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BOOK OF ABSTRACTS

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BIOLOGY

Investigating Toxin Production in Three Decades Deep Freeze Cyanobacterial Mats from Ponds and Hydro-terrestrial Environments Collected from Cape Royds, Rose Island, Antarctica

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Abstract

Cyanobacteria are the dominant phototroph in Antarctic freshwater and terrestrial environments. They play an important role as primary producers in these ecosystems. Cyanobacteria are also known to produce toxic secondary metabolites. There has been a growing research interest into the study of the distribution and occurrence of cyanotoxins, their potential toxicity as well as their ecological implications. The first scientific report on cyanotoxins was published in *Nature* in 1878. Cyanotoxins were commonly thought to be produced in warm, high light exposure, slow moving and eutrophic water bodies in temperate and tropical regions. Recent studies however change this paradigm with the discovery of nodularin and microcystin producing cyanobacteria in Antarctic mat samples. A more recent report indicated the presence of microcystin and MBBA and its isomers in a 100-year old dry herbarium Antarctic cyanobacteria mat collected during Captain Scott's discovery. The present research aims to investigate the presence of cyanotoxin encoding gene; microcystin, anatoxin-a, saxitoxin, cylindrospermopsin and nodularin in the culture isolates established from 14 deep freeze mats samples collected from various meltwater ponds and hydro-terrestrial environments on Cape Royds, Antarctica between 1984 and 1985. To date, three isolates comprised of a *Leptolyngbya*, *Nostoc* and *Geitlerinema* were tested positive for microcystin encoding gene. Polyphasic evaluation will be carried out for all toxin producing taxa encountered together with investigation on the implications of environmental stressor (temperature, salinity, nutrients availability and UV-B) on their toxin production.

Key words: Antarctica, microcystin, anatoxin-a, saxitoxin, cylindrospermopsin

Microbial synthetic biology for advancing biotechnological applications of Antarctic microbes

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Abstract

Antarctic is a home to extremophilic microbes that live in extreme environments particularly cold-adapted psychrophilic microbes that have been found to degrade xenobiotic compounds and capable to synthesize industrially-important antimicrobials and enzymes such as cold-active proteases and lipases, useful in medical and bio-based industries. Despite this, biotechnological applications of Antarctic microbes are relatively underdeveloped and predominantly limited to recombinant enzyme production using traditional microbial hosts such as *Escherichia coli* which owed to the lack of genetic information and genetic intractability of native microbial isolates. To address these issues, our research group focuses on employing microbial synthetic biology as biotechnological platform that offers effective and sustainable means for developing bio-products using genetically-engineered microbes. Our previous works in metabolic engineering of model microbial strains have enabled the increased production of biofuels and biochemicals and bioconversion of agro-industrial wastes such as glycerol. Similar bioengineering strategies are currently being employed for developing *Pseudomonas extremaustralis*, a psychrophilic and bioplastic-producing bacterium, as alternative microbial hosts for bioproduct development. Recent findings of improving furfural tolerance in engineered *P. extremaustralis* and potential uses of synthetic biology approaches on facilitating biotechnological applications of other Antarctic microbes will also be presented.

Keywords: Synthetic biology; Antarctic microbe; Metabolic engineering; *Pseudomonas extremaustralis*; Polar biotechnology

Phytoplankton as a food source for deep-sea foraminifera in the Southern Ocean

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Abstract

With the exception of the mineral-rich deep ocean floor, deep sea organisms rely on sinking particles produced in the upper ocean for food. The sinking particles consist mostly of faecal pellets and phytoplankton that sink individually or as aggregates. Based on the high performance liquid chromatography (HPLC) technique, we analysed the pigment content of the cytoplasm of four foraminifera species and its surrounding sediments collected at two deep-sea stations (51°S, 12°W and 50°S, 39°W at ~4100 m). HPLC results revealed high concentrations of algal pigments and their degradation products in the foraminiferan cytoplasm. The composition of the algal pigments in the foraminiferan cytoplasm reflected the phytoplankton composition measured at the surface ocean. Some foraminiferans contained more chlorophyll *a* than the degraded chlorophyll *a* indicate they were feeding on fresher phytodetritus. Other foraminiferans contained only degraded chlorophyll *a*, which shows that they utilised degraded phytodetritus. Interestingly, the concentrations of algal pigment in the foraminiferan cytoplasm were much higher than in the surrounding sediment. This suggests that the foraminiferans were collecting a diluted and sparse sinking particles and concentrated them in their cytoplasm. This unique ability is believed to contribute to the great quantitative success of foraminiferans in the deep sea.

Keywords: Phytoplankton, deep-sea, foraminifera, Southern Ocean, pelago-benthic coupling

Genome of a Thermophilic Bacterium, *Geobacillus* sp. TFV3 from Deception Island, Antarctica

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Thermophilic bacteria are bacteria which can survive and grow optimally at high temperature, ranging from 40°C to above 60°C. Analysis of the bacterial genomes of this particular thermal group is crucial to understand genes involved in thermal adaptation and provide some insight on different strategies adopted by thermophilic bacteria to thrive at high temperature. *Geobacillus* sp. TFV3, a Gram-positive bacterium, was isolated from the volcanic soil of Deception Island, Antarctica and was identified as a Geobacilli through 16S rRNA sequencing. The optimum growth temperature was determined to be around 65°C. The genome of strain TFV3 was then sequenced using PacBio sequencer, followed by genome assembly and annotation using various UNIX-based bioinformatics tools. The genome size of strain TFV3 is approximately 3.4Mb, with GC content of 51.8%. It contains 3,406 CDS, 27 rRNA, 88tRNA, 1tmRNA, 58 miscellaneous RNA, and 3 repeat regions. Results from Pangenome analysis suggested strain TFV3 be a novel bacterium, and *G. kaustophilus* Et7/4 appeared to be the closest phylogenetic species to strain TFV3 using whole-genome phylogenetic analysis. PROKKA annotation indicated that the genome harbored genes which are directly involved in thermal adaptation, such as 4 different heat shock proteins, 3 different molecular chaperones, 1 cold shock protein, and other degradation proteins like PNPase. Besides, it also possessed a number of genes responsible for different metabolism pathways, but were found to be indirectly involved in cold and heat adaptation, including several types of RNA helicases, oxidative stress enzymes, and also fatty acid metabolism enzymes.

Keywords: novel bacterium; thermophile; *Geobacillus* sp.; genome; Deception Island

Comparative Structural analysis of Haloacid Dehalogenase TypeII: Insight from cold-adaptive environment

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Abstract

Research into the structural properties of enzyme from psychrophilic organisms show they have enhanced structural flexibility at low temperatures with the fine balance between activity and stability of protein. Many hydrolytic enzymes were studied from cold temperature including for Haloacid Dehalogenase. For instance, *Psychromonas ingrahamii* which isolated from the cold environment had activity towards many haloacid substrates including L-Chloropropionic acid. Specifically, PinHAD dehalogenase produced by this psychrophilic bacterium could tolerate to various temperature for dehalogenation. To the best of knowledge, this is the only reported cold adapted Haloacid dehalogenase with wide range of temperature tolerant. However, structural insight on psychrophilic haloacid dehalogenase still lacking and crucial since it is required by pharmaceutical industries as biocatalyst. In this study, the structural difference between cold adapted dehalogenase (PinHAD) and other similar enzymes such as L-Deh from *Pseudomonas* sp. YL, *B. cepacia*, *S. tokodaii* and *Rhizobium* sp. RC1 will be computationally investigated and their key amino acids for temperature tolerant will be determined. The amino acids sequence of PinHAD together with mesophilic L-Deh will be aligned by using Multiple Sequence Alignment. Subsequently, their three dimensional structure proteins will be simulated in a solvents system and assessed their structural changes. Replica-Exchange Molecular Dynamics (REMD) technique will be applied to sample conformations at different temperatures. At the end of simulation, ionic interactions, hydrogen bonds, hydrophobic contacts and secondary structure formation will be calculated for comparison between psychrophilic and mesophilic L-haloacid dehalogenases.

Keywords: Haloacid Dehalogenase, Cold adapted, Replica-Exchange Molecular Dynamics (REMD)

Diesel-Degradation Potential of Antarctic Bacteria Isolated From Diesel Contaminated Soil

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Abstract

Increasing human activity in Antarctic lead to many incidents of diesel contamination in that region. Diesel is used as fuel to generate energy for daily consumption in scientific and military stations. In this study, a psychrotolerant bacterium was isolated from Diesel contaminated soil in Greenwich Island, South Shetland Islands, Antarctica using enrichment culture technique with diesel as sole carbon and energy source. Biodegradation analysis and the effects of addition of N and P towards the efficiency of biodegradation were conducted at low temperature. The samples were extracted using SPE column and subsequently analysed using GC-TOF/MS. Reduction and complete elimination were observed in several diesel components indicated the potential of the isolate to be used as diesel degrader in cold environment.

Keywords: Psychrotolerant, Diesel contamination, Biodegradation.

Effect of Ferum contamination on growth, biochemical composition and superoxide dismutase enzyme activity in *Chlorella* sp collected from Peninsular Antarctic

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Abstract

Global climate changes will likely results in high water temperatures, stronger stratification, and increased inflows of freshwater, chemical contaminants and nutrients to coastal water in many areas of the globe. In addition to it, the rapid exploration of human activities at the coastal area in polar region, the emissions of wastewater containing high concentration of metal like ferum; leading to serious chemical contamination problem in coastal waters. Algae are notable bioindicator species in environmental pollution studies. In view of this, efforts are made to investigate effect of ferum contamination on the growth, biochemical composition and superoxide dismutase activity of microalgae used as biomarker for evaluation on how microalgae responses and adapt to changes caused by climate change occurred at polar region. Results showed that the growth, carbohydrate, protein, lipid content and superoxide dismutase enzymes activity increased with increasing concentration of ferum until the threshold, beyond which the cells lost their resistance and died. The findings of the present study may contribute to the understanding of how the Antarctic algae respond to environmental stress, and to use growth, biochemical composition and superoxide dismutase enzymes activity levels to monitor the impact of climate change and increased contamination of the polar habitats.

Keywords : Chlorella sp, microalgae, growth, biochemical composition, Peninsula Antarctic,

Exploiting temperature and nutritional conditions for Poly microbial biofilm formation from Antarctic soil samples

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Microorganisms in Antarctica are able to live and thrive in this harsh environment. Psychrophiles have the ability to survive and proliferate at low temperature due to several adaptive features and one of it is through the production of extracellular polymeric substances (EPS) or biofilms. Temperature and nutrition were used as growth-limiting parameters for this study. The primary aim of this study was to assess the effects of temperature and nutrients on the growth of Antarctic bacterial biofilms. The soil samples from Signy Island, 12 from Gourlay peninsula and 12 from Berntsen point were used. The microbes from the soil supernatant were plated on 24 different microbial media, including defined media and complex medium with/without enrichments. The cultures were incubated at 4°C, 10°C and 15°C for a period of 15-30 days in a 24 well format and observed for the formation of biofilms. The biofilms formed were estimated by crystal violet method at the end point. This study highlighted that soil samples showed varied degree of microbial growth and biofilm formation. A total of 576 conditions with triplicates for three different temperatures were collected, the data was subjected to simple descriptive statistics were used to describe the overall trend of biofilm growth. As for the measure of dispersion, we are using the median absolute deviation (MAD) to complement with the parameter, median. The data were non-normally distributed and positively skewed. Bootstrap method was used, where each data set was resampled and the mean confidence interval was determined.

Key word: Biofilms, Antarctic soil, nutrition, temperature, bacteria

Phenotypic Evaluation on Selected Terrestrial Cyanobacteria from Signy Island, South Orkney Islands Antarctica

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Abstract

Members of the genus *Leptolyngbya* dominate microbial communities in Antarctic soil populations. However, their diversity is not very well understood. This study utilises a combination of morphology, ultrastructure and molecular approaches to confidently identify four *Leptolyngbya* strains inoculated from soil collected from Signy Island, South Orkney Islands Antarctica. Morphologically, all four strains in cultures showed diacritical characteristics that resembles the genus *Leptolyngbya*. However, the 16S rDNA and 16S-23S internal transcribed spacer (ITS) molecular analysis showed that all four strains are well separated from the *Leptolyngbya* clade. Three of these strains were more closely related to the genus *Wilmottia* while the remaining strain is a close relative of *Nodosilinea*. To date, only two *Wilmottia* species, *Wilmottia murrayi* and *Wilmottia* sp., have been characterized from Antarctica. Characterization for the genus *Nodosilinea* from Antarctica is currently unavailable. Increased understanding of the microalgae diversity on Signy Island will support conservation of the indigenous biota and aid future research on ecological processes, including consequences of environmental change.

Key index words: Taxonomy, 16S rRNA; 16S-23S ITS; cyanobacteria; *Leptolyngbya*

Assessment of Antarctic Bacterium *Rhodococcus* sp. strain AQ5-07 for Low-Temperature Degradation of Diesel

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Abstract

The omnipresence of recalcitrant petrogenic hydrocarbons in Antarctica is generally associated with extreme conditions that impede the natural degradation of hydrocarbon components. These have caused major perturbation in Antarctic ecosystem, suggesting that conventional bioremediation approaches are largely ineffective at present. However, several studies have reported that indigenous psychrotolerant isolated from hydrocarbon-polluted Antarctic soils demonstrated exceptional biodegradative capability towards petrogenic pollutants. The current study assessed the ability of the psychrotolerant phenol-degrader, *Rhodococcus* sp. strain AQ5-07, to assimilate diesel fuel as its sole carbon source. This study was also set out to optimise the conditions required in order to support maximal growth and biodegradation activities by applying conventional one-factor-at-a-time (OFAT) and multifactorial response surface methodology (RSM) approaches. Factors expected to influence the efficiency of diesel degradation namely initial hydrocarbon concentration, nitrogen source concentration and type, temperature, pH and salinity were studied. Strain AQ5-07 displayed an optimal cell growth and biodegradation activity at 0.75% v/v initial diesel, 1 g/L NH₄Cl, pH 7 and 1.5% w/v NaCl during OFAT analysis. Strain AQ5-07 was psychrotolerant based on its optimum growth temperature of 20-25°C. In conventionally optimised media, strain AQ5-07 showed *n*-dodecane mineralisation of 79.77%. However, the RSM-optimised conditions enhanced the reduction of *n*-dodecane to 93.78% within 2 days incubation. The outcomes suggested strain AQ5-07 as a potential candidate in sludge-phase bioreactor operations for hydrocarbons-contaminated sites in chronically cold environments including Antarctica. This study also confirmed the utility of RSM in medium optimisation.

