

2014

CFF-UNMC
Doctoral Training Partnership (DTP)
Book of Abstracts



DTP WEEK 2014 BOOK OF ABSTRACTS

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YIELD AND YIELD COMPONENTS OF BAMBARA GROUNDNUT (*VIGNA SUBTERRANEA* (L.) VERDC.) LANDRACES AS INFLUENCED BY LIMING TREATMENTS ON TROPICAL ACIDIC SOILS (Bam1-001)

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Abstract

Bambara groundnut (*Vigna subterranea* (L.) Verdc.), an underutilised pulse grain legume, presents great potential for increased food production on tropical marginal soils. However, the crop is among the few legumes for which studies on abiotic stress (such as pH) are very limited. A Screenhouse experiment was conducted to determine the effect of varying soil pH using lime on the performance of the crop. Treatments consisted of five (5) liming treatments (0, 0.5, 1.0, 1.5 and 2.0 t ha⁻¹ which resulted in the before sowing soil pH of 4.47, 4.63, 5.30, 5.68 and 6.33 respectively, and at harvest soil pH of 5.16, 5.71, 6.14, 6.36 and 6.55 respectively) and two (2) Bambara groundnut landraces (Ex-Sokoto and Kaaro) making a total of 10 treatment combinations. The treatments were laid out in completely randomized design (CRD) replicated three times. The results obtained revealed no significant ($P>0.05$) response of the landraces to lime application except in shelling percentage which was found to be decreased in the treatments applied with 2 t ha⁻¹ of lime. Ex-Sokoto landrace recorded higher number of pods plant⁻¹ (40 pods) and shelling percentage (70%) than Kaaro landrace which recorded 28 pods plant⁻¹ and shelling percentage of 66%. Other parameters were similar between the landraces. Thus, the findings of this research suggest that both the landraces could be adopted for Bambara groundnut production under tropical acidic soil conditions and the crop could be grown with or without application of lime.

FERTILITY IN BAMBARA GROUNDNUT: IDENTIFYING THE FACTORS THAT LIMIT FERTILITY IN BAMBARA GROUNDNUT, WITH PARTICULAR FOCUS ON THE EFFECT OF ENVIRONMENT ON POD SET (Bam1-009)

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Abstract

'Crop fertility' is a major issue and is likely to become more so in the ever changing environmental conditions, particularly under high temperatures, which leads to significant reductions in yield. The reproductive stage of development is a determinant factor of yield in crops cultivated for seeds or fruits. High-temperature stress can affect reproductive processes such as pollen viability, female gametogenesis, pollen-pistil interaction, fertilization, and grain filling. Even a small increase in temperature above the optimum can negatively affect pollen viability leading to low yields. Bambara groundnut (*Vigna subterrenea* L.) is an indigenous African legume cultivated mainly by subsistence farmers under traditional low input agricultural systems for its seeds. The most important physiological characteristic of Bambara groundnut is its drought tolerance, it produces reasonable yields under low rain fed and high temperature conditions where many of the other crops fail. However there is very limited evidence on how different landraces of Bambara differ in their response to temperature stress. This study aims to explore the effect of short periods of temperature stress on the reproductive tissue (anther and pollen), its function (pollen viability and germination) and pod set. The severity and variability of this effect will be determined using different landraces of Bambara groundnut. Little is known about floral transition in Bambara groundnut and almost nothing under stress conditions. Therefore the present research can be focused on identifying the factors that limit fertility in Bambara groundnut. And also using translational genomics approaches to extend the knowledge of temperature stress related genes of model crops to Bambara groundnut.

HARNESSING ROOT TRAITS OF WILD PROGENITOR OF DOMESTICATED LETTUCE FOR IMPROVED NUTRIENT USE EFFICIENCY (FoodP1-015)

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Abstract

The introduction of agricultural practices including the use of artificial fertilisers, herbicides and mechanisation in the mid-twentieth century has significantly improved the yield traits of domesticated plants. However, the increasing trend of global water scarcity and the high cost of artificial fertilisers limit the effectiveness of modern agricultural practices, particularly in developing countries and those with extreme climatic conditions. Introducing wild progenitor root traits into the domesticated crops could contribute to a more efficient low input farming, by taking advantages of the resilient characteristics of wild progenitors to abiotic stresses such as drought and low soil fertility. This research aims to investigate adaptive root traits in wild lettuce (*Lactuca serriola*) and its domesticated relative (*Lactuca sativa* cv. Salinas) and their responses in low nutrient conditions. This should provide useful information on traits to be maintained or selected as any suitable crops are improved through future breeding programmes. Preliminary studies of the project aim to understand and identify the basic root system architecture (RSA) of wild and domesticated lettuce, and to recognise and compare useful adaptive characteristics that suit low input farming. Both lettuces possess tap root systems, however, wild lettuce has a deeper root system with a longer primary roots and lateral outgrowth along its full length. Domesticated lettuce, on the other hand, has a shallower root system with relatively shorter primary roots and concentrated lateral growth in the basipetal area of the plant. Present studies expand these former investigations by looking at the differences in root characteristics of recombinant inbred lines (RILs) derived from a cross between *Lactuca serriola* and *Lactuca sativa* cv. Salinas under different inorganic phosphorus (P_i) concentration via *in vitro* methods. P_i was chosen as it is one of the main limiting nutrients in soils and current studies try to observe any differences of RSA from the preliminary studies and, in addition, uncover any possible related quantitative trait loci (QTLs).. In the course of this research, various methods will be used to study root characteristics, in both 2 and 3 dimensions of the RSA, which involve interdisciplinary specialisation such as physiology, agronomy and advanced imaging and graphics in order to obtain information on how RSA will respond to low input conditions. We believe that this project could provide a new perspective on how crops, generally, and roots, particularly, should be improved in the future. It should be based on the idea of using lower external inputs and enhancing the ability of the crop to uptake its own resources more efficiently and naturally, which in turn will pave the way for more sustainable agriculture.

