Seeds are a primary source of proteins for both humans and livestock. However, seeds of the major staple crops such as corn and soy are deficient in several of the essential amino acids (EAA), which animals must obtain from their diet. EAA deficency can lead to a syndrome in humans called protein-energy malnutrition, which is manifested by a series of severe symptoms including lower disease resistance, anemia, and retarded mental and physical development. The World Health Organization estimated that 30% of the population in developing countries suffers from this syndrome. To improve seed composition one needs to gain fundamental understanding of the genetic mechanism regulating seed amino acid (AA) composition. Several studies have shown that genome wide association mapping is an efficient approach to discover the genetic basis of several metabolites levels. However, seed AA composition is most often driven by small effect QTLs which are hard to detect using the current association panels. Our study suggests that in tightly correlated metabolic networks such as amino acids, using a combination of metabolic correlation-based network analysis and GWAS can help uncover additional genes that are part of the genetic architecture of these complex traits.

doi:10.1016/j.sajb.2017.01.024

The population size structure of *Aloe claviflora* in the Wolwekraal Nature Reserve in the Prince Albert district

G. Arena[a], S.J. Milton[a,b], W.R.J. Dean[a,b,c]
[a]*South African Environmental Observation Network (SAEON): Arid Lands Node, PO Box 110040, Hadison Park 8306, Kimberley, South Africa*
[b]*Renu-Karoo Veld Restoration CC., Prince Albert 6930, South Africa*
[c]*Percy FitzPatrick Institute of African Ornithology, University of Cape Town, Rondebosch 7700, South Africa*
E-mail address: arenag14@gmail.com (G. Arena)
**** Awarded best poster presentation***

The Wolwekraal Nature Reserve in the Prince Albert district of the Succulent Karoo has a history of Khoekhoe and San campsites, livestock farming and gravel mining. Current threats include illegal firewood harvesting and poaching, as well as a recent seepage of effluent from the neighbouring municipal sewage treatment. One of the aims of the reserve is to protect a suite of endemic species representative of the Prince Albert Succulent Karoo vegetation type from these threats. The reserve is also home to a healthy sized subpopulation of the *kraalaalwyn* (*Aloe claviflora*), aptly named for its' circular growth form of several aloes in a cattle pen-like formation which produce distinct horizontally-angled inflorescences. To date, despite its' wide distribution range across the semiarid and arid regions of southern Africa, there is no published data on this species. In this study we collected data on clump size, clone (rosette) size, inflorescences, and clone mortalities from this subpopulation in an attempt to determine the following research objectives, 1) size class distribution, 2) the relationship between clump size and number of clones per clump, and 3) the relationship between flowering, clone and clump size. Acquiring important baseline demographic information allows one to maintain long-term monitoring of mortality, recruitment, and flowering and growth rates under anthropogenic disturbance and climatic change to predict patterns in population structure of an arid-adapted *Aloe*.

doi:10.1016/j.sajb.2017.01.025

Mycotoxins, secondary metabolites of a cereal killer

K. Audenaert, G. Haesaert
Department of Applied BioSciences, Faculty Bioscience Engineering, Ghent University, Valentin Vaerwyckweg, 1, Ghent 9000, Belgium
E-mail address: Kris.Audenaert@ugent.be (K. Audenaert)

In agro-ecosystems, intensification of crop production, the use of agrochemicals and susceptible varieties influence virulence and diversity of plant pathogens and pests. It has been estimated that losses due to disease and pest symptoms in agricultural crops can feed 8.5% of the world's population. Biotic stresses comprise a vast group of organisms, but plant pathogenic fungi are considered the most important group causing devastating losses worldwide. On top of that, agro-ecosystems are under pressure due to restricted use of agrochemicals and due to climate change. An important group of plant pathogenic fungi are toxigenic fungi producing secondary metabolites called mycotoxins. Exposure to these mycotoxins may infer serious risks for animal and human health and lead to economic losses. Especially in African countries, the exposure to mycotoxins is high because of the importance of cereals in the daily diet. Cereals are highly susceptible to many toxigenic fungi. In this presentation, we will use several case studies investigated at Ghent University in the MYTOX research platform showing the plasticity of toxigenic fungal populations in the field. In addition, we will shed light on how, when and why mycotoxins are produced and how they can be controlled through agricultural practices and genotype choice. The presentation will show some prevention, intervention and remediation strategies in which the control of both the fungus and its mycotoxins will be discussed. Most recent developments in the field of ICT solutions will be presented to facilitate mitigation of mycotoxin risks by various stakeholders in the chain. Finally, we will shed light on how the omics era will help us to control toxigenic fungi both in the field and during storage and processing.

doi:10.1016/j.sajb.2017.01.026

Systematics of *Pteronia* L. (Asteraceae)

A.O. Bello[a], A.R. Magee[a,b], J.S. Boatwright[c], P.M. Tilney[a], M. Van der Bank[a]
[a]*African Centre for DNA Barcoding (ACDB), Department of Botany and Plant Biotechnology, University of Johannesburg, PO Box 524, Auckland Park 2006, Johannesburg, South Africa*
[b]*Compton Herbarium, South African National Biodiversity Institute, Private Bag X7, Claremont 7735, Cape Town, South Africa*
[c]*Department of Biodiversity and Conservation Biology, University of the Western Cape, Private Bag X17, Bellville 7535, Cape Town, South Africa*
E-mail address: anifatolayemi@gmail.com (A.O. Bello)

Pteronia L. is a large, often aromatic, shrubby genus comprising ca. 70 species most of which favour arid habitats within the Greater Cape Floristic Region. The genus is considered to be one of the priority genera for taxonomic research in South Africa. The genus was last treated by Hutchinson and Phillips in 1917 who recognised four sections based exclusively on leaf indumentum. A systematic study was carried out in order to investigate the phylogenetic relationships, infer biogeographic patterns and estimate the divergence times of *Pteronia* using DNA sequences, morphological and anatomical data. Phylogenetic analyses of the genus were based on nuclear and plastid DNA sequence data (ITS, ETS and *trnL-F*) for 84 samples (70 taxa) and confirmed the monophyly of the genus. Four main clades were recovered, of which the type group, the *P. camphorata* clade, emerging as the most