Keywords Diesel, Antarctica, *Rhodococcus* sp. strain AQ5-07, Biodegradation, Response-surface methodology (RSM).

Characterisation of two Antarctic cyanobacterial isolates from Signy Islands with tolerance towards UV-B Radiation

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Abstract

The ozone layers are becoming thinner each day, and ultraviolet radiations from the sun have been penetrating directly onto organisms in Antarctica. The intense effects of UV radiation have caused certain organisms there to produce certain pigments and proteins to protect themselves from the denigrative effects of the UV radiation. The compounds produced can be harvested for consumer usage. Thus, this research purposes are to assess the ability of the Antarctic cyanobacterial isolates to withstand UV-B radiation up until 72 hours and to characterise the two cyanobacteria species from Signy Islands, Antarctica. The samples were classified as cyanobacteria A and cyanobacteria B and were observed under light microscope for characterisation via diacritical features and irradiation under UV-B (302 nm) for up to 72 hours. The post-irradiation results showed that cyanobacteria B has better tolerance towards UV-B radiation. The samples were observed under microscope and results shown that both were not from a similar species. The characterisation of cyanobacteria A and cyanobacteria B were different, by looking into their diacritical features of the samples which are dimensions and internal structures for the specific cyanobacteria. The identified genus of the two isolates shown similarity with *Leptolyngbya* sp.. Observations were also done macroscopically to observe the pigment of the samples after exposures towards UV-B (302 nm) radiation. The determination of species via morphological characteristics were not enough thus, molecular identification through 16S rDNA should be recommended.

Keywords: cyanobacteria; Antarctic; characterisation; UV-B irradiation; UV-B tolerance

Aerobic degradation of phenol by Antarctic bacterium *Arthrobacter* sp. AQ5-15 in the presence of heavy metal

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Abstract

The menace of phenol pollution from daily waste discharge and accidental oil spill still occur as a result of increasing activities in the Antarctic continent including areas related to study and supply of research stations, tourism and marine transportations. The increased level of phenol concentration in the Antarctic environment brings significant risk to the aquatic as well as terrestrial lives due to its highly toxic and persistence properties. These activities also result in elevated levels of heavy metals, which may adversely affect the efficiency of phenol degradation by microorganisms due to high toxicity. The sustainability of this continent can be achieved by effective remedial technologies and better utilisation of resources. This study has revealed that bacteria *Arthrobacter* sp. strain AQ5-15 isolated from Antarctica were able to degrade phenol at low temperature in the presence of various heavy metals. Optimisation of the degradation showed that this strain is psychrotrophic and prefers a near-neutral environment to function efficiently. Subsequently, this strain exhibited 100% degradation of 0.5 g/L phenol in the presence of heavy metals named Pb and Zn. The potential of this cold-adapted strain to degrade phenol completely in the presence of heavy metal proved that this strain could be a potential inoculant for phenol bioremediation in extremely cold environment.

Keywords: Antarctica; Phenol; Heavy metal; *Arthrobacter* sp.; Bioremediation

Toxicity of copper and lead in a tropical and an Antarctic isolate of *Chlorella* after short- and long-term exposure

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Abstract

Environmental contamination by heavy metals such as copper (Cu) and lead (Pb) is of concern as it may impact on algae, which play important role as primary producers. The Antarctic is not spared from heavy metal contamination due to leachates from waste dumping sites, shipping and construction activities at research stations. Most toxicity testing of Cu and Pb on algae was based on short-term response (72 or 96- h) but not the effects of prolonged exposure. The primary aim of this study, was to compare the response of a tropical and an Antarctic *Chlorella* to Cu and Pb. The tropical *Chlorella* was isolated from Cameron Highlands, an area with active agricultural activities in Malaysia while the Antarctic *Chlorella* was isolated from Signy Island, a site that is impacted by heavy metal contamination in Antarctica. The algae were exposed to CuSO₄ and Pb(NO₃)₂ ranging from 0- 300µM for 20 days and the following biomarkers were assessed: growth rate, pigment contents and oxidative response. Results showed that inhibition effect of Cu and Pb was observed in tropical *Chlorella* after 4 days with EC₅₀ of 130 µM and 237 µM respectively and similar inhibition effect (EC₅₀- 110 µM; 290 µM respectively) was observed after 20 days for both toxicants. To the contrary, greater inhibition effect was observed in Antarctic *Chlorella* after 20 days of 5 to Cu with a lower EC₅₀ decreased from 210 µM (day 4) to 105 µM (day 20). Both tropical and Antarctic *Chlorella* produced significant amounts of reactive oxygen species (ROS) (27 folds higher) after being exposed to 300 µM of Cu for 20 days. However, Pb (300 µM) was only able to induce the production of ROS in the tropical *Chlorella* but not the Antarctic strain. In conclusion, inhibitory effects of Cu were observed in the tropical *Chlorella* on day 4, but in the Antarctic *Chlorella*, this was only evident on day 20. Hence, toxicity testing of Cu on Antarctic algae may require a longer exposure (>96 hours) in order to assess the negative impacts of the toxicant.

Keywords: Copper, Lead, Tropical *Chlorella*, Antarctic *Chlorella*, Reactive oxygen species

The growth of the Antarctic isolate, *Rhodococcus sp.* on diesel under the effect of selected heavy metals

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Abstract

Co-contamination of diesel and heavy metals is one of environmental concerns in Antarctica. Bioremediation by bacteria can be challenging due to the complex composition of diesel and the inhibitory effect of heavy metals. The growth of *Rhodococcus sp.*, which is an Antarctic isolate that can grow on diesel as carbon source, was studied by observing and comparing the growth on diesel on day 4 (logarithmic phase) under the effect of selected heavy metals (Pb, Cr, As, Cd, Cu, Zn, Ni, Hg and Co) at 10°C. The sample presence with Zn showed the second most inhibited growth. Further experiment of various concentration of Zn was conducted to observe and compare the growth of *Rhodococcus sp.* under the effect of different concentration of Zn (1, 2, 5, 10 and 20 mg/l). Overall, findings showed that the selected heavy metals had effect to the growth of the *Rhodococcus sp.* on diesel in the order: Hg > Zn > Cd > Cu > Co > Ni > As > Pb > Cr. The growth of *Rhodococcus sp.* on diesel supplemented with Hg and Zn showed only 2.95% and 5.71%, respectively when compared to the no-metal control. The growth of strain in the presence of 2 mg/l of Zn(NO₃)₂ was better than that of in the presence of 1 mg/l of Zn(NO₃)₂. However, the presence of 5 mg/l of Zn(NO₃)₂ onwards (5 mg/l, 10 mg/l and 20 mg/l) significantly inhibit the growth of *Rhodococcus sp.*

Keywords: *Rhodococcus sp.*; mercury; hydrocarbon degradation; co-contamination

Optimisation of biodegradation conditions for diesel oil removal by cold-adapted *Arthrobacter* sp. strain AQ5-05 from Antarctica using Response Surface Methodology approach

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Abstract

The Antarctica is known as the world's most pristine environment. Increasing human activities at these regions demand the use of petroleum hydrocarbon notably diesel oil for fueling generators, aircraft, ships, and operational vehicles. Antarctica has thus suffered from prolonged contamination due to these man-made activities which resulted into polluting its ecosystem. Diesel oil spillage is a major challenge in the Antarctic continent due to its antimicrobial properties couples with the habitually low temperature and insufficient nutrient which delayed the rate of microbial processes and abiotic degradation. The use of microorganism has been proposed as a means of cleaning oil spills on the continent. However, the introduction of foreign organisms in this region is not supported by the Antarctic Treaty. This present study is aimed at optimising the growth conditions and diesel degradation activity of the Antarctic local bacterium *Arthrobacter* sp. strains AQ5-05 by applying Plackett-Burman design to screen out irrelevant parameters affecting the rate diesel degradation, afterwards the significant parameters obtained were further optimised using response surface methodology (RSM) via central composite design (CCD). The optimum temperature, pH, and salinity were found to be 16.30 °C, 7.67 and 1.12 % (w/v), respectively. Furthermore, second order polynomial regression model accurately presented the experimental data interpretation with an R^2 value of 0.999, Adjusted R^2 , Predicted R^2 , and F values of 0.994, 0.981, and 1840.3 respectively. The optimised conditions for diesel mineralisation identified *via* RSM increased diesel degradation from 34.5 to 56.4% for strain AQ5-05. This study therefore confirmed the potential use of these cold-tolerant bacterium strain in the biodegrading diesel-polluted Antarctic soils at low environmental temperature.

Keywords: Antarctica; *Arthrobacter*; bioremediation; diesel; response surface methodology

Potential antimicrobial activity of bacteria isolated from soil sample of Ross Island, Antarctica

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Abstract

Worldwide encounters antibiotic resistance issue and researchers actively conducting studies to discover new antibiotics in order to deal with this problem. This research aimed to screen extracellular antimicrobial activity of bacteria isolated from soil sample which was collected from the Ross Island, Antarctic. The microorganism from soil sample was cultured on nutrient agar. Five single colony was isolated, inoculated in nutrient broth, and incubated on a shaker at 20 °C with rotation of 200 rpm. The liquid culture was centrifuged at 13,000 rpm for 10 min to get supernatant. The supernatant of bacteria was used for screening of antimicrobial activity. *Staphylococcus aureus* and *Escherichia coli* were used as a test pathogens and chloramphenicol was used as a control. Out of five against *E. Coli*, two isolates showed antimicrobial activity. For *S.aureus*, all five isolates showed antimicrobial activity. However, all extracellular antimicrobial activities against both test pathogens were graded as weak. Another process to get concentrated supernatant, and intracellular screening should be implemented in this research to get more clear zone of inhibition. These positive results showed that there are potential to continue this research to discover new bioactive compound with antimicrobial activity from Antarctic bacteria.

Keywords: Antarctic; psychrotolerant; psychrophiles; antimicrobial; bioactive compound

Putative antimicrobial peptide-coding genes from antarctic bacterium *Pedobacter* sp. strain BG5

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Abstract

Pedobacter sp. BG5 produced antimicrobial compounds that inhibited the growth of food pathogens. However, to date, it is not known whether the antimicrobial compounds were conferred by genes in the plasmid or chromosome. There is a possibility that genes in the plasmid, pMWHK1 encoded the antimicrobial compounds. Four out of the eight open reading frames, *orf5*, *orf6*, *orf7*, and *orf8* of plasmid, pMWHK1 were analyzed in this study. *Orf5* has high homology to an antitoxin compound whereas *orf6*, *orf7*, and *orf8* were hypothesized to encode antimicrobial compounds. This work was performed to determine whether *orf6*, *orf7* and *orf8* of plasmid pMWHK1 conferred the antimicrobial properties of *Pedobacter* sp. strain BG5. Additionally, an experiment was set-up to determine whether *orf5* is an antitoxin gene. All the putative genes were transcribed from an arabinose promoter in the pBAD plasmid in *Escherichia coli* TOP10. Upon expression of *orf6*, antimicrobial activity assays were performed using a lawn of tester strain on an agar plate. Among the gene products, the one encoded by *orf6* mildly inhibited the growth of a tester strain, *Bacillus cereus* K3. *Orf6* also reduced the growth rate of host *E. coli* TOP10 expressing it. Nevertheless, the expression *orf5* was unable to counter the effect of the antimicrobial toxin of *orf6*. Gene products of *orf7* and *orf8* did not inhibit the host or the tester strains.

Keywords: *Pedobacter* sp., antimicrobial compound, plasmid, antitoxin gene

Optimization growth rate of bacteria-producing cold-active proteolytic enzyme from Antarctica region

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Abstract

Diverse of microbial diversity were discovered in the Antarctica region. The capability of these microorganisms to live at lower temperature was very fascinating. In this study we optimized the growth condition of the bacteria using One Factor at Time (OFAT) approach. The parameters selected were pH, temperature and sodium chloride (NaCl) percentage. The initial absorbance of the bacteria was adjusted to 0.1 in the tested media and incubated in orbital shaker at 200 rpm. The growth rate of the bacteria was calculated after 24 hours incubation period. The optimized conditions were obtained after running triplicate test. Majority of the bacteria isolated with cold active proteolytic enzyme activity were psychrotolerant and tolerated with 4 % NaCl. Coastal environment and cold temperature influenced the bacteria's growth. The relationship of bacteria growth rate with the proteolytic enzyme activity was analyzed. Higher bacteria growth rate produced higher proteolytic activity. Growth characteristics affected the enzyme production. In conclusion, optimum bacteria growth conditions is important to maximize the enzyme activity and production. This would benefits for high scale enzyme production for industrial purposes.