INVESTIGATING DROUGHT TOLERANCE OF CROPS: GENOMICS-BASED APPROACHES TO IMPROVE DROUGHT TOLERANCE IN BAMBARA GROUNDNUT (Bam1-007)

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Abstract

Drought is a key constraint to crop yield in farming systems. As water resources for agronomic uses become more limiting, improving drought tolerance is of utmost importance for crop breeding and food security. However, drought tolerance is a complex process. Plants respond to drought stress conditions via a series of physiological, cellular, and molecular processes. Recently, many drought-inducible genes have been identified by molecular and genomic approaches in various plant species, such as in *Arabidopsis* and rice. Now, more accurate targeting of genes and analysis of the function of these genes is critical to further our understanding of the molecular mechanisms governing plant drought stress response and tolerance, ultimately leading to the enhancement of stress tolerance in crops through genetic manipulation. Bambara groundnut (*Vigna subterranea*) is an underutilised crop grown as a secondary food source by subsistence farmers in Africa. Bambara groundnut is a species with potential having excellent nutritional content, the ability to fix nitrogen and produce yields in marginal soils and is drought tolerant. Though it is known to be drought tolerant, there is limited information on how Bambara groundnut responds and adapts to drought. This study focuses on the analysis of the drought-response transcriptome, and physiological responses to drought in Bambara groundnut. The main objective of the experiment is to investigate drought tolerance in Bambara groundnut in different landraces at a molecular and a physiological level. Therefore, the principal focus of the experiments is to profile the response of Bambara groundnut transcriptome to drought stress via cross-hybridisation of Bambara groundnut RNA with the soybean GeneChip array; to identify genes of potential importance to drought tolerance; to identify key gene networks that respond to drought stress and relate their regulation to adaptive potential occurring during drought stress; and to evaluate their effects on plant growth, reproductive development and plant morphology in different landraces. Network analysis and detailed bioinformatic analysis identified key drought induced genes in DipC and Tiga Necaru (TN) landraces. Drought related genes will be identified and confirmed by quantitative RT-PCR. Identified genes will help in the development of new molecular markers and further QTL analysis could provide markers for crop breeding of genotypes that provide stable crop yields under widely varied environmental conditions. Identifying genetic, morphological and physiological variation for drought response in different landraces of Bambara groundnut will help in identifying a number of contrasting lines for comparative analysis. It is hoped that the data obtained in this research work will build towards a foundation for knowledge-based plant breeding.

CHANGEABLE LIGHTING RECIPE TO ENSURE PLANT GROWTH AND DEVELOPMENT UNDER LED LIGHT GROWING SYSTEM (ResT-02)

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Abstract

To maintain our agriculture and improve the economic and environmental sustainability of crop production in the foreseeable future using limited clean resources, energy for our growing systems must be utilised as efficiently as possible. As an innovative lighting technology, LED lights not only have extremely high photoelectric conversion efficiency, but also can supply narrow wavelength light that makes them suitable as a light source for plant growth. But each species of crop has significantly different responses to different light conditions and their requirements will even change during each growth stage. Thus, a large number of studies on common crops will need to be conducted, to explore the role of specific lighting spectra in plant growth and development and to choose suitable lighting for increasing yield and quality. This project exploits new developments in plant health/quality, and the low cost, efficiency and controllability of LEDs to deliver new lighting systems with control over spectral quality and intensity that deliver greater 'crop per watt'. Also, the project will also help understand the physiological and molecular mechanisms behind the influence of light quality and intensity on plant growth and development. The future work will focus on suitable spectra while reducing lighting intensity, to identify conditions for efficient crop growth for commercial production and also explore related genes or molecular markers for further seed selection or breeding.

HOW DOES GEOGRAPHY AFFECT OR REFLECT GENETIC VARIATION IN BAMBARA GROUNDNUT? (CropB1-003)

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Abstract

The initial objective in this research project is to improve the understanding of the relationship between genotype, environment and geographic localisation, and how this relationship impacts on traits such as crop yield. This project uses Bambara groundnut as an example to try to understand the relationship between genotype, environment and geographic localisation. This crop has been receiving significant attention from the scientific community recently and a number of results of previous experiments are available, that makes Bambara groundnut an appropriate candidate for the experiments planned. It is expected that results from this study could be extended to other similar underutilised crops. Currently, some exploratory methods (Principle Component Analysis and Clustering) have been applied to analyze the relationship between the results of molecular analysis (DNA microsatellite markers, scored as a matrix of presence and absence of each allele size) and geographic location.

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METABOLIC AND PHYSIOLOGICAL TRAITS ASSOCIATED WITH BAMBARA GROUNDNUT (*Vigna subterranea* (L.) Verdc) ADAPTATION IN CONSTRASTING ENVIRONMENTAL CONDITIONS (Bam1-003)

