, is a member of the Cucurbitaceae family and is endemic to the Namib. This keystone species forms tangled thickets that accumulate wind-blown sand and plant litter, resulting in hummock formation. These hummocks harbour a host of biota and provide essential ecosystem services in this desert environment. There is, however, limited information on !nara plant-fog relations, and how hummock formation contributes to this interaction. The effect of the hummock on water balance in the soil was investigated by measuring moisture content and temperature. Various strategies to exploit fog and dew as alternative sources of

water were tested. These include direct aerial absorption through the stems and the movement of coalesced water along the stems. A Wingscape time-lapse camera together with a Lascar humidity logger, and a Leaf-Wetness Sensor were used to determine presence and duration of moisture. Chlorophyll *a* fluorescence was employed to evaluate the overall vitality of the plants before and after fog events. Preliminary results indicate likely direct absorption of water through the stem and an increase in the chlorophyll *a* fluorescence intensity after a fog events. These results indicate that the Inara plant may greatly benefit from fog as a supplementary source of moisture.

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Physiological and biochemical responses of sorghum to drought stress

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Drought is a major threat to global food security and is anticipated to worsen, severely curtailing the global economy, as forecast by many climatic models predicting increased frequency and duration of drought episodes. Understanding plant adaptive responses to drought stress could prove crucial in developing new biotechnological solutions to avert crop yield losses to drought. Sorghum is an African indigenous crop well adapted to thrive on marginal lands, making it a suitable model system to study drought stress. We are using drought-tolerant and susceptible sorghum varieties to study the biochemical and molecular changes underpinning the adaptive responses to drought. Detailed morphological analyses of plants subjected to drought stress and then re-watered to recover revealed striking differences between the sorghum varieties. Relative water content, fresh and dry biomass, and other growth parameters for both roots and shoots were protected in the drought-tolerant variety, while the susceptible variety was adversely affected and had poor recovery after irrigation. Examination of physiological responses, such as stomatal conductance and stabilisation of chlorophyll, mirrored the morphological adaptations we observed. Systematic analysis of the major stress defence systems is on-going. The ultimate goal of this project is to use these sorghum varieties as an experimental system to identify differentially expressed proteins during drought stress and recovery. This will provide key data for better understanding plant adaptive responses to drought and driving agri-tech innovation in this area.

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Phytophthora cinnamomi: A driver behind endangered flora in the CFR?

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Phytophthora cinnamomi is a generalist plant pathogen that was introduced into the Cape Floristic Region (CFR). By 1984, it had been isolated from 83 indigenous plant species in the South Western Cape. Numerous populations of plant taxa are now declining in the CFR. We reviewed the threat posed by *P. cinnamomi* based on the current red list statuses of these species (<http://redlist.sanbi.org>). Thirty of the 83 susceptible host species are listed as threatened, of which five are critically endangered. We then ranked all threatened and rare species according to their vulnerability, with the most vulnerable species considered to be those with the smallest distribution size. Taxa at the higher end of this vulnerability scale should receive immediate focused attention to minimize the threat of extinction due to the exotic *P. cinnamomi*. Based on our findings, we recommend further research regarding the distribution, prevalence and impact of *P. cinnamomi* in the CFR. We also suggest that Cape Citizen Science (<http://citsci.co.za>) could be a platform for providing observational data on the current distribution of *P. cinnamomi*.

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A 'footprint' of desiccation tolerance in the genome of the resurrection plant *Xerophyta viscosa*

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Desiccation tolerance is common in seeds and various other organisms but only a few higher plants possess vegetative desiccation tolerance. These 'resurrection species' may serve as ideal models for the ultimate design of crops with enhanced drought tolerance. To understand the molecular and genetic mechanisms enabling vegetative desiccation tolerance we produced a high-quality whole-genome sequence for the resurrection plant *Xerophyta viscosa* and assessed transcriptome changes during its dehydration. Data revealed induction of transcripts typically associated with desiccation tolerance in seeds, and involvement of orthologues of ABI3 and ABI5, both key regulators of seed maturation. Dehydration resulted in down regulation of genes located in genomic 'anhydrobiosis-related islands' (ARIDs), possibly reflecting the cessation of growth that allows for the expression of desiccation tolerance. Vegetative desiccation tolerance in *X. viscosa* was found to be uncoupled from drought-induced senescence. We propose that vegetative desiccation tolerance arose by redirection of genetic information from desiccation tolerant seeds and, hence, this may open a unique possibility to 'unlock' vegetative desiccation tolerance from the genome of desiccation sensitive crops.

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Optimising propagation techniques for *Aloe peglerae* and *Aloe reitzii*

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