Keywords: Bacteria; cold-active protease; Antarctica; OFAT; Growth rate

Structural adaptation and potential application of lipase from Antarctic *Pseudomonas*

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Abstract

Cold active lipases have huge biotechnological prospects due to their high catalytic activity at low temperature. The utilization of organic solvents as reaction media for low molecular weight ester synthesis coupled with low temperature process for enzymatic reaction provides numerous industrially attractive advantages. Previously, a gene encoding a lipase from an Antarctic *Pseudomonas* sp was expressed in *E. coli*, purified and characterized. This cold-active lipase exhibited alkaliphilic profile and was particularly active at low temperature in water-immiscible solvent. Thus, it was of interest to investigate the effect of temperature and organic solvent towards the lipase structure via biophysical and computational approach. Molecular dynamic simulations and protein-solvent interaction analysis showed that the interaction of organic solvent and lipase was based on hydrophobicity effect. The synthesis of short chain flavour ester was conducted. The cold active lipase was able to synthesize ethyl hexanoate with best conversion of ester obtained at low temperature. These unique properties of this Antarctic lipase will provide considerable potential for many industrial applications and organic synthesis at low temperature in the near future.

Keywords: Lipase; *Pseudomonas*; Structural adaptation; Antarctica

The comparison of soil metagenome analysis between tropical and polar region

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Abstract

The soil environment contains an enormous diversity of life with the highest microbe diversity on the earth (Roesch et al., 2007). There are billions of bacterial cells, and around 100,000 different bacterial species can be found in a teaspoon of soil (Torsvik et al. 2002). However, not all the bacterial species can be easily cultivated and identified through traditional way. Recently, the emerging of the next generation sequencing technique have revolutionized the soil metagenomic field by allowing massive parallel sequencing occurs in a high throughput way to access the soil bacteria diversity. Our objective was to study the species differentiation by analyzing the metagenomic data between polar regions and tropical region. The high throughput 16S rRNA illumina sequencing was employed to reveal and compare the taxonomic information of 14 soil microbial communities in between tropical, Arctic and Antarctic region. The results showed that a total of 52 bacterial phyla were found within the soil samples in tropical and both polar regions. The three most dominant phyla groups within all the tropical soil samples were the phyla Proteobacteria, Actinobacteria and Chloroflexi while for both polar regions, the most dominant groups were represented by phyla Proteobacteria, Actinobacteria and TM7. By comparing the bacterial abundance values based on their OTUs, we found that there were some similarities of taxonomic diversity and composition within both polar soil bacteria and tropical soil bacteria. Due to the complexity of soil metagenome, a small proportion of bacteria phyla group were still unable to be detected and classified.

Keywords: Soil bacteria; metagenomic analyses; 16S rRNA illumina sequencing; bacterial diversity and composition

Structure and function of a novel cold regulated cold shock domain containing protein from an obligate psychrophilic yeast, *Glaciozyma antarctica*

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Abstract

Cold shock domain (CSD)-containing proteins are one of the groups of the evolutionarily conserved nucleic acid-binding proteins in all three domains of life consisting of an ancient beta-barrel fold that serves to bind nucleic acids. The cDNA of a novel CSD-containing protein was cloned from *Glaciozyma antarctica* designated as Ga_CSD1. The Ga_CSD1 was cloned in pET30 Ek/LIC and pet32 Ek/LIC cloning host, sequenced, expressed and its resistance towards cold was characterized. The full length of Ga_CSD1 open reading frame is 1338bp which encodes for an N-terminal CSD with conserved nucleic acids binding motif RNP1 and RNP2. The deduced amino acid sequence of CSD of Ga_CSD1 shares high homology between 40% to 66% with other CSD proteins in vertebrate, invertebrate and bacteria. Protein expression of recombinant Ga_CSD1 in both pET30 Ek/LIC and pet32 Ek/LIC shows overexpressed soluble expression in both supernatant and pellet form in 20°C. The effects of CSD protein overexpression on colony formation shows that *E. coli* cells are able to grow at 37°C and 20°C but not in 4°C while *E. coli* Ga_CSD1 cells are able to grow in all temperatures tested. In addition, *E. coli* Ga_CSD1 cells shows higher growth rate compared to *E. coli* cells in 10°C. Structural analysis of Ga_CSD1 shows some interesting findings such as more aromatic interactions for efficient binding in low energy environment, a longer loop that may contribute to structural flexibility and clustering of charged amino acids on the protein surface that is vital for protein stability and flexibility.

Keywords: Cold shock protein, cold adaptation, stress tolerance, *Glaciozyma antarctica*, psychrophilic yeast

Soil bacterial diversity of Browning Peninsula, Windmill Islands, East Antarctica revealed by NGS approach

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Abstract

Browning Peninsula is located near south of the Windmill Islands in east Antarctica. Browning Peninsula is known to be a barren ice-free polar desert landscape. There were limited studies done on the bacterial diversity in Browning Peninsula with different sequencing approaches such as 454 pyrosequencing. In this study, we screened the soil bacterial taxonomic composition using next generation sequencing technology utilizing illumina miseq platform targeting v3-v4 hypervariable regions of the 16S rRNA. In total of 2,207,103 reads that passed the quality filtering, 28 phyla were identified, and the top phyla were Cyanobacteria (27.65%), followed by Proteobacteria (25.97%), Actinobacteria (9.25%), Firmicute (8.64%), Chloroflexi (8.47%), and Bacteroidetes (4.24%). In contrast to other soil ubiquitous bacteria, cyanobacteria were significantly dominated the bacterial composition in the soil of Browning Peninsula. Thus, it can be concluded that Cyanobacteria act as primary producer in the extremely dry, nutrient-poor, barren landscape of Browning Peninsula.

Keywords: Browning Peninsula; east Antarctica; bacterial; 16S rRNA

Polyphasic characterization of toxin producing cyanobacteria from cryopreserved Antarctica Cyanobacteria mats

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Abstract

The first report on cyanobacteria producing cyanotoxin in Antarctica was made recently but there is no reason to assume the toxicity production is a new phenomenon in Antarctica. Recently, the findings from 100-years old Antarctic cyanobacterial mats collected from Ross Island and Mc Murdo Ice Shelf during Captain R.F. Scott's discovery expedition revealed that microcystins, BMMA and BMMA isomers were discovered. This new findings represent the oldest polar cyanobacterial samples found to contain cyanotoxin. According to this, we anticipated that the recent increasing discoveries of cyanobacterial toxin in Antarctica due to the increased number of studies since 2000 rather than the new emergence or introduction of toxin strains in recent years. In this study, we examined twenty cryopreserved mats samples from Cape Royds, Granite Harbour and Cape Crozier in Antarctica between 1986 and 1987. All these samples are being identified using morphological and molecular phylogenetic analysis for species delineation. As for toxins production, strains successfully isolated into unialgal cultures were screened for genes involved in the biosynthesis of microcystin, anatoxina, saxitoxin, cylindrospermopsin and nodularin using Polymerase Chain Reaction (PCR). To date, three species belonging to the genus *Leptolyngbya*, *Geitlerinema* and *Phormidium* were positive for the presence of microcystin encoding genes.

Keywords: Polyphasic; Cyanobacteria; Cyanotoxin; Cryopreserved; Microcystin; Antarctica

Thermal stress response in polar and temperate *Pseudogymnoascus* spp. soil fungi

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Abstract

Global temperatures are predicted to rise due to climate change. In polar systems, studies to link shifting environmental parameters to physiological response and thus functional activity are lacking in soil fungi. *Pseudogymnoascus* fungi, commonly isolated from polar soils, have been shown to secrete high levels of extracellular hydrolase enzymes, suggesting a role as important decomposers. In this study, we sought to measure transcriptional changes in these fungi in response to a transient heat. Arctic, Antarctic and temperate strains were cultured at 15°C (ideal growth temperature) for 5 days then transferred to 25°C (heat challenge temperature) for 2 hours. Possible orthologs of *Saccharomyces cerevisiae* HSP70 and HSP90 genes were identified among available *Pseudogymnoascus* spp. protein predictions, and their expression following heat treatment was measured by quantitative real-time PCR. Consistently across all strains, two HSP70 homologs and the HSP90 homolog were upregulated, of which two were statistically significant in polar strains. Conversely, one HSP70 homolog was downregulated in all strains, demonstrating functional differences of homologous genes in the HSP70 family. RNAseq analysis of one of the Arctic strains revealed 2,992 differentially expressed genes, many of which are involved in pathways of protein synthesis and metabolism. Taken together, our findings suggest that short-term exposure to thermal stress elicits an extensive transcriptional response in *Pseudogymnoascus*, and that approaches in gene expression analysis may be used to identify molecular markers of heat stress and pave the way for future in-depth functional studies toward understanding the effects of climate change-associated warming on polar soil fungi.

Keywords: stress; heat; fungi; qPCR, RNAseq

Review on genes involved in pathways of mycosporine-like amino acids biosynthesis

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Abstract

Cyanobacteria are photoautotrophs depending on sunlight as their primary source of energy. However, their dependence on solar radiation caused them to be exposed to harmful ultraviolet rays. UV rays can directly damage cellular DNA or indirectly through formation of ROS (Reactive Oxygen Species). Massive loss of stratospheric ozone as a result of chlorinated fluorocarbons (CFCs) has been reported after the discovery of the ozone hole in the Antarctic in 1985. Attention had been directed not only to the Antarctic but also to the Arctic due to the autocatalytic destruction of the stratospheric ozone that has led to the enhanced radiation of harmful UV-B (280-320nm). Cyanobacteria which is a major component of terrestrial and freshwater habitats of Antarctica produces MAAs (mycosporine-like amino acids); a versatile secondary metabolite that not only works as a sunscreen compound, but also may serve as an antioxidant molecule, act during salinity, thermal and desiccation stress, an accessory pigment in photosynthesis and an intracellular nitrogen reservoir. This paper reviews current information on the pathways of MAAs biosynthesis such as shikimate and pentose phosphate pathway and the involvement of several key genes such as non-ribosomal peptides synthetase, dehydroquinase synthase, O-methyltransferase, ATP grasp, NRPS-like and D-Ala-D-Ala ligase that forms several MAAs like mycosporine-glycine and shinorine.

Keywords: Mycosporine-Like Amino Acids, Shikimate pathway; Pentose phosphate pathway, Mycosporine-glycine, Shinorine.

Functional traits of benthic communities in the West Antarctic Peninsula

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Abstract

A study in West Antarctic Peninsula was conducted in January 2016 to determine the macrobenthic ecosystem functions. The organisms were classified into biological traits (feeding, mobility, adult life habit, body form, body size, reproductive technique, and type of larva) to determine the dominant traits of macrobenthic organisms at different latitude stations. In addition, the collected data were also analysed using a more sophisticated (as opposed to community structure) indices namely Biological Traits Analysis and Functional Diversity. Data interrogation found out that traits related to resource utilisation (i.e. feeding, mobility) imposed more influence on the communities compared to traits related to life cycle (i.e. reproductive technique, type of larva). A spatial aspect of this study showed that the functional diversity in the West Antarctic Peninsula was negatively correlated with the latitude, where high latitude station was less functionally diverse than the low latitude station.

Keywords: West Antarctic Peninsula, macrobenthos, functional diversity,

Unlocking the secrets of cold adaptation in psychrophilic yeast *Glaciozyma Antarctica*

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Abstract

Antarctica is a land of extremes. Extreme cold, extreme low nutrients, extreme high ultraviolet (UV) radiation, extreme dehydrated conditions and frequent freeze-thaw cycle. Thus, the most successful organisms that can thrive in Antarctica are the microorganism, with high adaptation to withstand extreme conditions. Due to these adaptations, the types of compounds produced by these microorganisms might be of novel origins with good pharmaceutical properties. *Glaciozyma antarctica*, a psychrophilic yeast first isolated from Antarctica, was chosen to determine the role of secondary metabolites in cold adaptation. This microbe was grown at different temperatures of -18 and 12 °C and then extracted with ethyl acetate. The chemical profiles of each extracts were analyzed using LCMS. Results showed that some compounds were only produced at 12 and vice versa. At 12 °C, six compounds were detected: cyclo(-Pro-Gly), cyclo(-Pro-Val), thymidine, spongothymidine, vidarabine and uracil. Meanwhile, eight compounds were detected from the -18 °C extract, which were (-)-glaciantarcin (151), cyclo(-Pro-Ala) (152), cyclo(-Pro-Leu) (125), cyclo(-Pro-Phe) (127), cyclo(-Pro-Tir) (154), spongothymidine (158), thymine (161) and phenazine-1-carboxylic acid (162). This preliminary finding showed that different compounds are produced when microbes are subjected to extreme cold, and might play a role in cold adaptation.

Keywords: psychrophiles; *Glaciozyma antarctica*; secondary metabolites; cold adaptation

Application of Response Surface-based Optimisation for optimising pure canola oil-degrading parameters under temperate conditions using the cold-adapted Antarctic bacterium *Rhodococcus* sp. AQ5-07

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Abstract

The Antarctica natural environment is often considered as among the most virgin areas in the world. However, the existence of pollutants from industrial areas debunked this status. At present, the Antarctic environment is no longer clean. Canola oil released into the Antarctic environment from kitchens, restaurants, slaughterhouses and food processing industries or by accidental oil spills. These deposits of lipids have led to serious anthropogenic problems such as odour problems, pipes blockage, congestion of treatment filters among others, hence killing marine organisms. The damage can be severe if the release of this waste occurs in temperate waters where biodegradation by existing marine microorganisms is limited due to the cold conditions. Plackett–Burman design was used to screen the significant parameters that affect pure canola oil (PCO) degradation rate. After the design was applied, response surface methodology (RSM) through the use of central composite design (CCD) was used to optimised the significant parameters in order to obtain the most superior degradation conditions. The optimum substrate oil concentration, nitrogen source (NH₄)₂SO₄, yeast extract and pH were found to be 2.92% (v/v), 1.31 g/L, 0.39 g/L and 7.68, respectively. Second order polynomial regression model has accurately showed the interpretation of experimental data with an R^2 value of 0.9405, Adjusted R^2 , Predicted R^2 and F values of 0.8850, 0.7432, and 16.94, respectively. This study demonstrates the possible use of an Antarctic bacterium with the potential to be used in bioremediation of vegetable oil and wastewater treatments in a low temperate environment.