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Abstract

Global food production must not only respond to the demands of a growing world population, but also to the hazards posed by climate change. Higher temperatures, unpredictable rainfall and weather patterns, changes in growing seasons, increased occurrences of drought and extreme weather events will exert a greater strain on agriculture. Nowhere will these changes have a more detrimental impact than the continent of Africa. It is expected that warming throughout Africa will be greater than the global average, with decreasing precipitation leading to higher occurrence of drought in many regions. Climate change will not only cause shifts in food production and yield loss due to more unpredictable and hostile weather patterns, it will also affect food prices and increase malnutrition, especially amongst children. Improving crop productivity and nutritional content in the most vulnerable countries will therefore be vital for mitigating the adverse effects of climate change. A key strategy available to adapt to a changing climate is the development and promotion of underutilised crop species. With only three plant species accounting for more than 90% of the world's caloric intake, it is clear that an abundance of genetic resources and potentially beneficial traits are being neglected. Bambara groundnut (*Vigna subterranea* (L.) Verdc) is an African grain legume in which considerable interest has gathered for its potential to contribute to food security in Africa. This is primarily due to its ability to withstand periods of drought and harsh climatic conditions, along with its high nutritive content and ability to contribute to soil fertility through nitrogen fixation. Research suggests certain physiological and metabolic traits contribute to the plant's resilience, namely a reduction of transpiration by stomatal control, a high root:shoot biomass ratio, an increase in partitioning of dry matter to roots and a reduction in leaf area development. However, evidence for the nature and extent of drought resistance is limited. This work attempts to uncover some of the processes which will help improve the productivity of this important crop in drought-prone environments.

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PHYSIOLOGICAL GROWTH AND YIELD RESPONSE OF UNDERUTILISED LEAFY VEGETABLES TO A PROJECTED CLIMATE CHANGE IN SOUTH AFRICA

(CropB-R2-001)

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Abstract

The African continent has been identified as particularly vulnerable to the changing climate due to its envisaged low adaptive capacity and vulnerability. The South African region is regarded as one of the most vulnerable regions in Africa. Changes in temperature, CO₂, and precipitation under the scenarios of climate change for the next 30 years present a challenge to crop production. The IPCC report finally includes possible scenarios of future climate that would greatly affect agricultural production throughout the world. All these changes are exposing farmers to new and, in many cases, unfamiliar conditions. Underutilised edible leafy vegetables play an important role in the African agricultural and nutritional systems. In spite of all these amazing good nutritional qualities, underutilised leafy vegetables are not widely consumed in South Africa. However, these crops are regarded as crops for the future, but there are still knowledge gaps in smallholder farming systems and rural areas of SA. Thus the objective of this study is to determine the physiological growth and yield response of underutilised leafy vegetables to a projected climate change in South Africa. The trials will be conducted inside the rain shelters at ARC-VOPI station in South Africa and in the growth chambers at UNMC. Different temperatures, CO₂ concentrations and water levels will be used as treatments, arranged as randomized complete block design with six replicates on separate experiments. The following variables will be collected: plant height, soil water content, chlorophyll content, LAI, stomatal conductance and photosynthesis, fresh and dry biomass. The data will then be subjected to analysis of variance (ANOVA) with SAS software and will also be simulated using Aqua Crop model. The results of this study will reveal the impact of climate change on leafy vegetables.

CONSTRUCTION OF GENE CO-EXPRESSION NETWORK AND IDENTIFICATION OF FUNCTIONAL MODULES IN BAMBARA GROUNDNUT UNDER COLD-TEMPERATURE STRESS (Bam1-004)

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Abstract

A gene co-expression network is the interaction of groups of co-expressed genes and it help us to better understand how each gene interact with other genes under a particular condition. In the network, each node represents a gene and the edge represents the correlation coefficient between the two genes of interest. One important property of these kind of networks is the modular structure, in which nodes are densely connected with each other. Nodes belonging to the same module interact with each other to carry out a specific biological function. Using these methods we can predict functions for unknown genes which fall in same module. Further we can find out functional modules by applying various clustering methods on these networks. Bambara groundnut (BG) belongs to the legume family. BG is a less studied crop and cultivated as landraces only although it is nutritionally rich crop. Despite its importance, no information is known particularly about its genes and their interactions with each other, neither in a stress condition nor in a normal condition. Therefore, here we have made an attempt to discover a list of genes with functions and their interactions with each other in cold-temperature stressed BG using Highest Reciprocal Rank (HRR)-based co-expression network analysis. In this study we used *Glycine max's* microarray chip (Xspecies technology) to generate expression data for BG under cold-temperature stress. The chip contains 37,593 probes. HRR-based co-expression network methodology were used to construct a co-expression network and then the network was partitioned using a powerful algorithm, HCCA (Heuristic Cluster Chiseling Algorithm), to find out functional modules. Finally we have identified and annotated a list of genes which are expressed, along with their interactions with other genes, within the largest functional module.

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TOWARDS A COORDINATED CROP IMPROVEMENT PROGRAMME IN BAMBARA GROUNDNUT: MAGIC POPULATIONS AS PERMANENT MULTI-UTILITY GERMPLASM RESOURCE FOR IDEOTYPE DEVELOPMENT, GENETICS AND/OR GENOMIC ANALYSIS (Bam1-006)

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Abstract

Bambara groundnut (*Vigna subterranea* L. Verdc) has potential to contribute to global food and nutritional security. However, typical of most underutilised crop species, there are no or very few improved varieties/cultivars of Bambara groundnut developed via controlled breeding programmes. Landraces which have been selected by farmers remain the main source of planting materials. The concept of ideotype crop varieties/cultivars that combine superior yield potential and desirable agronomic traits with maximum adaptability to specific ecologies is the aim of breeding programmes. Availability of improved varieties is also one of the main motivating factors leading to large-scale cultivation of crops by farmers. Uniformity of agronomic traits allows synchronization of cultural practices (leading to efficiency and cost effectiveness in farm management) and it is one condition needed for successful mechanisation of agriculture. The development of varieties of Bambara groundnut with uniform and desirable agronomic traits is necessary, if the potential of this underutilised crop species is to be effectively harnessed for global food and nutritional security. Moreover, not much is known about the genetic inheritance of important agronomic traits in Bambara groundnut. To effectively utilise resources and save valuable time, the need for permanent multi-utility germplasm resources to tackle various genetic questions while generating valuable novel recombinants of genotypes for introduction, evaluation and selection within different ecosystems is of huge significance. The 'second/next generation' breeding populations appear to meet these strategic breeding needs and could present a paradigm shift for breeding and genetic studies in plant species. Of the various types of the 'second/next generation' breeding populations, Multi-parental Advance Generation Inter-cross (MAGIC) appears very useful to plant breeders and is becoming increasingly popular. It has the advantage of integrating multiple sources of alleles into a single population which at the early generations of population development allows conventional linkage mapping and QTL analysis, along with fine mapping at later generations. As such, MAGIC populations represent a potentially new way to integrate the best aspects of linkage analysis with association mapping, while generating novel recombinants as potential ideotypes for selection within different ecosystems and different agricultural systems, including sole-cropping and inter-cropping.

