The genus *Cotula* comprises about 55 species centered mostly in southern Africa, but with a few species extending into Tropical Africa, Eurasia, South America and Australia. Preliminary data suggests that *Leptinella* is embedded within *Cotula* and that *Cotula mexicana* may be better placed within *Soliva*. Both *Leptinella* and *Soliva* have been revised while *Cotula* remains largely forgotten. As morphological variation within the genus remains largely unexplored, uncertainty in which characters, if any, currently define *Cotula* remains, as well as what distinguishes it from *Leptinella* and *Soliva*. The aim of this project is to revise all the species of *Cotula* and refine generic circumscriptions within the *Cotula*-clade using both morphological and phylogenetic data. As a first step towards that ultimate goal we here focus on subdividing the genus into smaller, more manageable taxonomic units using morphological characters and phylogenetic analyses of nuclear (ITS) and plastid DNA regions (*psbA-trnH* and *trnC-petN*). Despite their largely uniform general morphology, we have uncovered tremendous variation in floral and, particularly, fruit characters which can be used to define broader grouping as well as separate many of the species. A broad overview of the main species groups within the genus, the floral and fruit diversity and the phylogenetic relationships will be presented.

**ENABLING THE PROCESSING OF BIOINFORMATIC WORKFLOWS WHERE DATA IS LOCATED THROUGH THE USE OF CLOUD AND CONTAINER TECHNOLOGIES**

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The use of “big data” to inform biomedical decisions poses complex problems of storage, privacy and data security. This is especially true for fields such as e-health which deal with human health records. Organisations holding such data need to be able to assure regulators and patients of the security of their data storage and handling. In addition, when dealing with large datasets, movement of data for processing can pose a challenge. Many applications that are used to process various types of data have strict software package dependencies, imposing competing requirements on the administrators of institutional computing platforms. Software containers are a lightweight and generally better performing, albeit less diverse alternative to virtual machines. The advancement and increase in adoption of these container technologies have resulted in adoption for use in a variety of scenarios and fields. This allows researchers to replace the shipment of data with shipment of code by packaging their software into containers. Researchers are allowed to define their own toolchains and workflows to do analysis with rather than being limited to what has been allowed by the organisation managing the data set. Utilizing the growing cloud environment ecosystem, with platforms such as OpenStack, it is possible to provide researchers with an easy to use interface to execute custom workflows remotely, without the hassle of software dependency management and direct technical knowledge and reducing the need to send potentially large data sets from one location to another.

THE ENCAPSULATION AND QUANTIFICATION OF OLEA AFRICANA IN NANOLIPOSOMES

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Most bioactive compounds in plants are water-soluble, which limits their ability to pass over lipid rich cell membranes. A suitable method for altering the distribution patterns of water-soluble agents, is the encapsulation in liposomes. In this study an aqueous leaf extract of Olea africana (OA) was characterized using High-Performance Liquid Chromatography (HPLC) to quantify the content of Oleuropein, the main bioactive compound, and the HPLC-method was validated. The extract was encapsulated in liposomes using the lipid film hydration method. Following extrusion, liposomes were monodispersed with an average size of 109.6 nanometres and a charge of -20.3 millivolts. The encapsulation efficiency of Oleuropein in liposomes, using HPLC, was 24%. Confocal microscopy results show that liposomes were inside H9c2 cardiomyoblasts. OA leaves have been shown to contain antioxidants and to be cardioprotective. The extract encapsulated in a liposome can potentially improve its bioavailability and subsequently its cardioprotection.
INVESTIGATING SECONDARY METABOLITES IN THALASSOMONAS VIRIDANS

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The continued emergence of bacterial resistance to currently used antibiotics has become an alarming concern to many industrial nations and has added to the urgency of discovering novel drugs. Natural products isolated from marine microorganisms have received much attention in recent years due to their applications in human health, ranging from novel antibiotics to anti-cancer therapies. *Thalassomonas viridans* is a Gram-negative marine microorganism isolated from oysters off the coast of Japan. The genome sequence of this microorganism revealed several biosynthetic gene clusters including; non-ribosomal peptide synthases (NRPS), polyketide synthases (PKSs), PKS-NRP hybrids, lantipeptides and bacteriocins. Functional screening revealed that *T. viridans* had bioactivity against *Staphylococcus aureus*, *Bacillus cereus*, *Pseudomonas putida* and the multi-drug resistant *E. coli* 1699 when cultured in marine broth supplemented with different carbohydrate sources. The observed activity led to the objective of identifying the biosynthetic gene cluster(s) responsible for production of the active compound(s). A bioactivity-guided approach was taken to identify the compounds using HPLC fractionation that resulted in a semi-pure fraction that retained activity. Further size fractionation has indicated that the active compound is >50 kDa in size. This indicates that the active compound is likely not a non-ribosomal peptide or polyketide but points towards a larger secondary metabolite, such as a class III bacteriocin. Protein purification is currently being employed to identify the active compound in the >50 kDa fraction.