Keywords: Antarctica; Biodegradation; Canola oil; *Rhodococcus* sp.; wastewater

Investigating the response of polar marine phytoplankton *Chlorella* sp. towards elevated oceanic CO₂ using a metabolomics approach

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Abstract

Anthropogenic activities are causing carbon dioxide levels to rise rapidly at an unprecedented rate, which expected to increase 2.5 times by year 2100 if there are no significant mitigation efforts. Oceans are major physical carbon sinks, with 40% of anthropogenic CO₂ are absorbed by polar Southern Ocean. Other than trapping heat and warming the ocean, CO₂ dissolved brought down the oceanic pH. Marine phytoplankton are important as major primary producers as the base of most marine food webs and are central to the marine biological carbon cycle. Laboratory and field investigations on responses of marine phytoplankton grown under increasing levels of acidification have returned different outcomes. Phytoplankton are highly diverse, shaped by multiple endosymbiotic events. Moreover, phytoplankton strains which are ubiquitous globally are likely to adapt to local environments and may respond differently. In this current investigation, polar *Chlorella* sp. were acclimated to current (~400 ppm(parts-per-million)) and future predicted (~1000 ppm) oceanic CO₂ levels and cellular primary metabolites were extracted for gas-chromatography mass spectrometry (GCMS) analysis to probe metabolic changes. Physiological parameters (growth, photosynthesis, pigment levels and cell volume) were measured alongside biochemical (fatty acid levels) features. All phytoplankton share the same primary metabolites, the end products of cellular metabolism. Hence the output of this research will circumvent the problem of varying responses in marine phytoplankton. Our goal is to build a substantial experimental foundation in observing metabolism of marine producers under the effects of ocean acidification.

Keywords: oceanic CO₂; polar phytoplankton; metabolomics

Cold Stress response of a cold-adapted bacterium *Cryobacterium* spp. SO1 from Fildes Peninsula, Antarctica

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Abstract

Bacteria have evolved to survive in respective ecological niches they inhabit to. For instances, bacteria isolated from the glacial environment have evolved to survive in the subzero habitat. A reduce of surrounding temperature is probably affecting the organisms' molecular mechanisms. It will be interesting to define the cold stress response adopted by study bacterium through transcriptomic analysis. For that, a cold-adapted bacterium isolated from Antarctica, *Cryobacterium* spp. SO1 was used in this study. To understand how *Cryobacterium* spp. SO1 response to cold stress, a drop of 10°C was introduced to the optimally grown culture and the RNA were extracted for transcriptomic sequencing. A total of 169 million raw reads were obtained, 161 million reads were pass filtered. The reads were then mapped to the genome of strain SO1. As detected, more than 85% of the reads were mapped back to the genome. Pairwise comparison between transcriptome data between optimal temperature and cold stress revealed a total of 182 differentially expressed genes (DEGs), out of that, 66 genes were up-regulated remaining 116 genes were down-regulated. From the dataset, the usual discussed thermal-stress related genes such as cold-shock proteins (CSPs) were not differentially expressed in strain SO1. It may indicate *Cryobacterium* spp. SO1 either has different adaptation strategies or the introduced cold is too mild to threaten their life, therefore CSPs and relevant genes were not expressed.

Keywords: *Cryobacterium* sp. SO1; Cold-stress; Transcriptomes; DEGs

UVB-Induced DNA damage and repair in *Pseudogymnoascus* spp. isolated from Arctic and Antarctic regions

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Abstract

Solar radiation regulates all biological activities on Earth. Prolonged exposure to UV radiation can cause deleterious effects to all organisms especially those inhabit in the polar regions during the summer. In study, we compared the repair of UV-induced DNA damage under two repair conditions, light and dark, each of which induced the photoreactivation (Phr) and nucleotide excision repair (NER) pathways, respectively. Two types of DNA damage, namely cyclobutane pyrimidine dimers (CPDs) and pyrimidine 6-4 pyrimidone photoproducts (6-4PPs) were quantified using ELISA during repair incubation at 0, 2, 6, and 10 h. Results showed that Antarctic strains were more resistant to UVB-induced CPD compared to Arctic strains. In comparisons between different light condition, CPDs were repaired significantly faster in light than in dark conditions. The expression of two DNA repair genes, *RAD2* and *PHR1* (each encoding a protein in NER and Phr, respectively) during the repair duration of 0 and 2 h in the two different repair conditions were then measured using qPCR to determine the principal DNA repair pathway. The expression of *PHR1* was downregulated and *RAD2* was upregulated after UVB exposure in both light and dark repair conditions. These observations suggest that the Phr pathway may not be involved in the repairing of UVB-induced DNA damage in *Pseudogymnoascus*. The difference in *RAD2* expression between the two repair conditions was insignificant, further supporting that an alternative repair mechanism may be involved in the repairing of CPDs in the presence of light.

Keywords: Nucleotide excision repair; photoreactivation; cyclobutane pyrimidine dimer; 6-4 pyrimidine pyrimidone photoproducts; DNA repair

The genome of psychrotolerant *Pseudanabaena* strain isolated from high arctic: A NGS approach revealing complex association of genes and adaptation

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Abstract

The whole genome of filamentous cyanobacteria strain *Pseudanabaena catenata* obtained from the High Arctic Svalbard archipelago was characterized using Illumina Miniseq platform. The genus *Pseudanabaena*, despite its substantial roles in ecosystems and pharmaceutical applications has been overlooked due to its relatively small cell/filament sizes. Therefore, the successful sequencing and genomic analysis of the entire genome of this strain provides further understanding of complex association between genetics and physiology in this genus. The genome sizes of strain *P. catenata* USMAC16 was approximately 5.5 Mb with G+C content of 43.8%. A total of 2292 protein coding genes and 2261 genes matching hypothetical proteins were identified. Genome analysis identified two phycocyanin (*cpc*) gene clusters in which three homologues of *cpcA* and *cpcB* were present. A number of genes coding for cold adapted features such as *gyrA* and *B* coding for DNA gyrase, *htpG* coding for chaperone protein HtpG and *desA* coding for fatty acid desaturase were present in the genome of this strain which explains its psychrotolerant behaviour. This study has integrated next generation sequencing (NGS) approaches and has revealed information on the physiology and adaptation of *Pseudanabaena* strain towards dynamic environments.

Keywords: Genome; Illumina sequencing; *Pseudanabaena*; psychrotolerant; Svalbard.

Census of the bacterial community of the King George Island and Deception Island, Antarctica

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Abstract

The global temperature has increased by about 0.6 °C over the past century, and its effect is significant. Global warming may affect the equilibrium of the soil bacterial communities. Thus there is increasing concern that it might trigger a surge in the population of pathogenic bacteria. King George Island (KGI) and Deception Island (DCI) are members of the South Shetlands islands in West Antarctica, both with their landscape and local environmental factors, which may result in spatial heterogeneity of soil bacterial diversity. The two sites are suitable for long term monitoring of bacterial diversity change due to temperature rise, as the temperature there is known to rise relatively faster than east Antarctica. This project was conducted to census the soil bacterial diversity of Fildes Peninsula, KGI and DCI. 16S rDNA of soil bacteria of the two sites were sequenced using the Illumina MiSeq sequencer. The results showed that the major phyla present in KGI and DCI were the Actinobacteria, Proteobacteria, Chloroflexi, Verrucomicrobia, Bacteroidetes, and Acidobacteria. Distribution and evenness of the soil bacterial communities varied at the genus level and demonstrated some interesting features. For instance, *Sphingomonas* sp. was found to be the dominant genus of the two sites while subsequent six major genera from the two sites differ. Besides, genus, *Legionella* with members encompassing pathogenic bacteria were also found at low abundance at the two sites.

Keywords: Bacterial diversity, South Shetland Islands, 16S rDNA and soil

Cloning and expression of $\Delta 12$ fatty acid desaturase

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Abstract

Fatty acid desaturase catalyzes the addition of a double bond in a specific position of fatty acyl chain through the reaction called desaturation. This enzyme helps regulate the fluidity of membrane lipids and play vital roles in the biosynthesis of polyunsaturated fatty acids (PUFAs), which serves as precursors to regulate human health and development. Though fatty acid desaturase has been studied widely in advanced organisms, there are very limited studies of this particular enzyme in prokaryotes. To date, the structural study in microorganisms revealed that there is no structure has yet been crystallized and elucidated from prokaryotes. Fatty acid desaturase gene can be found in psychrophilic organisms, with the capability of adapting and living in an extreme cold condition. Currently, study about psychrophiles has come to attention of researchers as they have mechanisms to survive a very cold temperature and has the capability of working at high catalytic activity at particular temperature. Few psychrophilic organisms have been isolated from Antarctica including *Arthrobacter* sp. to understand their survival mechanism. Introduction of a double bond and composition of Histidine boxes of amino acid could be factors contributing towards the identification of cold-adapted enzyme. In order to understand the structure of $\Delta 12$ fatty acid desaturase gene, cloning and expression have been conducted. Model structure of the enzyme has been successfully predicted by means of homology modeling. On that account, the discovery of highly potential cold-adapted enzyme may give opportunity towards the nutraceutical and pharmaceutical industry.

Keywords: Fatty acid desaturase; psychrophiles; *Arthrobacter* sp.; expression

Response of phytoplankton groups to physico-chemical conditions in the Southern Ocean

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Abstract

Responsible for about half of global primary production, marine phytoplankton play an important role in global carbon cycle. Changes in ocean temperature and acidity are expected to alter physical processes, nutrients and carbonate system in the Southern Ocean. However, it remains unclear how phytoplankton will respond to these changes. We report the relationship between total dissolved inorganic carbon (DIC) and major phytoplankton groups collected along a transect (44°S to 53°S, centred at 10°E) crossing the Antarctic Polar Front (APF) on cruise ANT-XXVIII/3 “Eddy Pump” on board RV Polarstern in austral summer 2012. There are distinctive correlations between DIC and phytoplankton groups and across the APF. North of the APF, DIC shows a strong positive correlation with diatom-1, but a weak correlation with dino-1 and hapt-8. In contrast, a positive correlation was observed between DIC and diatom-2, but only a weak correlation with diatom-1 and dino-1 south of the APF. The results hint that different phytoplankton groups will respond differently to changes in physico-chemical conditions in the Southern Ocean.

Keywords: Phytoplankton, Southern Ocean, Antarctic Polar Front, carbon cycle

Effects of lead (Pb) toxicity on the morphology, oxidative stress response and metabolomic profiles of *Chlorella vulgaris* and *Micractinium inermum* isolated from Signy Island, Antarctica

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Abstract

The aim of this study was to assess the toxic effects of lead (Pb) on *Chlorella vulgaris* and *Micractinium inermum* in terms of morphological changes, oxidative stress response and metabolomic profiles. The microalgae isolated from soil samples of Signy Island, Antarctica were subjected to 10-day Pb toxicity testing. *Micractinium inermum* isolated from Berntsen Point (Pb content=127.643 µg/g) was more sensitive to Pb than *C. vulgaris* isolated from Goulay Peninsula (Pb content=0.893 µg/g). Cells exposed to Pb showed large amounts of starch granules, abundant vacuoles with electron-dense polyphosphate bodies, and alteration in chloroplast structure. The ROS levels of *M. inermum* exposed to Pb were significantly lower than the control, while superoxide dismutase (SOD) activity increased but no significant change in catalase (CAT) activity. In comparison, the ROS levels in *C. vulgaris* exposed to Pb at EC₁₀ were significantly higher than the control, with significant increase in both SOD and CAT activities. The metabolic responses of microalgae exposed to Pb were analysed using ¹H NMR spectroscopy. Subsequent PLS-DA scores plot showed that Pb-treated cells were clearly separated from the control. A total of 31 metabolite changes were detected in *M. inermum* exposed to Pb (9 up-regulated; 22 down-regulated) while a total of 10 metabolite changes (3 up-regulated; 7 down-regulated) were detected in *C. vulgaris*. The metabolites that confer potential oxidative protection such as glutathione and malate were up-regulated in both *M. inermum* and *C. vulgaris* exposed to Pb. In summary, exposure of the microalgae to Pb caused ultrastructural damage, induced oxidative stress and increased production of protective metabolites against oxidative stress.

Keywords: Antarctic microalgae; lead toxicity; ultrastructural changes; oxidative stress; metabolomic profiles

Heavy metal and antibiotic resistance in Antarctic bacteria isolated from Signy Island

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Abstract

Antarctic bacteria encounter a myriad of stresses from their pristine environments, including anthropogenic causes. These stresses elicit various defence mechanisms that not only buttress the microbes from damaging stress, but also manifest a cascade of changes that impact bacterial recalcitrance towards antimicrobial and heavy metal activity. Heavy metals, in particular are raising concerns among researchers, over their potential effects on human health as they are able to remain stable in the environment for prolonged periods. Antibiotic resistance has been recognized as a threat to global health ever since its emergence that limits therapeutic options available when treatment is warranted. The main objective of this study was to determine the relationship between heavy metals and antibiotic tolerance of culturable Antarctic soil bacteria isolated from two locations; Berntsen Point and Gourelay Peninsula in Signy Island. The polymicrobial biofilms from soil samples were estimated by crystal violet assay. Microbial isolates that showed resistance to heavy metals like copper and zinc at various concentrations (0.03- 4 mM) were subjected to 56 different kinds of antibiotics. With regards to antibiotics assays, the isolates showed different percentage of resistance. The isolates tested were *Arthrobacter sp.*, *Psychrobacter sp.*, *Rhodococcus sp.*, *Sporosarcina sp.*, and *Flavobacterium sp.* which are usually found in the soil environment. Moderate incidence of co-resistance to both antibiotics and metals were observed among the strains isolated. The results were varied depicting many ranges of conditions are able to support polymicrobial biofilm formation *in vitro* under psychrophilic conditions.