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SEMI-DESTRUCTIVE SAMPLING METHOD TO MEASURE OIL PALM (*Elaeis guineensis* Jacq.) ABOVE GROUND BIOMASS (BioP1-002)

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Abstract

Oil palm (*Elaeis guineensis* Jacq.) above ground biomass consists of its main components i.e. frond, trunk, bunch and frond base. Non-destructive methods for biomass estimation were reported in earlier publications. However, research studies have been conducted on single planting material origin i.e. Deli x AVROS and arguably may not be applicable to planting material of different origins and improved varieties. This study aims to estimate the above ground oil palm biomass using a semi-destructive method (SDM) in comparison to a non-destructive method (NDM) as reported in earlier publications. The oil palm genotype tested in this experiment was FELDA Standard Cross 3 (SC3) of Deli x Yangambi origin. Samples were taken from four central palms (preferably) in two replicates, and consisted of four palm ages, giving a total of 32 palms. Sampling of above ground biomass consists of leaf, bunch, trunk and frond base, following the non-destructive method (NDM) reported in earlier publications and a semi-destructive method (SDM) as comparison. Sample dry weights were measured to determine the relationship between NDM and SDM. Oil palm biomass estimation is a challenging task due to substantial volume of plant parts taken for measurements, exhausting manpower and time. This has limited the number of palms sampled in this study (only two replicates) and sampling error could be high. Nevertheless, SDM enables sampled palms to be resampled for further verification, if and as required.

ESTIMATING GREEN VEGETATION FRACTION USING MULTISPECTRAL DUAL BAND INDICES (BioP-008)

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Abstract

Vegetation cover is very much related to leaf area index, which is a very important biophysical parameter for crop monitoring. Although the applicability of conventional dual band vegetation indices has greatly increased following the availability of very high-resolution spectral sensors, nevertheless these indices do suffer from saturation at moderate to higher percentages of vegetation cover. The approach undertaken in this paper attempts to identify a robust multispectral Normalized Differential Index (NDI) which is able to both reduce saturation effects and simultaneously achieve a high degree of accuracy for fractional vegetation cover. Different combinations of multispectral bandwidths in the green, red and infrared regions were evaluated to obtain the optimal band combination. The tests were conducted using three different crop types with distinctly different canopy structures. Performances of the optimal NDI combinations were also compared against established vegetation indices (VIs). Preliminary results obtained from only green erectophile vegetation cover indicate comparatively better performances from the optimal NDI combination, R – M and Optimized Soil Adjusted Vegetation Index (OSAVI). The optimal NDI was obtained using the 670nm and 750nm multispectral bands for the red and near-infrared bands respectively.

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ANTIOXIDANT POTENTIAL OF UNDERUTILISED LEGUMES (FoodP1-019)

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Abstract

Global food security is an important issue due to the significant increase in global population and thus food demand. This may lead to an imbalance between crop production and food demand especially in relation to staple food commodities. Consequently, the price of staple food may increase and hence reduce the ability of consumers to afford staple foods in the near future. Therefore, alternative nutritious food sources whose production is both sustainable and cost effective are required. Underutilised leguminous plants are emerging crops that attract attention in this respect. The legumes (seeds of leguminous plants) are rich in macronutrients such as protein, dietary fibre, and micronutrients such as vitamins and minerals. They also contain a great diversity of other potentially beneficial phytochemicals such as flavonoids, phenolic compounds, lignans and proanthocyanidins. Studies have shown that phytochemicals found in legumes exhibited putative biological activities such as antioxidant, anticancer and antidiabetic properties. However, this research has focused on commercial rather than underutilised legumes. The objective of this study was to determine the phenolic content and antioxidant activities of a number of underutilised legumes. This is a preliminary study prior to phytochemical profiling of these underutilised legumes. Five underutilised legumes - adzuki bean, mung bean, black eyed pea, lablab bean and pigeon pea - were selected for this study. Four commercial legumes - soybean, chickpea, red kidney bean and lentil - were also analysed for comparative purposes. Methanolic extracts of each of the beans were assessed for total phenolic content and antioxidant activity. Soybean contained the highest phenolic content among the legumes tested, which was 1.46 mg GAE/g dry weight. The phenolic content of the underutilised legumes were in decreasing order adzuki bean (0.75mg GAE/g dry weight) > mung bean > pigeon pea > black eyed pea > lablab bean (0.27 mg GAE/g dry weight). Adzuki bean's methanolic extract also showed the highest antioxidant activity among the nine tested samples. The adzuki bean extract gave a value of 49% of free radical scavenging ability in the DPPH assay and 0.31mM FeSO₄/g dry weight reducing potential in the FRAP assay. The order of free radical scavenging ability in the DPPH assay was adzuki bean > red kidney bean > lentil > soybean > pigeon pea > lablab bean > black eyed pea > mung bean > chickpea (3.8%). The order of reducing power in the FRAP assay was adzuki bean > red kidney bean > soybean > black eyed pea > pigeon pea = mung bean > lentil > lablab bean > chickpea (0.05mM FeSO₄/g dry weight). In conclusion, most of the underutilised legumes demonstrated strong antioxidant activity, but adzuki bean exhibited the strongest antioxidant activity among the nine legumes and was significantly higher than soybean. Future studies will be carried out to develop phytochemical profiling techniques for selected legumes using advanced detection techniques and equipment such as high performance liquid chromatography (HPLC) and liquid chromatography mass spectrometry (LCMSMS). The outcome of this study will produce an

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important identification and quantification tool to monitor the level of phytochemicals present in legumes during the food supply chain and to ensure the production of legumes with good nutritional quality.