PREDOMINANT AIR-SEA STATES DURING COASTAL MARINE HEATWAVES

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As the mean temperatures of the world's oceans increase, it is predicted that marine heatwaves (MHWs) will occur more frequently and with increased severity. However, it is hypothesised that more proximate variables may be responsible for these extreme events. An improved understanding of the mechanisms driving MHWs may allow us to better forecast their occurrence at specific localities. To this end, we have utilized atmospheric (ERA-Interim) and oceanographic (BRAN) reanalysis data to examine the air-sea state around southern Africa during coastal (<400 m from the low water mark) MHWs. Self-organising maps (SOMs) were used to cluster the mean air-sea states during MHWs into 1 of 9 types to determine the predominant patterns. It was found that warm water forced onto the coast via anomalous ocean circulation was the predominant oceanographic pattern during most MHWs. A range of distinct air temperature and wind patterns were found with warm air temperatures over the continent and strong north-westerly winds featuring most prominently during MHWs. It may therefore be possible to forecast the occurrence of MHWs when such air and sea states are projected to occur simultaneously. The lack of any strong air-sea patterns during roughly one third of the MHWs implies that sub-meso-scale activity may have been responsible for them and that finer scale observations may be necessary to deduce their physical drivers. These findings motivate for the implementation of local scale real-time in situ monitoring of at-risk coastal locations in conjunction with the development of a forecasting and disaster prevention system.

**USING MOLECULAR DYNAMICS TO ILLUSTRATE THE CHANGES IN THE GLYCAN SHIELDS OF TWO HIV-1 ENVELOPE TRIMERS AFTER THE LOSS OF A GLYCAN.**

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The glycan shield of the HIV-1 envelope trimer forms a barrier between the virus and the humoural immune response, thereby protecting the virus from neutralisation. As the glycoprotein mutates to escape further immune attack, the composition of the glycan shield can vary substantially between isolates and over time. The loss of a single glycan on the viral surface, or the shift of a glycan by only a few residues, has been shown to have a significant effect on the neutralisation sensitivity and antibody breadth developed.

Here, we analyse the changes in the glycan shields of two HIV-1 envelope glycoproteins when a single glycan-site mutation (N301A) is introduced. The antibody neutralisation...
assays for these two viruses indicated that the loss of the N301 glycan resulted in a shift
from resistant to sensitive for only one of the isolates, which suggests that further
structural features and glycan interactions influence the conformation of the glycan
shield. Trimeric homology models were generated using these subtype C pseudovirus
sequences (~90% identity), and their N301A mutants. All four models were
computationally glycosylated with high-mannose glycans (Man-9) and molecular
dynamics simulations were carried out for 500 ns using Amber 14.

Our results show a significant difference between the dynamics of glycans on the original
and N301A mutant models. We observe a difference in the range of movement for some
glycans, as well as a change in their interaction with adjacent glycans (whether within or
between monomers), which forms one explanation for the variation seen in the
experimental neutralisation assays.

This study illustrates the complexity of the glycan shield, where the impact of a loss of a
glycan depends on the potential of the remainder of the glycan shield to compensate for
this loss through structural rearrangement. Such rearrangements, however, can have a
substantial effect on the virus’ neutralisation profile.

NOVEL PHAGES OF HEALTHY SKIN METAVIROMES FROM SOUTH AFRICA

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Bacteriophages are the most abundant biological entities on Earth. In Nature, they can
affect biogeochemical cycling of nutrients, cause the collapse of trophic structures and
drive host diversification. Since 2008 next generation sequencing has been directed at
gaining a better understanding of the interactions between humans and their
associated microbial communities. Some skin metagenomic studies have investigated the viral
diversity present and, recently their possible influence on the healthy skin microbial
populations, and tried to establish global patterns of skin-phage evolution. However, the
detail associated with the phages which potentially play a role in skin health has not been
investigated. While skin metagenome and metavirome studies have indicated that the skin
virome is highly site specific and shows marked interpersonal variation, they have not
assessed the presence/absence of individual phages which we do here. Our study adds to
this interpretation; however, we demonstrate that identical phages are present on different
individuals and in different body sites and that under varied conditions these may be
present on the skin, and we investigate the structural organization of these novel phages.
Here, we took a semi-culture independent approach (metaviromic) to better understand
the composition of phage communities on skin from South African study participants and
find that a bacteriophage related to the S. capitis phage Stb20 may be a common skin commensal virus potentially regulating its host and its activities on the skin.