Keywords: Heavy metal; antibiotic resistance; co-resistance; Antarctic soil bacteria; biofilm

Study on the population genetics and mycotoxin genotypes of *Fusarium* spp. In Antarctica

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Abstract

Members in the genus *Fusarium* are widely distributed in many geographic regions of the world. This group of fungi is well known as plant pathogens of many important cereal crops, *e.g.*, wheat, maize, rice and sorghum, and of other native and economically important plants in the temperate and tropical regions. Most species in this genus can produce an array of important secondary metabolites such as mycotoxins. The extreme condition in Antarctica influences the diversity and life-styles of *Fusarium* spp. for adaptation. *Fusarium* spp. were reported to have been isolated in soils, plants and permafrost in sub-Antarctica. However, there are lack of information on the origin of this economically important fungal genus. Using population genetic approach, this research would answer several questions regarding the origin, diversity, population structure, and adaptation of genus *Fusarium* in Antarctica. Amplified fragment length polymorphisms (AFLPs) will be used for genotyping the isolates and analyse their population structure. Besides AFLPs, vegetative compatibility group (VCG) and sexual compatibility tests will also be conducted to understand the life cycle of this fungus in the population. Furthermore, trichothecenes mycotoxin genotyping will be conducted to further understand the fitness of *Fusarium* spp. in Antarctica. This research will increase our understanding on the evolution of mycotoxins in plant pathogens using *Fusarium* as a model, and the population structure of genus *Fusarium* in adapting to the extreme cold environment.

Keywords: population genetics; trichothecene; *Fusarium* sp., mycotoxin

Cold adaptive evolution of HSP70 of an Antarctic psychrophilic yeast, *Glaciozyma antarctica*: HINTS from a comparative analysis of the full size 3D structure and its interdomain interactions

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Abstract

HSP70 chaperone protein are the central components of cellular network in protein folding mechanisms. They involve in the folding of newly synthesized proteins, protection of the hydrophobic regions of denaturated proteins, the regulation of apoptosis, the immune response, and several other cellular processes. Although a large number of publications have been emphasizing on the structure and function of HSP70, the knowledge on cold adapted mechanisms acquire in psychrophilic eukaryote is still currently unavailable. In this work, a reliable full-size 3D structure of *Glaciozyma antarctica*'s HSP70 (Ga_HSP70-1) was constructed using comparative modeling. Analysis on the primary sequence and tertiary structure of Ga_HSP70-1 show several fascinating findings. Based on the performed molecular modeling, several residue substitutions are found in the nucleotide binding domain (NBD-N terminal). Interestingly, a stretch of 17-amino acids that are highly conserved in fungi was found missing in Ga_HSP70-1. Analysis on its interdomain interactions shows some possible cold adapted evolution mechanism which allow Ga_HSP70-1 to function in low energy environment.

Keywords: chaperone; Hsp70; model; tertiary structure; ATPase and substrate-binding domains

Protein cold adaptation strategy: A comparative structural analysis of α -crystalline domain of a conserved hypothetical protein of *Glaciozyma antarctica*

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Abstract

A 37 kDa hypothetical protein Ga_HP010 of *Glaciozyma antarctica* is a conserved protein containing α -crystalline domain found in a variety of organisms including human. The α -crystalline domain consists of 100 residue amino acids is folded into several β -strands organized into two β -sheets which is the basic building block for most small heat shock proteins (sHSPs). It is known that sHSPs act as molecular chaperones by folding protein intermediates to form stable complexes. However, there is little information available about these structures functioning in low energy environment. Herein, we present a comparative structural analysis of a cold adapted α -crystalline domain of a conserved hypothetical protein, leading to the identification of potential residues which contribute to cold adaptation strategy. In this work, the full length of Ga_HP010 was amplified and cloned for sequence analysis. The α -crystalline domain has 63.8% sequence similarity with *Rhodotorula toruloides* chord-domain-containing protein while the tertiary structure is 53.2% similar with human chord-domain-containing protein. Sequence alignment shows that the amino- and carboxy-terminal extensions of the α -crystalline domain differing in sequence from species to species and even between sHSPs from the same organism. Interestingly, comparison of 3D structures of α -crystalline domain between Ga_HP010 and human shows longer dimerization loop in Ga_HP010 which connect the β -sheets. Another intriguing finding is the missing of one β -strand in Ga_HP010 where in human, the β -sheet is composed of 3 β -strands whereas in Ga_HP010, only 2 β -strands followed by an extension loop. Analysis on protein-protein interactions reflects the cold adaptation strategies acquire by Ga_HP010.

Keywords: Molecular chaperones; small heat shock proteins; the α -crystallin domain, conserved hypothetical proteins, protein folding

Effects of elevated temperatures on growth and photosynthetic performance of polar *Chlorella*

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Abstract

Global warming has been the subject of concern in today's world with elevating temperatures causing the melting of polar ice as well as increasing sea level. The aim of this study was to investigate the physiological and photosynthetic performance of two polar *Chlorella*, namely *Chlorella vulgaris* UMACC 250 and *Chlorella vulgaris* UMACC 234 to elevating temperatures as might be experienced under future warming scenarios. The cultures were exposed to three different temperatures of 4°C, 8°C and 12°C. The growth and photosynthetic activity were determined every 2 days or a period of 10 days. At the end of the experiment, the cultures were harvested and analyzed for protein, carbohydrate and lipid. A general trend of growth and photosynthetic performance were observed for both *Chlorella* strains when the cultures exposed to elevating temperatures. There was a decrease in the growth on day 4 to day 7. However, both *Chlorella* strains were able to tolerate and survive much better at 8°C and 12°C compared to their ambient temperature (4°C). The final chlorophyll-*a* and carotenoid content showed increasing trend with increased temperatures for both strains. The photosynthetic activities were analyzed using pulse-amplitude modulation (PAM) fluorometry. The photosynthetic parameters including maximum quantum efficiency (Fv/Fm), relative electron transport rate (rETR), light harvesting efficiency (α) and photoadaptive index (Ek) were derived from the rapid light curves (RLCs). At the beginning of the experiment, both *Chlorella* strains indicated a slight decline in photosynthetic activities and growth. However, they showed the ability to recuperate with *Chlorella* UMACC 250 recovers much better compared to *Chlorella* UMACC 234. Both strains showed similar trend in their carbohydrates content at 12°C, while *Chlorella* UMACC 234 showed decreasing protein content with increased temperatures. The results indicated that both polar *Chlorella* strains were able to survive and acclimate at increased temperatures throughout 10 days of exposure.

Keywords: Polar; *Chlorella*; photosynthesis; pulse-amplitude modulation (PAM) fluorometry

***In silico* analysis of cold-adaptive aromatic ring-hydroxylating dioxygenases**

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Abstract

Anthropologic activities from scientific and military stations in Antarctica increase the risk of oil pollution due to its necessity in generating energy for daily consumption. Many studies have been conducted in identifying potential bacteria that able to degrade polyaromatic hydrocarbon (PAHs) using cold-adapted Aromatic Ring-Hydroxylating Dioxygenases (ARHD). However, there is very limited information available regarding its structure and behaviour at different temperature. In this study several ring-hydroxylating dioxygenases were obtained from molecular structure database, which originated from both cold and temperate environments. The amino acid sequence analysis was conducted in order to determine their conserved region and their evolutionary distance between these two origins. The structure similarity of ARHD originated from cold environment and temperate was performed and subsequently the temperature variation simulation was conducted. Several differences were observed in cold adapted ARHD indicated unique characteristics in its structure and behaviour compared to temperate ARHD. The understanding of cold adapted ARHD molecular structure may lead to efficient utilisation of bacteria that possessed this enzyme in bioremediation of aromatic hydrocarbon pollutants.

Keywords: Aromatic Ring-Hydroxylating Dioxygenase (ARHD); Cold adapted; molecular simulation

Adaptation and ecosystem resilience of blue-green algae towards carotenogenesis regulatory mechanism

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Abstract

Blue green algae (cyanobacteria) which known for its vibrant bluish green basically contains, phycocyanin, phycoerythrin and a number of yellow pigments, mainly carotenoids. The same species of blue green algae may vary in colour depending on the surrounding condition. The main issue that researcher want to address through this research is unclear mechanism regarding the pigmentation of blue-green algae towards its defense mechanism in certain degree of stress condition. In this research carotenoid biogenesis is investigated in blue green algae cell culture as a potential model system. The value of this experimental system for investigating variables controlling carotenoid accumulation is then tested by assessing the effects of environmental variables, such as drought stress, light intensity and nutrient strength on carotenoid accumulation. Our findings revealed that blue green algae pigmentation depending upon the spectral composition of the light. The lower the light intensity, the more accessory pigments effective in photosynthesis will be formed to catch a high percentage of the light. However, it was believed that it is beyond light intensity. It could be more key factors that can trigger blue green algae to change its colour accordingly to particular environment. Therefore, the necessity of this research is to develop a better understanding regarding blue-green algae (cyanobacteria) typologies and defensive behavior in different region. Anticipated benefits of the research may have potential in contributing to the defense/protective mechanism as well as ecological indicators in various fields in the future.

Keywords: carotenoid; environmental stress; cyanobacteria; chromaticity

Profiling of fatty acids in microalga from Antarctic

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Abstract

Microalgae are equipped with remarkable adaptive mechanisms that allow them to survive in all sorts of habitat even in subzero temperature such as in Antarctic. This research aims to determine the fatty acid compositions of a polar microalga using different type of solvents. The highest fatty acid compositions was detected when hexane was used as solvent which was 65.92%. Meanwhile, methanol solvent gave the lowest fatty acid compositions, which was 10.52%. Among the fatty acids, polyunsaturated fatty acids were the highest composition in the microalgal sample consists mainly of oleic acid and α -linolenic acid. This study confirms the variations of fatty acid compositions present in microalgae, which have many potentials to be exploited especially for healthcare and aquaculture applications.

Keywords: microalga; Antarctic; fatty acids

Fatty acid profiles of Antarctic Cyanobacteria *Leptolyngbya*

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Abstract

Cyanobacteria are robust microalgae that are equipped with remarkable adaptive mechanisms that allow them to survive in all sorts of habitat even in subzero temperatures such as in Antarctica. In total of 4 cyanobacteria previously isolated from Antarctic polar ice was used in this study. Morphologically, these cyanobacteria were found to be closely similar to the genus *Leptolyngbya*. Analysis using 16S rRNA sequence further confirmed their identity as *Leptolyngbya* spp. and they are designated as *Leptolyngbya* sp. A, B, D and E. Following fatty acid analysis using GCMS, it was determined that unsaturated fatty acids predominate the fatty acid profiles for *Leptolyngbya* sp. A, B and D while saturated fatty acid was found to be dominant in *Leptolyngbya* sp. E. *Leptolyngbya* sp. D contained almost 100% of linoleic acid whilst *Leptolyngbya* sp. A and *Leptolyngbya* sp. B contained 59.35% and 83.33% of linoleic acid respectively. Besides linoleic acid, palmitoleic acid (18.45%), oleic acid (19.45%) and lauric acid (2.74%) were also present in *Leptolyngbya* sp. A. As for *Leptolyngbya* sp. B, other than linoleic acid, only oleic acid (16.67%) was detected. Findings from this study demonstrated the potentials of Antarctic cyanobacteria that could be further exploited for other application such as biofuel and healthcare industries.

Keywords: cyanobacteria; *Leptolyngbya*; Antarctic; fatty acid profiles

Discovery of antibiotic resistant bacteria from Antarctic regions

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Abstract

Increasing anthropological activities such as scientific exploration not only discovered previously unknown beneficial bacteria but also bacteria that possessed antibiotic resistance. This study was conducted to screen bacteria isolated from Antarctic region with positive antibiotic resistance characteristic. Several bacteria were isolated from sediments and soils from several locations on Southern Victoria Land, Antarctic. These bacteria were spread on the nutrient rich media and tested with certain antibiotics; chloramphenicol, gentamycin and tetracycline. Then, DNA of each bacteria strain was extracted and amplified using primers 27F and 1492R. From the results, most of the bacteria were susceptible except some strains. Based on the phylogenetic analysis, these bacteria belong to *Paenibacillus* sp and *Pseudomonas* sp. These findings indicated the presence of antibiotic resistance gene in bacterial community in Antarctic region.