DETERMINATION OF THE CONTENT OF PROTEIN AND ANTI-NUTRITIONAL FACTORS IN UNDERUTILISED LEGUMES (FishP1-004)

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Abstract

In the aquaculture industry, farming of carnivorous fish requires large amounts of fishmeal and fish oil. The rapid expansion in farming of carnivorous fish has triggered the researchers to investigate the potential of using plant-based aquafeed as an alternative to traditional fishmeal to improve the sustainability of the aquaculture industry. Unfortunately, there is a drawback in using plant-based aquafeed due to the natural presence of anti-nutritional factors (ANFs) in plants. These ANFs may slow down the growth of the fish by altering protein utilisation and digestion, affecting mineral and antivitamin utilisation in fish metabolism. Hence, the aim of this study is to reduce the ANFs, especially protease inhibitors, present in underutilised legumes through various processing methods. The outcome of this study could facilitate the use of ANF-free legumes as plant-based aquafeed in the aquaculture industry. The current study is divided into three phases: 1) determine the ANFs and protein content in targeted underutilised legumes, 2) optimise a best combination of processing methods in reducing the ANFs in legume and process it into plant-based aquafeed, 3) conduct a feeding trial on *Siakap* using plant-based aquafeed. In Phase 1, a total of six underutilised legumes, namely adzuki bean, mung bean, chickpea, hyacinth bean, black-eyed pea and pigeon pea have been selected for this study. The protein yield of these legumes was determined using the Bradford method. Meanwhile the ANFs present in legumes were determined using enzymatic assays to detect trypsin inhibitor activity, chymotrypsin inhibitor activity, α -amylase inhibitor activity and condensed tannin activity. Adzuki bean and mung bean had the highest protein yield, which were $129.91 \pm 1.59 \text{g}/100 \text{g DW}$ and $125.31 \pm 3.36 \text{g}/100 \text{g DW}$ respectively. Among the targeted legumes, pigeon pea had the highest trypsin inhibitor activity, which was $0.81 \pm 0.08 \text{TIA}/\text{mg DW}$, whereas pigeon pea and mung bean had the highest chymotrypsin inhibitor activity, which were $1.67 \pm 0.67 \text{CIA}/\text{mg DW}$ and $1.61 \pm 0.76 \text{CIA}/\text{mg DW}$ respectively. The highest α -amylase inhibitor activity was recorded in black-eyed pea, which was $0.18 \pm 0.01 \text{AIA}/\text{mg DW}$. Chickpea possessed the lowest protein content, which was $57.95 \pm 2.03 \text{g}/100 \text{g DW}$. The lowest trypsin inhibitor activity was recorded in black-eyed pea ($0.30 \pm 0.04 \text{TIA}/\text{mg DW}$) while pigeon pea showed the lowest α -amylase activity ($0.07 \pm 0.01 \text{AIA}/\text{mg DW}$). No detectable chymotrypsin inhibitor activity was found in chickpea and hyacinth bean. Condensed tannin was not found in any of the tested legumes. All targeted legumes possessed a significant amount of ANFs that need to be removed through various processing methods. In Phase 2 of the study, the effect of combining different processing methods such as soaking, wet heating, autoclaving, dry freezing and enzymatic hydrolysis on ANFs, protein content, amino acid profile and *in vitro* protein digestibility in these legumes will be evaluated.

DEVELOPMENT OF A STRATEGY TO IMPROVE THE GROWTH AND HEALTH OF FISH FED WITH PREBIOTIC PLANT-BASED DIET (FishP1-003)

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Abstract

Aquaculture is one of the alternatives offered in providing seafood sustenance to the world. However, a large number of issues challenge the sustainability of aquaculture practices, such as the occurrence of diseases and dependency on capture fisheries for fish meal production. One of the solutions proposed is the inclusion of prebiotics in aquaculture, which has been applied successfully in other terrestrial farm animals, which aims to improve the health and growth of fish through the improvement of gastrointestinal microflora. Therefore, the current study is being conducted to develop a strategy to improve the growth and health of fish fed with a prebiotic plant-based diet. This study highlights the development of a method applicable to determine the suitability of plant material to be applied as prebiotics in fish, taking into consideration the health and growth of fish, as well as the nutritional content of the fish as a result of the modified diet. This method will include the consistent analysis of growth and health of the fish throughout the feeding period, nutritional quality of the meat obtained from the fish, resistance of the fish against pathogenic bacteria, as well as the monitoring of beneficial bacteria populations in the gastrointestinal tract. In this study, the strategy is being developed using resistant starches isolated from underutilised legumes as potential prebiotics for *Siakap* (*Lates calcarifer*). The underutilised legumes used in this study include adzuki beans, mung beans, red lentils, chick peas and black-eyed peas. In Phase 1, starch is isolated from the legumes and the resistant starch contents are compared. The efficiency of resistant starch enhancement is also compared, comparing between enzyme hydrolysis and acid hydrolysis in terms of resistant starch content and its effect on the growth of potential probiotic bacteria isolated from gastrointestinal tract of barramundi from an aquaculture source. Findings from this phase of the study will contribute towards the development of the feed material in Phase 2 and the feeding trial in Phase 3. One of the problems faced in the bridging of knowledge across various disciplines is the lack of knowledge in several mechanisms, such as the roles of bacteria in the fish gastrointestinal tract, which is lacking in comparison to terrestrial animals, as well as the effect of metabolites produced by these bacteria towards the host. Therefore, the benefits of probiotics and prebiotics in aquatic animals may not be used to their optimum potential.