Keywords: Bacteria; Antarctic; Antibiotic-resistance

Response of *Chlorella* isolates from polar regions and lower latitudes to ultraviolet radiation (UVR) stress: Growth, pigmentation and oxidative stress response

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Abstract

Increased levels of UVR as a result of anthropogenic ozone depletion have been reported in many parts of the world including Antarctica and the adjacent geographic regions, as well as the Arctic region. Microalgae from different geographical latitudes receive varying levels of UVR. The aim of the present study was to assess the effects of UVR, particularly increased UVB radiation on the growth, pigmentation and oxidative stress response of *Chlorella* species isolated from different latitudes, namely Antarctic (*Chlorella* UMACC 237), Arctic (*Chlorella* UMACC 263), temperate (*Chlorella vulgaris* UMACC 248), and tropical (*Chlorella vulgaris* UMACC 001) regions. The microalgae were exposed to three light treatments: PAR+UVA+UVB, PAR+UVA, and PAR alone, on 12h:12h light-dark cycle for 8 days. The Antarctic and Arctic *Chlorella* were grown at 4°C, while the temperate and tropical *Chlorella* were cultured at 18°C and 28°C, respectively. Growth response, photosynthetic pigment contents (chl-a, chl-b and carotenoids), reactive oxygen species (ROS), lipid peroxidation levels, and superoxide dismutase (SOD) and catalase activities of the *Chlorella* isolates were assessed. Results showed that increased UVB caused the reduction in specific growth rate (μ) in the Arctic and temperate *Chlorella*. Significant increase in cellular contents of chlorophyll a and b were observed when the tropical and temperate *Chlorella* were subjected to increased UVB radiation. However, the reversed trend was observed in cellular contents of carotenoids for these *Chlorella* spp. Both the Antarctic and Arctic *Chlorella* showed significant increase in ROS and lipid peroxidation, indicating that the polar *Chlorella* spp. were under oxidative stress caused by UVB. However, both polar *Chlorella* spp. were able to survive under increased UVB condition by producing higher amounts of carotenoids and increasing their catalase activity. Overall, the results showed that the *Chlorella* isolates from different latitudes responded differently to UVB stress.

Keywords: Ultraviolet radiation; *Chlorella*; pigment; oxidative stress; growth

Effects of sunscreen UV filter, oxybenzone on green microalgae

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Abstract

UV filters are widely used in sunscreen and personal care products due to its properties to give protection to our skins against UV light. Oxybenzone or commonly known as benzophenone-3 was one type of UV filter found as the active ingredients in many pharmaceutical products. Although oxybenzone had been extensively studied as environmental toxicant in the ecosystem, but little is known about the toxicity effects on microalgae. The growth (OD₆₂₀, chl- *a*, carotenoid) and biochemical properties of oxybenzone on polar microalgae (*Chlorella* UMACC 400 and *Chlorella* UMACC 401) and temperate microalgae (*Chlorella pyrenoidosa*, *Chlamydomonas reinhardtii*, *Scenedesmus quadricauda*) have been investigated. These microalgae were cultured in triplicates and exposed to different oxybenzone concentrations (0, 100, 200 300 and 400 mg/L) at 4 and 18°C, respectively for 96 h. The results showed that the highest concentration of oxybenzone (300 and 400 mg/L) had an adverse effects towards the reduction of the growth rate and biomass of these microalgae. The exposure of oxybenzone at higher concentrations also leads to the cell structure impairment after 96 h. In addition, it was also showed that the protein content increased significantly when exposed to 400 mg/L oxybenzone concentrations. It was observed that exposure to 200 mg/L to 400 mg/L oxybenzone concentrations does not give significant effects towards *S. quadricauda* growth. Further investigation needs to be done to determine the effects of oxybenzone on microalgae at the relevant environmental concentrations.

Keywords: Polar; *Chlorella*; oxybenzone; benzophenone-3; emerging contaminants.

Understanding *Pseudogymnoascus* sp. response towards temperature stress: A proteomic approach

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Abstract

Mass spectrometry (MS)-based proteomics is a powerful tool that has helped researchers to identify and quantify complex protein mixtures in various cells. Under temperature stress, fungi will undergo numerous physiological changes and metabolic modifications for survival. Changes in protein abundances can give an overview of the complex protein response under high and low temperature stress. In this study, *Pseudogymnoascus* sp. (isolate HND16 R1-1 sp2), a fungus isolated from Arctic soil, was selected as a model organism, in an attempt to provide an overview of how polar fungi respond towards temperature stress via a proteomic approach. Firstly, an optimisation of protein extraction protocols was carried out. Three different chemical extraction methods; 1) TCA-acetone, 2) TCA-acetone-phenol, and 3) phenol-guanidine hydrochloride were used. The quantity and quality of proteins extracted were found to be best when using TCA-acetone extraction. This was demonstrated through total protein content and 1D SDS-PAGE resolution. Subsequently, *Pseudogymnoascus* sp. was exposed to three different temperatures that represented optimal (15°C), low (5°C) and high (25°C) temperature stress for 5 days and TCA-acetone was used to extract proteins for comparative analysis by 2-dimensional (2D) gel electrophoresis. There were significant differences in the proteome profiles between samples exposed to low and high temperature stress, thus showing the physiological response of *Pseudogymnoascus* sp. via its proteome. Future works will be carried out on five other strains representing different regions. This will be followed by the identification of proteins that change in abundance using tandem mass spectrophotometry.

Keywords: Fungi; temperature stress; proteomics; 2D electrophoresis

Expression, characterization and homology modelling of a putative cold active lipase from *Glaciozyma Antarctica*

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Abstract

Psychrophiles are one of the extremophiles which found in nature that are able to adapt and live in extreme cold temperature. Study about psychrophiles has become an interest among researchers to unravel and understand how they are able to survive extreme conditions. Previously, a psychrophilic yeast was isolated from an Antarctic sea ice and was identified as *Glaciozyma antarctica* PI12. The yeast genome was successfully sequenced and annotated. A number of low identity gene encoding putative lipolytic enzyme were identified. This include a putative lipase that belongs to Hormone Sensitive Lipase (HSL) family and have 30 percent identity to the esterase from the bacterial hormone-sensitive lipase family. The 3D structure of HSL lipase was predicted using computer-aided software and showed the presence of the potential active site at conserved amino acid Serine, Histidine and Aspartate. The predicted structure resembles extended loop region that could be important for cold adaptation. The recombinant lipase was successfully expressed in *E.coli* that have higher activity towards medium chain ester substrates. The analysis of the structure and functionality of this lipase may provide new insights about the cold enzyme adaption especially from psychrophilic yeast.

Keywords: Psychrophiles; Putative lipase; *Glaciozyma Antarctica*; Recombinant cold-adapted enzyme; Homology modelling

Arrhenius plot analysis, temperature coefficient and Q₁₀ value estimation for the effect of temperature on the growth rate on acrylamide by the Antarctic bacterium *Pseudomonas* sp. strain DRYJ7

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Abstracts

Several models are available to model the effect of temperature on the growth rate of microorganism on substrates. One of the models is Arrhenius and is very popular due to it having few parameters. An apparent activation energy based on the Arrhenius plot on the growth on phenol by *Pseudomonas* sp. Strain DRYJ7 on acrylamide is reported for the first time. The bacterium was grown in minimal salts media supplemented with 1000 mg/L of acrylamide as a nitrogen source and glucose as the carbon source. The plot of $\ln \mu_m$ (specific growth rate) against $1/T$ for growth on acrylamide was carried out spanning the range of temperature from 15 to 30°C. Regression analysis from 15–30°C results in activation energy of 15.26 kJ mol⁻¹. A relative 10 °C increase in the surrounding temperature, usually results in doubling the reaction rate, with corresponding Q₁₀ value of 2, which is true for a number of biological reactions. The Q₁₀ values, determined from the Arrhenius plot of 2.012 and a theta value of 1.05 obtained in this work, are within the normal range for many biological values. This is the first time that values for the activation energy, Q₁₀ and theta for the growth of a bacterium on acrylamide is reported.

Keywords: Antarctica; acrylamide-degrading; temperature; *Pseudomonas* sp.; Arrhenius plot

Physiological resilience of Antarctic actinobacteria

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Abstract

Actinobacteria are Gram positive bacteria found in diverse natural environments including extreme environments such as the Arctic and Antarctic. Actinobacteria are able to produce bioactive secondary metabolites such as antibiotics, enzymes, anti-inflammatory agents and other compounds of biotechnological interest. The objectives of this study were to isolate and characterise actinobacterial strains from Antarctic soil samples and to screen them for biological activities such as enzyme production, antimicrobial properties and anti-inflammatory properties at two different incubation temperatures. Five actinobacterial strains, namely 21, A18, A95, A17 and PQP2 were isolated, purified and identified to belong to the genera *Kitasatospora*, *Micrococcus*, *Rhodococcus* and *Streptomyces*. Only strains A18 and A95 showed growth and produced catalase as well as protease at two widely different incubation temperatures of 15°C and 28°C. Crude extracts from strain 21 inhibited the growth of *Bacillus cereus*, *Bacillus subtilis*, *Staphylococcus epidermidis*, *Staphylococcus aureus* and *Bacillus megaterium*. Crude extracts from strains A17, A18 and A95 that were incubated at 15°C showed anti-inflammatory properties. Amongst the strains that grew at 28°C, only the crude extract of strain A95 showed minimal anti-inflammatory activity. These preliminary results indicated that certain Antarctic actinobacteria which are able to adapt to a large temperature change may have higher physiological resilience.

Keywords: antibacterial activity; anti-inflammatory activity; protease

Optimization of protein extraction methods for *Pseudogymnoascus* sp. fungi

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Abstract

As primary decomposers in the soil microbial community, fungi synthesize a variety of enzymes and metabolites as well as undergo modifications under stress. Proteomics has proven to be a crucial tool in understanding these processes. However, the robust fungal cell wall makes protein extraction difficult. A successful proteomics approach depends on high protein content and abundance following extraction. In this study, *Pseudogymnoascus* sp. polar fungi was used as a model and three different extraction methods were compared for their efficiency in extracting the proteome from the fungi. The whole experiment was done in triplicates. 1g of fungal biomass was lysed using mechanical methods such as mortar and pestle and sonication as well as a non-mechanical method using urea buffer. Next, three different protein extraction methods, which are phenol chloroform, sucrose and acetone, were carried out. Bradford assay was performed to calculate the protein content of the protein extracts. Lastly, SDS-PAGE and 2D-PAGE were carried out to determine the abundance of the proteins. The average protein content precipitated using phenol chloroform, sucrose and acetone methods were 4.28 mg/ml, 0.82 mg/ml and 5.71 mg/ml respectively. The 1D-PAGE profile of proteins extracted using acetone was very similar to the 1D-PAGE profile of proteins extracted using phenol chloroform, while the proteins extracted using sucrose were not well resolved. In 2D-PAGE gels, the proteins were not well resolved into protein spots. Nevertheless, protein extractions using the phenol chloroform and acetone methods resulted in 2D gels which were comparable to each other.

Keywords: *Pseudogymnoascus* sp., protein extraction, phenol chloroform, sucrose, acetone

Protective mechanisms and responses of micro-fungi: Maintaining cellular and DNA integrity under ultraviolet irradiation

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Abstract

Fungi are important microbes that contribute to the process of nutrient cycling in the natural environment and maintain many symbiotic relationships with plants and other microbes. Fungal microbial communities are integral to the understanding of not only typical soil and rock habitats, but are especially important to the functioning of many extreme environments. In the polar environments, they are constantly challenged by various abiotic and biotic stress factors. Their growth, conidia production, survival, germination, pathogenicity, virulence and bioactive compound production can be strongly influenced by exposure to solar ultraviolet radiation. Various adaptive mechanisms are used to protect the cells and to maintain DNA integrity, allowing survival of exposure to solar ultraviolet irradiation in natural environments. Despite having such abilities, failure to protect cells against damage induced by ultraviolet radiation can compromise genetic integrity and survival, and alter species composition within the fungal community. Here we present the biological and environmental factors that influence the protective mechanisms employed by micro-fungi in response to exposure to solar ultraviolet radiation, thus providing some insight about adaptive responses in micro-fungi.

Keywords: Photoproducts; Pigmentation; DNA repair; Cross-protection; Regional adaptation

Isothermal modelling on the removal of copper using *Durvillaea antarctica*

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Abstract

Heavy metals pollution in the Antarctica is emerging as an important problem due to anthropogenic activities. Bioremediation of metal pollution especially copper in Antarctica in the future using biosorption is the most environmental-friendly method. Biosorption using *Durvillaea antarctica*, an alga that lives in the Antarctic region does not involve the introduction of new potentially foreign species. In this study, the isotherms of copper biosorption by the alga is modelled according to various models ranging from one to five parameters models such as Henry, Langmuir, Dubinin-Radushkevich, Freundlich, BET, Toth, Sips, Fritz-Schlunder IV, Baudu and Fritz-Schlunder V. All gave visually acceptable fitting with the exception of the Henry model. Statistical analysis based on root-mean-square error (RMSE), adjusted coefficient of determination ($\text{adj}R^2$), bias factor (BF), accuracy factor (AF) and corrected AICc (Akaike Information Criterion) showed that the Sips model is the best model. The calculated Sips parameters k_S value of 12.52 (95% confidence interval from 3.593 to 21.439), q_mS value of 0.97 (95% confidence interval from 0.905 to 1.026) and nS value of 0.67 (95% confidence interval from 0.531 to 0.806).

Keywords: Biosorption; *Durvillaea antarctica*; Isotherms; Copper; Sips Parameters

Distribution of soil heavy metals across ecologically distinct habitats on Signy Island, Maritime Antarctica and its association with bacterial community composition and metabolic profiles.

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Abstract

Heavy metals are natural components commonly found in soil. They contaminated soils across the globe due to accumulation of heavy metals through emissions from rapid expanding industrial activities, application of fertilizers and pesticides, disposal or spillage of metal wastes, atmospheric deposition and others. Lead (Pb), chromium (Cr), arsenic (As), zinc (Zn), cadmium (Cd), copper (Cu), mercury (Hg), and nickel (Ni) are the most common heavy metals found at contamination sites. In Antarctic, due to geographical isolation, harsh environment and generally low human activities, lower heavy metals concentrations are recorded in the soil as compared to other soil systems. However, in recent decades, in association with global warming and increasing human presence in Antarctica such as research station construction and the elevated scientific research activities, elevated metal concentrations have been detected near scientific research stations. High levels of lead (Pb), zinc (Zn) and copper (Cu) contamination have been recorded at historical landfill sites across Antarctica, including Thala Valley around Casey Station and Marble Point in the McMurdo Sound region. According to studies, various microbial have different tolerances towards heavy metal toxicity in the environment, which may therefore impose a selection pressure on the bacteria community in the soil. Increased concentrations of heavy metals in soils may enhance populations of metal – resistant microbes but it will reduce the diversity of other soil microbial communities. As a result, compositional shift of microbial diversity may occur. This study aims to elucidate responses of microbial functions toward different terrestrial habitats at Signy Island. Detailed soil metabolomics analyses will be conducted to evaluate correlation of bacterial community metabolic profiles with environmental factors.

Keyword: Antarctica soil, NMR, heavy metal, environment

Production of a lipopeptide biosurfactant by a psychrotolerant bacterium, *Rhodococcus* sp. ADL36 isolated from Antarctic pristine soil

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Abstract

Production of biosurfactants is one of the strategies employed by cold-adaptive Antarctic strains to increase the bioavailability of these hydrocarbon substrates and facilitates their uptake into the cells. Screening for the capacity to produce surface-active molecules was conducted on *Rhodococcus* sp. ADL36, a diesel-degrading bacterium isolated from pristine Antarctic soil. The strain showed a positive drop collapse test, oil displacement activity, microplate assay, and high emulsification index at 45%. The biosurfactant produced was able to reduce the surface tension of water from 72 mN/m to less than 30 mN/m. The assessment on the stability of the cell-free supernatant demonstrated high stability across the temperature, pH and salinity tested although no correlation was found between the surface and emulsification activity. Based on the positive relationship between the assessment of macromolecules content and infrared analysis, the extracted biosurfactant synthesised was classified as a lipopeptide. This is the second report on lipopeptide-producing from this phenotype and the first from the polar region.

Keywords: Screening, diesel-degrading *Rhodococcus* sp., Antarctica, biosurfactant characterization, lipopeptide

Kinetic Analysis for the Removal of Copper Using *Durvillaea antarctica*

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Abstract

Existing techniques for the treatment of pollutants include membrane separation, ion exchange, precipitation, and transformation and biosorption. Of all of this technology, biosorption has several positive aspects which include low operating expenses, very efficient detoxification of toxicants at low concentrations, low amount of disposal materials and does not need nutrient requirements as in bacterial-based remediation, the latter of which is limited by the presence of heavy metals and other toxicants. The reduction of copper by *Durvillaea antarctica*, an alga that lives as south as the Antarctic region can be an efficient and low-cost tool for remediation of copper. In this study, the kinetics of copper biosorption is modelled according to the pseudo-first order, pseudo-second order and Elovich models. Statistical analysis based on root-mean-square error (RMSE), adjusted coefficient of determination ($\text{adj}R^2$), bias factor (BF), accuracy factor (AF) and corrected AICc (Akaike Information Criterion) showed that the pseudo-second order model is the best model. Kinetic analysis using the pseudo-second order model at 0.15 mM copper gave a value of equilibrium sorption capacity q_e of 0.150 mmol g⁻¹ (95% confidence interval from 0.149 to 0.151) and a value of the pseudo-second-order rate constant, k_2 of 8.605 (95% confidence interval from 7.016 to 10.194).

Keywords: Biosorption; *Durvillaea Antarctica*; kinetics; copper; pseudo-second order

POLAR METEOROLOGY AND ATMOSPHERIC CHEMISTRY

The atmospheric circulation features of teleconnection between the Indian Ocean sector's sea ice extent and the Indian summer monsoon rainfall

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Abstract

The teleconnection between the Antarctic Sea Ice Extent and Indian monsoon rainfall (ISMR) had been statistically discovered in previous studies, yet the mechanism behind this process has remained unsolved. In this study, atmospheric circulation of teleconnection between the variability of sea ice extent over the Indian Ocean sector during April- May-June (AMJ) and variability of ISMR has been examined. Reanalysis data and two CMIP5 models data namely ACCESS1-0 and ACCESS1-3, starting from 1979 until 2013 were utilized in this study. Reanalysis results reveal that the AMJ SIEIO is significantly correlated with ISMR via the meridional wave train and anomalous meridional circulation along the Indian Ocean. The proposed mechanism can be illustrated as follow: the polar front jet (subtropical jet) at high latitude (mid-latitude) is enhanced (reduced) during high ice phase (low ice phase) years, which leading to the strengthening (weakening) of Ferrel cell (Hadley cell) and also strong ascending (descending) motion over the India latitudes which hence induce the convective activity o. The strong (weak) convective activity over the India region will influence the strengthening (weakening) of ISMR which leads to more (less) rainfall.

Keywords: Sea Ice Extent in the Indian Ocean (SIEIO), high ice phase, low ice phase, Indian Summer Monsoon rainfall (ISMR), convective activity.

In-situ observation of wind speed and direction using SOnic Detection and Ranging (SoDAR) in Jang Bogo Station during winter 2017 season

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Abstract

This study evaluates the performance of the SOnic Detection And Ranging (SoDAR) instrument installed in Jang Bogo Station, Antarctica. The SoDAR was installed on December 2016 and recorded data was available from May 2017. Data measured by this instrument is wind (direction and speed). The data is a high temporal resolution with measurement measured in every 15 minutes. The measurement is up to 500 meters from the surface, with the minimum measurement is at 30 meters. Although located at least 900 meters apart, a comparison to the Automatic weather station shows a similarity in the mean wind speed (at the lowest measurement, SODAR is 30 meters, AWS is at 3.3 meters. A comparison with sounding data shows a similar wind direction and speed for the whole atmospheric column, at least at 00 UTC. Measurements from May to October 2017 detected 845 strong winds events of equal to and above 10.8 m/s (Beaufort scale 6). A study for winds dynamics from 10 to 12 Jun 2017 shows dominant southwesterly-westerly winds in the surface and aloft during two strong wind events, and more varies winds condition in a column of atmosphere during calm days. This valuable dataset is important to investigate the wind dynamics from the surface to at least 500 meters height at a more frequent measurement.

Keywords: SODAR, Jang Bogo station, Antarctica, strong wind event, winds

Ship hull Inspection using Remotely Operated Vehicle

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Abstract

This paper describes the application of Remotely Operated Vehicle (ROV) for underwater ship hull inspection. Mostly, ship hull will occur the rust, cracks, corrosion, and marine growth due to reactions by sea water. There is a schedule diver to go for visual inspect before doing a service repair a damaged section but it is costly and harmful to human life and a safety issue highly to consider during this operation. Underwater, Control, and Robotics Group (UCRG) USM has been developed a Remotely Operated Vehicle (ROV) to complete the underwater mission such as ship hull visual inspection. There is an advantage to human to explore the mission even though in a dangerous underwater environment or impractical for dive people such as Antarctica which is coldest continent in the world. ROV is generally guided by a human pilot through a link cord providing its power and data communication to perform a localized inspection. The ROV equipped an underwater camera, lighting source, and several sensors to collect the data and information regarding the ship hull condition during the inspection. Thrusters provide movement around the ship hull to record the image and video.

Keywords: Remotely Operated Vehicle; Ship hull Inspection; Antarctica

Amazon and Antarctic stable isotope ratios in the 2016 – 2017 Southern Brazilian rainfall

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Abstract

The south of Brazil stands out because it is strongly influenced by air masses coming from the Amazon and Antarctic regions. This study determined the rainfall stable isotope ratios collected in Porto Alegre (30.0°S, 51.2°W) from January 2016 to December 2017. The oxygen isotope ratios, determined by the Cavity Ring-Down Spectroscopy method, were compared with isotopic composition data, from 1965 to 1983, made available by the IAEA. To identify the atmospheric environment and the origin of the air masses, we analyzed the geopotential height fields, wind vectors, zonal wind, precipitable water and temperature at 925, 850, 500 and 200 hPA, daily and monthly using NCEP Climate Forecast System Version 2 data. Two extreme events, in January (29/01) and February (02/02) 2016, presented marked characteristics of Antarctic air mass in the $\delta^{18}\text{O}$ record (much smaller than the Amazonian values). In September 2016 (13/09) event, the opposite was observed, denoting the influence of Amazonian air mass. Further, in the January 2016 to December 2017 period, a superior annual amplitude in the stable isotope ratios (when compared to the IAEA values) is attributed to a greater contribution of extreme events caused by air masses coming either from the Amazon and Antarctic regions.

Keywords: extreme precipitation events, Rio Grande do Sul, South American Low-Level Jet, Stable Isotopes

The surface climatology of the Antarctic Peninsula

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Abstract

Over the past decades, a number of recent studies that focused on Antarctic climate variability have highlighted the remarkable warming observed over the Antarctic Peninsula. With current high level of interest in climate change because of the marked warming that has been observed over the area, AWS offers one of the most completed set of data. The University of Wisconsin-Madison (UW-Madison) and British Antarctic Survey (BAS) have Automated Weather Station (AWS)s installed throughout the region of Antarctic Peninsula. Using the data acquired from both of the UW-Madison and BAS network, meteorological parameters such as temperature, pressure and wind speed are analysed on annual time basis. The AWSs are identified to be separated into three different regions that are influenced by different environmental and physical factors; western, eastern and also the area around the Caird Coast. The trends outline the general characteristics of the region within different areas and the western region faced the coldest and warmest temperature recorded for all region at -53.75°C and 28.06°C respectively. The AWS stations at the eastern region experienced the highest wind speed. The climatology produced highlights the trend of the area and the challenges it has in providing a long term observation data. Results from this study are essential and serve as a baseline data for future researchers within the meteorological community.

Keywords: Antarctic Peninsula; Automated Weather Station; surface climatology; meteorology

Surface Ozone Variations during Austral Summer at Great Wall Station, Antarctica

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Abstract

Tropospheric ozone concentration variation in polar regions is known to be greatly influenced by photochemical reaction production, synoptic transport and downward transportation of stratospheric ozone. Due to clean atmospheric environment of Antarctica region and given the complexity of ozone chemistry, the surface ozone data contain important values for the evaluation of ozone variation trends. This study is reporting the display of surface ozone concentration variations during Austral summer at Great Wall Station, Antarctica. Surface ozone was measured continuously using EcoTech Ozone Analyser for a period of a month in December 2018/January 2019. During this period, the observed hourly surface ozone concentrations were not greatly varied. The highest increase of hourly ozone concentration was 47% from its daily mean, while 49% for maximum of hourly decrease. Surface ozone concentrations at Great Wall Station during Austral summer were comparable with other measurements during summer but comparatively lower values when comparing with values during winter at other Antarctic stations. The surface ozone concentrations at Great Wall Station exhibited diurnal variations but less distinctive on daily averages. The background surface ozone can be used for further investigation on ozone transport and chemistry over the Antarctic region.

Keywords: Antarctic, Austral summer, polar region, surface ozone, variations

A further investigation into the use of an inverse model for sea ice thickness retrieval

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Abstract

Sea ice has long been identified as one of the key indicators of climate change. Many research works on climate change utilize various parameters gathered from the sea ice as input into different theoretical models or simulations. The collection of such data however, can be difficult due to the harsh environment of the polar regions. The use of microwave remote sensing as a tool to collect data from the polar region has been ongoing for many years. Yet, deciphering the data into useful physical parameters has been one of the challenges faced by many researchers. Thus, the development of inverse models is essential to solve this issue. An inverse scattering model, integrating a forward model using Radiative Transfer theory and an optimizer known as Simulated Annealing (RTISM-SA) was developed. This inverse model is a modification of a previous model, and offers better convergence and a more generalized setting to allow convenience in switching target parameters for inversion. In this paper, the validation results and performance of the inverse model in sea ice thickness retrieval shall be discussed.

Keywords: Inverse model; sea ice; thickness; retrieval

Extreme values modelling of temperature, precipitation and wind speed in Antarctica

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Abstract

There are two topics which will be separately discussed i.e. Temperature versus Precipitation and Wind Speed in Antarctica. The statistical behavior of extreme minimum and maximum temperature for four stations i.e. Casey, Macquarie Island, Mawson and Davis, are analyzed with respect to their extremal properties from January 1989 to December 2012. Both the Generalized Extreme Value and Generalized Pareto Distributions will be used to fit for yearly, monthly and threshold datasets. Later the extreme precipitation and wind speed datasets from 1961 to 2011 are being model using the Generalized Extreme value for three stations i.e. Bellingshausen, Mirny and Novolazarevskaya. Estimated models for all stations have been constructed using maximum likelihood estimation method and the diagnostic plots were used to check whether the models are fitted well to the raw data. The return levels then are obtained to give some forecasting values for the temperature, precipitation and wind speed datasets for all stations.

Keywords: Extreme modelling; temperature; precipitation; wind speed; return level

Atmospheric surface ozone and isoprene measurement during MASEC'16

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Abstract

The Antarctic continent is known to be an unpopulated region due to its extreme weather and climate conditions. However, the air quality over this continent can be affected by long-lived anthropogenic pollutants from the mainland and maritime region. Surface O₃ and isoprene C₅H₈ both produced from anthropogenic and biogenic sources. Both gases are greenhouse gases (GHGs) which has strong relationship and contributed to the climate change. The main objective of this study is to report the first in situ observations yet known of surface O₃ and C₅H₈ over Ushuaia, the Drake Passage, and Coastal Antarctic Peninsula (CAP) on board the *RV Australis* during the Malaysian Antarctic Scientific Expedition Cruise 2016 (MASEC'16). Hourly O₃ and C₅H₈ data was measured continuously for 23 days using portable instrumentation. Our key findings were that the surface O₃ mixing ratio during MASEC'16 increased from a minimum of 5 ppb to ~ 10–13 ppb approaching the Drake Passage and the

Coastal Antarctic Peninsula (CAP) region. The anthropogenic and biogenic O₃ precursors which is C₅H₈ from Ushuaia and the marine region influenced the mixing ratio of surface O₃ over the Drake Passage and CAP region. The C₅H₈ were indicated that the emission from ocean surface were significantly influenced the surface O₃ formation measured over the CAP. Significant positive correlation was observed between isoprene and surface O₃ concentrations ($r^2 = 0.77$, $p < 0.001$). Measurements showed that C₅H₈ mixing ratio were the highest over region of King George Island, Deception Island and Booth Island with values of ~5.0, ~0.9 and ~5.2 ppb, respectively. Backward trajectory analysis showed that air masses may have lifted the isoprene emitted by marine algae which may influenced the surface O₃ formation. We believe our findings provide valuable data set of surface O₃ and isoprene over the under sampled CAP.