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DIETARY CALCIUM AND ZINC DEFICIENCY ARE PREVALENT IN AFRICA AND ASIA (CropB1-010)

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Abstract

Globally more than 800 million people are affected by chronic hunger with greater than two billion people having one or more micronutrient deficiencies (MNDs), a.k.a. hidden hunger. More than 6% of global mortality and morbidity burdens are associated with undernourishment and MNDs. Owing to the difficulty of determining human micronutrient status, little is known about prevalence of calcium (Ca) and zinc (Zn) deficiencies, which can affect human physical and cognitive development. Here we assess global supplies and deficiency risks of dietary Ca and Zn, and their recent historical trends. Food supply and composition data for Ca and Zn, demographic data, and Estimated Average Requirement (EAR) thresholds for Ca and Zn were integrated in a relational database management system. A total of 145 countries with population > 1 million were included in this study. Global dietary Ca and Zn supplies, and deficiency risks were assessed between 1992 and 2011. In 2011, 3.5 and 1.1 billion people were at risk of Ca and Zn deficiency respectively due to inadequate dietary supply. To our knowledge, these are the first global estimates of dietary Ca deficiency risks while our Zn deficiency risk estimates are consistent with recent studies. Approximately 90% of those at risk of Ca and Zn deficiency in 2011 were in Africa and Asia. The global mean dietary supply of Ca and Zn in 2011 was 684 ± 211 and 16 ± 3 mg *capita*⁻¹ d⁻¹ (\pm SD), respectively. Between 1992 and 2011, global risk of deficiency of Ca and Zn decreased from 76 ± 23 to $51 \pm 32\%$, and 22 ± 19 to $16 \pm 14\%$ (\pm SD), respectively. In 1992, 86 out of 138 countries had Ca deficiency risks >50%, decreasing to 69 countries out of 145 in 2011. Similarly, in 1992, 48 countries had Zn deficiency risks >25%, decreasing to 39 countries in 2011. This trend corresponds with an overall increase in Gross National Income and global food supply, notably mineral-dense animal products. With the United Nations (UN) Millennium Development Goal 1 (MDG1) aiming to halve hunger by 2015, deficiency risks of Ca should have decreased from 76 to 47%, and that of Zn from 22 to 14%, in the period 1992-2011. There are 101 and 86 countries which are unlikely to halve Ca and Zn deficiency risks, respectively, by 2015. We conclude that continuing to reduce Ca and Zn deficiency risks through dietary diversification and food and agricultural interventions including fortification, crop breeding and use of micronutrient fertilisers will remain a significant challenge in the post-MDG1 era. However, there is also a pressing need to identify and/or generate data with a better spatial resolution to support policies to address these and other MNDs.

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THE ROLE OF FISH AND OTHER AQUATIC ANIMAL SPECIES IN THE MALAYSIAN DIET – BARRIERS TO INCREASING CONSUMPTION OF FARMED SPECIES (FishP1-005)

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Abstract

The dependence of Malaysian on fish is apparent. The extensive Malaysian coastline, which is about 4800 km in length, has given rise to many small scale industries related to the harvesting of fish. On another hand, fish is acceptable to all, irrespective of religious observances. As such, fish tends to dominate over other animal protein sources (i.e. poultry, eggs, pork, beef and mutton) in this country. The fact that fishery resources are an important source of nutrients for humans is well known. However, it is worth pointing out that the nutritional contributions of fish and shellfish to Malaysian diet have yet to be quantified. The Malaysian Adult Nutrition Survey (MANS) provides the first national estimates of energy and nutrient intakes, food consumption patterns and meal patterns of the Malaysian adult population but did not provide insight into the quantifiable contribution of fish and shellfish to energy and nutrient intakes of its respondents. On top of that, the current Malaysian Food Composition Table, which was published in 1997, has limited number and scope of nutrients analysed for fish and shellfish per se. National promotion of fish consumption and fishery activities, whether for nutritional or economic exploitation, need to be balanced against concerns for sustainability of marine fish stock and its potential depletion. The average increment of fish consumption in Malaysia is constant at about 1.6% yearly since the year 2000 but actual annual fishery landings in Malaysia do not observe a similar growth trend. In fact, three-quarters of ocean fish stocks had been exploited up to their maximum sustainable yield by year 2000. The fish supply and demand equilibrium can be achieved by promoting aquaculture activities. Prior to that, it is important that consumer attitudes toward aquacultured fish and the variables that drive fish purchasing decisions are fully understood. Consumer-held perceptions of aquacultured fish have received increasing attention in western countries recently but are still poorly understood in Malaysia. Gaining insight into the Malaysian consumer's perception of farmed fish will determine whether the aquaculture field will be successful in achieving its growth potential. With sufficient scientific evidence, public policy can be made to regulate and improve aquaculture practices hence promising the quality of aquacultured products before encouraging the replacement of wild-caught fish with aquacultured fish in Malaysia. Given the significance of fish and shellfish in nutritional value and food security and the emerging role of sustainable aquaculture, this research is designed to assess the role of fish and shellfish and their products in maintaining appropriate nutrient intakes in different communities within the Klang Valley and Selangor and to identify potential barriers to replacing wild-caught fish with those which have been aquacultured.

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ISOLATION AND NUTRITIONAL ANALYSIS OF CHLOROPLAST-RICH MATTER, A POTENTIAL FARMED BARRAMUNDI FISH-FEED SUPPLEMENT (FishP-006)

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Abstract

Barramundi in the aquaculture industry has become one of the most commonly farmed fish in South East Asia. However, commercially used plant-based feed ingredients contain anti-nutritional factors (ANF) which hamper fish growth. The chloroplast, a photosynthetic organelle, has been suggested to be rich in essential fatty acids (EFA) and vitamins important for fish growth and thus, represents an alternative nutritionally-rich fish feed supplement. To understand the possible utilisation of chloroplasts in fish-feed, chloroplast-rich-matter (CRM) was isolated from spinach leaves and analyzed for the nutritional content. CRM was isolated from spinach leaves by means of homogenization, filtration, and high-speed centrifugation. The final pellet of CRM was subsequently freeze-dried. The CRM powder was analyzed for protein, lipid, fatty-acids, chlorophyll and carotenoid, vitamin E and pro-vitamin A using a BCA protein analysis kit, the Bligh and Dyer method, spectrophotometric methods, GC-MS, and HPLC, respectively. Results demonstrated that chloroplast-rich matter was composed of 51.5% of protein, 27.7% lipid, and 6.6% chlorophyll. The majority of fatty acids in CRM was shown to be alpha-linolenic acid (ALA; 57.2%); while vitamin E and pro-vitamin A content was 31.6 mg/100 g and 602 mg/100 g of CRM, respectively. The high content of protein, ALA, and pro-vitamin A suggest the possible use of CRM as a protein, ALA, or pro-vitamin A supplement to improve the growth and health status of farmed barramundi. Future work will be aimed at expanding the nutrient profiling to vitamin C, amino acids, and mineral analysis. Selecting a suitable neglected, underutilised plant species (NUS) to isolate and nutrient profile the chloroplasts, should be done in order to provide a cost-effective, nutritionally-rich, chloroplast supplement, in conjunction with adding value to underutilised plant species. To achieve future aims, it will be necessary to combine the knowledge systems of barramundi aquaculture and neglected, underutilised plant species.

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ISOLATION AND IDENTIFICATION OF PARTIAL RAB GENE FRAGMENTS IN MALAYSIAN MANGO

(FoodP1-016)

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Abstract

The world's overdependence on few major crops is alarming as it leads to non-balanced diets. Introducing underutilised fruits rich in nutraceutical values will allow for diversification of the human food availability which in turn will help improve food quality and food security. Mango (*Mangifera indica*) fruit was chosen as a model in this study mainly because the South East Asia region is the centre of origin for mango. Therefore, a wide variety of mangoes can be found but many of the mango varieties are still not widely studied and underutilised. Mango (*Mangifera indica*) is an important tropical fruit consumed widely both fresh as well as in its processed form. However, the softening and spoilage of mango fruits is a major challenge as they are unfit for long term storage, leading to major losses. Without a doubt, there is a pressing need for knowledge to understand this mechanism and so studies at the genetic level will be highly beneficial if genes associated with ripening are to be isolated and used for biotechnological improvement. Previous molecular studies suggested that several enzymes such as polygalacturonase and pectin methylesterase are working in concert in the fruit ripening process. In addition, the role of the Rab gene families in mango fruit ripening has been identified as an exciting potential avenue of research. Recently, these genes have been validated to be involved in the softening of the tomato fruit using reverse genetics approaches. To our knowledge, no substantial data has been made available on these genes in the Malaysian mangoes.

In this study, genomic DNA and total RNA was extracted from Malaysian mango using modified CTAB method respectively. The NCBI BLAST search program was used to identify Rab protein and nucleotide sequences from closely related plant species such as peach, tomatoes, oranges and apples. The Rab sequences were aligned and conserved motifs identified with the help of the online Clustal Omega program. Using the online CODEHOP tool and PCR technique, distinct degenerate primers were designed and partial Rab gene sequences amplified.

In this study, the ripening stages of three mango varieties were established based on various physicochemical characteristics including colour, firmness, soluble solid content(SSC) etc. DNA yields ranged from 13-21 µg per 300mg of tissue while 2-20µg of total RNA was obtained routinely per gram of frozen fruit tissue. Partial *Rab* gene fragments of expected sizes were successfully isolated using the CODEHOP PCR strategy with either cDNA or genomic DNA as templates. NCBI BlastX search revealed matches between the partial *Mangifera* sp *Rab* sequence and several other *Rab* genes of other plants available on the database. These included *Theobroma cacao*

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(93%), *Citrus sinensis* (92%), *Vitis vinifera* (92%) amongst others. Reverse transcription followed by end-point PCR demonstrated the suitability of the total RNA preparation for downstream application. Their possible involvement in mango softening will be elucidated further. The study aims to provide a greater understanding of the ripening related process in reducing postharvest losses.

Effective manipulation requires knowledge of the molecular networks that control the fruit softening process. Studies at the genetic level are required if genes are to be used to improve this quality. Nonetheless, the pieces are in place for rapid advances to be made in the manipulation of rapid softening in the near future.

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POSTHARVEST MANAGEMENT OF ANTHRACNOSE IN PAPAYA USING PLANT EXTRACTS

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Abstract

Colletotrichum gloeosporioides is a plant pathogenic fungus that causes anthracnose in papaya. Up to present, synthetic chemicals such as Prochloraz, Thianbendazole, Benonmyl, Imazalil are used alone or in combination with other postharvest disease management practices to control anthracnose. However, consumer concern about chemical residues and the toxicological effect of fungicides to human health has necessitated the introduction of novel non-chemical approaches to control the disease. Natural products such as turmeric rhizome (*Curcuma longa* Linn) and ginger (*Zingiber officinale* var. Bentong) have been reported to possess antimicrobial properties. Studies of their antimicrobial properties is limited to the field of ethnomedicine, pharmacology and other agronomic practices whilst it is significantly underutilised in the field of postharvest disease management in fresh fruits and vegetables, particularly papaya. A preliminary screening of the antimicrobial properties of these underutilised plants against *C. gloeosporioides* isolated from papaya and their efficacy to control anthracnose was investigated at different concentrations at ambient temperature.