Keywords: Surface Ozone, Isoprene and Coastal of Antarctic Peninsula

Torpedo-shaped Micro Autonomous Underwater Vehicle for coral reef inspection

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Abstract

Coral reef often called the rainforest of the sea supports about 25 percent of ocean fish. Coral reef provide shelter, food and places for fish to reproduce. However, coral reef is being endangered by human activities and natural phenomenon. Coral is collected to produce jewelry and dynamite is used by fisherman to catch fish. We propose the use of micro Autonomous Underwater Vehicle (μ AUV) is the inspection of coral reefs. A torpedo-shaped μ AUV prototype suitable for inspection purposes is design and developed at Underwater, Control and Robotics Group (UCRG), Universiti Sains Malaysia. μ AUV is designed to be small, lightweight, portable and can be operated by a single user. This allow easier launch and recovery of the μ AUV without needing and launch and recovery mechanism. The μ AUV perform the inspection just below water surface to allow its antenna to locate its position while camera located inside the μ AUV capture images clearly underwater. The μ AUV is primarily designed but not limited to perform coral reef mapping. Besides that, it can be deployed to perform underwater vegetation imaging and be deployed in area where diver can't be deployed such as Antarctica which has extremes climate and is the coldest continent on earth.

Keywords: Coral reef; micro autonomous underwater vehicle, torpedo-shaped

Study of lightning flash activity over Western Antarctica

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Abstract

The distribution of cloud-to-ground (CG) lightning flash activity over the Western Antarctica is studied using a Boltek lightning detector (LD-350) sensor installed at Carlini Base station (CARL: 62.23°S, 58.63°W). Data obtained from the detection system between February and December 2017 have been analysed. Three composite active thunderstorms (labelled Storms region A, B, and C) were detected by the sensor within a 1,000 km radius from the station in the common locations and areas. Out of a total of 2,019,923 flashes, 43.01% were positive CG and 56.99% were negative CG flashes. During the summer and fall seasons, the CG flashes (both positive CG and negative CG) experienced a percentage of more than 96%, compared to less than 4% during the winter and spring seasons. Thus, lightning flash activity during summer and fall are more intense than winter and spring seasons found in this study. The majority of detected lightning strikes greater than 85% were located closest to the station of Carlini Base produced by Storm region B and less than 15% were produced by Storm region A and Storm region C, located in the ocean areas over the Amundsen/Bellingshausen Sea and the Weddell Sea.

Keywords: Antarctica; cloud-to-ground; seasonal analysis; thunderstorm

The role of atmosphere and ocean on recent trend in Antarctic sea ice

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Abstract

The Antarctic sea ice has increased in recent several decades, in contrast to the marked sea ice melting in the Arctic. Analysis indicates that the Antarctic sea ice has increasing trends in all seasons, especially with larger trends in spring and autumn. However, spatial distribution of the Antarctic sea ice trend is not uniform seasonally. During decaying seasons (DJF and MAM), there is a significant sea ice melting trend in the Amundsen and Bellingshausen Seas due to onshore winds and currents, pushing the sea ice toward the coast and at the same time providing warm air and water from offshore to the coast that leads to warming trends of surface air and ocean. However, in other sectors, especially in the Ross Sea and eastern Weddell Seas, ice significantly increases with time due to surface air and ocean cooling, associated with the increasing Southern Annular Mode (SAM) and deepening of Amundsen Sea Low (ASL). In growing seasons (JJA and SON), sea ice has increasing trends in most places at the margin of sea ice in all seasons, in association with the surface air and ocean cooling that is closely linked to the strengthening of the SAM and deepening of the ASL.

Keywords: Antarctic sea ice; Atmosphere circulation; Ocean circulation; Amundsen Sea Low; Southern Annular Mode

Climatology of strong wind events at Terra Nova Bay, Antarctica

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Abstract

Terra Nova Bay is on the western Ross Sea and is known for extremely strong downslope winds originating from the continental interior. These cold dry winds modify a relatively warmer and moister atmospheric boundary layer at the outlet of glacial valleys. Automated Weather Station data from Antarctic Meteo-Climatological Observatory and from Jang Bogo station were used to establish the climatology of the wind field over area surrounding Terra Nova Bay. Based on the preliminary analysis of the wind speed, the criteria were developed to define strong wind events (SWE). SWE is defined as an event having wind speed higher than two standard deviations above the mean wind speed that last for more than ten hours. The wind speed during the event is allowed to dip below the threshold for less than 10 hours at a time. The ratio of wind speed above the threshold must be 50% higher than wind speed below the threshold for the duration of an event. Analysis showed that 80% of the events last two to three days, and small number of the events last more than 5 days. Most of the events occurred during winter where the temperature difference is highest, followed by spring and autumn. There are only small number of SWE events during summer. AWS near coastal region exhibit high wind speed in long term average, whereas the plateau and inland AWS exhibit lower wind speed in long term average. The wind speed is significantly lower during summer (December to February) compared to other seasons. Not all AWS has the same major wind direction between all year round and SWE.

Keywords: Terra Nova Bay, Strong Wind Event, climatology, AWS

POLICY, GOVERNANCE AND SOCIAL SCIENCES AND HUMANITIES

Antarctica Legislation: Importance and Challenges

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Abstract

Malaysia policy on the Antarctic is that Antarctic is the common heritage for the common benefit to the entire world. The vision of the government strategy can be transpired through the Antarctic Committee as the members of the Antarctic Committee comprised of policy makers and technical experts. The expectation outcome from this provision is for the development of policy on Antarctic with technical and scientific considerations in order to solve the societal and environmental problems. Malaysia has to carry out own initiative, by way of carry out activity, to earn the recognition as Consultative Party unlike New Zealand and Australia. The creation of career development drives for improved technologies that create opportunity for high-technology industry. Development of these systems requires highly-skilled workers, climate scientists and software experts are needed to make best use of them. Systems capable of operating in the hostile polar oceans are also likely to have applications in other extreme environments. One of the main considerations of the States in implementing the Annex VI is on the cost of compliance with the legal regime. The concern is concentrated on the issue that the cost of compliance might outweigh the benefits of the law to the government and citizens. The cost-benefit analysis may favour States with significant economic impacts in Antarctic but States with no significant involvement in activities in Antarctic may find the costs of compliance outweighing the benefits it may gain.

Keywords: Legislation; committee; consultative; high-technology; industry;

Evolution of Malaysia's policy and governance for Antarctica

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Abstract

This paper examines the evolution of Malaysia's policy and governance for Antarctica. Malaysia's policy on Antarctica since 1983 has evolved from being focused on diplomacy to science and followed by governance. Malaysia's interest in Antarctica started when the Prime Minister of Malaysia raised the issue of Antarctica at the United Nations General Assembly (UNGA) in 1982. Malaysia argued that the United Nations (UN) is the best and fairer body to govern Antarctica as a common heritage of mankind and secondly questioned the exclusivity of the Antarctic Treaty System (ATS). Malaysia's stand has resulted in the tabling of "Question of Antarctica" in the UNGA from 1983 to 1992. In 1997, the Malaysian Cabinet decided that Malaysia would undertake research in Antarctica. The consistent enthusiasm and interest among Malaysian scientific community to expand Antarctic research has contributed to the government decision for Malaysia to become a party to ATS. When the Cabinet in August 2011 decided for Malaysia to be a party to ATS and to ratify Madrid Protocol, the decision was for Malaysia to become a consultative party so that Malaysia can be active in the governance of Antarctica. It was also decided for a legislation to be formulated to fulfil the country's obligations in the ATS and Madrid Protocol. Having acceded to ATS in 2011 and ratified the Protocol in 2016, the next step is for Malaysia to become a consultative party. This will enable Malaysia to participate in consensus based governance of the continent. To acquire consultative status, Malaysia must demonstrate substantial research activity and the country must have Antarctic Act in place, as decided by the Cabinet. The Bill is currently undergoing the legal scrubbing process and will subsequently be tabled in the Parliament. To move forward, the Government through MESTECC is preparing the National Polar Roadmap to provide priorities and strategies for Malaysia's current and future engagement in the Antarctic continent with possible expansion to Arctic region.

Keywords: Malaysia; Antarctica; policy; Antarctic Treaty System; National Polar Roadmap

Internationalisation at home: Enculturing socio-scientific issues of the polar regions in higher education curriculum

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Abstract

Internationalisation at Home (IaH) is the purposeful integration of international and intercultural dimensions into the formal and informal curriculum for all students within domestic learning environments. Within these integrated practices, non-mobile students are given the opportunity to expose with global perspectives as well as to interact with international peers. Number of higher education institutions (HEIs) have taken a pro-active approach to promote an understanding of international issues through integration of global challenges into the existing curriculum. The study aims to explore perspective of socio-scientific issues (SSI) derived from global sustainability challenges of the polar regions' ecosystem and its potential to be integrated in HE curriculum for enhancing IaH strategy. Complexity of the polar regions' issues has potential to spark an array of learning that could cultivates international knowledge and mindset for student in understanding global and transboundary issue which it is consequently contribute in fostering scientific literacy as well as enhancing global citizenship. Further empirical research is needed to understand the relationship how SSI of the polar regions enriching IaH strategy in HEIs. This study proposes a new body of fundamental social knowledge related to the IaH strategy in HE through integration of global issues into curriculum content.

Keywords: global curriculum; global citizenship; sustainability;

Internationalisation practice in university research: An experience of Polar research's collaboration

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Abstract

Research strategies are among the core elements devoted to the internationalisation catalyst for the universities, and this move has expanded considerably during the past decade. Yet, there are also universities enhance international outlook by developing a set of research missions that aim to address global sustainability challenges, which become the important driver of internationalisation through development of strategic international partnerships and collaborations. With an increased interest in polar research across the globe, together with the long history of scientific collaboration within the nations, thus, it is time to explore the theoretical understanding of how the involvement in polar research can potentially enhance internationalisation of university. Through conceptual analysis, it clearly indicates that polar research initiatives have the potentials to enhance the internationalisation of universities through their outputs in joint-publication, mobility and a shift in the role of polar research to foster global citizens and knowledge diplomacy. Further empirical research and evidence-based policy making are needed to understand the relationship between polar research collaborations in this context. This study sheds light on the theories and lends a new body of fundamental social knowledge related to the internationalisation of research strategies in university through global research initiatives.

Keywords: global citizenship, knowledge diplomacy, research internationalisation, joint publication

School engagement through collaboration in the case of University of Malaya and Sultan Mizan Antarctic Research Foundation, Malaysia

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Abstract

The authors aim to share the experience of the involvement in the school engagement activities funded through the Social Innovation program funded by the Ministry of Science, Technology and Innovations of Malaysia (MOSTi) in 2016 and 2017 between University of Malaya and Sultan Mizan Antarctic Research Foundation. A total of 16 science schools throughout the country participated in the interactive forum themed 'Malaysia's Journey to the Ice: Women in Antarctica'. The collaboration between the university and the foundation initially involves merely experience sharing of the women researchers in Antarctica with the school students, aimed at increasing the student awareness and interest in science, polar science in particular. The objective, has however, evolved and expanded to include capacity building and research component focusing on science communication which witnessed 'learning by doing' results through co-evaluation of program.

Keywords: school engagement activities; social innovation program; interactive forum; capacity building; science communication

Knowledge, awareness and practice on climate change among community in kuala lumpur

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Abstract

Cities are responsible for 75% of world carbon dioxide emission, making it as significant contributor to climate change. Urban population will be the early responders towards the impacts of climate change, therefore it is essential to assess the knowledge, awareness and practice (KAP) of community for framing mitigation activities. Thus, the study intends to identify the level of KAP among community in Kuala Lumpur (KL). A cross-sectional study via a self-administrated questionnaire was carried out among 234 respondents within the age of 15 years old and above. Simple random sampling was applied to select five out of eleven districts in KL (Bukit Bintang, Cheras, Bandar Tun Razak, Wangsa Maju, Titiwangsa) while convenient sampling was used for recruitment of subjects from community settings. Spearman correlation tests was used to analyze the association between knowledge, awareness and practice scores. Chi Square test was used to identify the association between knowledge and awareness with educational status. The knowledge about climate change among community in Kuala Lumpur was reported to be moderate while the awareness level was very high. The practice of community on climate change was at moderate level. There was positive and weak association between knowledge and awareness ($r = 0.302$) whereas the association between knowledge knowledge was also found to be positive and weak ($r = 0.142$). There was positive and weak association between awareness and practice ($r = 0.196$). Educational level had significant association with knowledge and awareness level. The community had some knowledge about the issue, however they did not aware of what actions to be taken to deal with the issue. The government need to disseminate information about climate change through mass media and social media. Combinations of top down and bottom up approaches are important for the adaptation and mitigation strategies.

Keywords: Knowledge, Awareness, Practice, Climate Change, Community