Concentration (treatment) of 2.5 mg/ml, 5 mg/ml, 7.5 mg/ml and 10 mg/ml was prepared from stock obtained from methanolic extracts of ginger and turmeric rhizome. Stock was prepared by addition of distilled water after re-dissolving each crude extract (ginger and turmeric rhizome with small amount of methanol). An *in vitro* antifungal study was performed to ascertain the efficacy of plant extracts against *C. gloeosporioides*, in the concentrations denoted above, using the poison food technique. In this technique, freshly prepared PDA (potato dextrose agar) was amended with the treatments above and poured into a 9 cm petri dish. Fungal agar disc of 5 mm was placed in the centre of the amended PDA and incubated at 25°C for 10 days (when the fungus in the control petri dish has completely covered its surface). For the *in vivo* study, the efficacy of plant extracts to control anthracnose on fruits caused by the fungus was done using the treatments 5mg/ml, 10mg/ml and 15mg/ml for each crude extract solution prepared. During the *in vivo* studies, all fruits were inoculated (dipped in spore suspension of 10^5 spore/ml for 1 min and dried for 5 hr), followed by application of treatment (dipping of fruits in extract solution at different concentrations for 2 min). Control fruits were inoculated only.. Fruits were then stored at $25\pm 2^\circ\text{C}$ for 28 days and 15 days respectively.

There was significant effect ($P < 0.05$) of treatment in controlling *C. gloeosporioides*, as this was evident in the percentage (%) inhibition of mycelia growth and conidia germination irrespective of the crude extract. The efficacy of treatment to control *C. gloeosporioides* was dose dependent and fungistatic, even at the highest concentration (10 mg/ml), for all extracts used in this study.

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Scanning electron microscopy (SEM) markedly showed distorted, shrivelled and swollen fungal hyphae and conidia especially between 2.5-5mg/ml, when fungus were treated with either ginger or turmeric rhizome compared to control, whereas at 7.5mg/ml or 10 mg/ml there was little or no conidia germination. At 7.5 mg/ml, the % inhibition of mycelia growth was 71.41% and 86.28% in turmeric rhizome and ginger respectively. The highest % inhibition in mycelia growth (88.46%) was observed in ginger crude extracts at 10 mg/ml.

In the *in vivo* studies, the onset of anthracnose was delayed until after day 9 in ginger-treated fruits. This delay was observed at 10 mg/ml and 5 mg/ml which was not different from the control fruits, but it occurred much earlier, thus after day 6 at 15 mg/ml in ginger treated fruits. Whereas 100% disease incidence (DI) was observed after 12 days for all treatment including control, the disease severity varied. After 12 days, the disease severity was low at 10mg/ml [(score = 2.4 (25% decay))] but was highest at 15 mg/ml [(score = 3.8 (50% decay))].

Similarly, the onset of anthracnose occurred after day 9 in turmeric rhizome treated- fruits which were not different in the control fruits. At day 12, 33%, 67% and 70% DI was recorded in 5 mg/ml, 10mg/ml and 15 mg/ml treated fruits respectively compared to control (33%). The order of disease severity is as follows; control [(score = 1.2 (9%)], 5mg/ml [(score = 1.6 (15%)], 10 mg/ml [(score = 1.8 (18%)] and 15 mg/ml [(score =2.8 (28%)] at day 12. Turmeric rhizome markedly reduced anthracnose disease and severity even until 15 days. After 15 days all fruits had decayed. Irrespective of the extract used, fruits treated at 15 mg/ml gave a high disease severity which could be due to phytotoxic effect. We conclude that all the extracts, especially turmeric rhizome, can act as a potential natural antimicrobial agent to control postharvest anthracnose in papaya fruits especially at 5mg/ml or 10mg/ml.

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PROFILING OF THE GLYCEMIC INDEX OF UNDERUTILISED FRUIT AND VEGETABLE (FoodP-031)

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Abstract

Glycaemic Index (GI) is a term used to describe the effect on blood glucose of consuming a carbohydrate rich meal. It is accepted knowledge that the digestion and the absorption of carbohydrate lead to an increase in the levels of blood glucose. The extent and rate of elevation depend on a number of factors. For optimum health, it is essential that blood glucose is maintained between 3.0-5.5mmol per litre. This is achieved by the pancreatic hormones insulin and glucagon that work synergistically to control the levels of circulating glucose. When this system is compromised, for example when the pancreas or insulin receptors are damaged, blood glucose levels cannot be controlled. This leads to the development of type two Diabetes Mellitus (T2DM). As nutritionists, we are interested in consuming a diet that provides optimum health. With respect to carbohydrate and GI value, this means avoiding foods that result in a sudden peak in blood glucose (known as high GI foods). The GI value of a food ranges from 0 to 100, with the highest value being for pure glucose. Complex carbohydrates, especially from whole grains, have a lower GI value.

There is anecdotal (and scientific) evidence to suggest that fruits, vegetables and herbs (including underutilised species) can be used to control T2DM. For example, bitter melon (*Momordica charantia*) contains charantin, momordicin, cucurbitanoids, which are responsible for the hypoglycaemic principle. Bitter melon extract was shown to have an anti-hyperglycaemic effect in streptozotocin-induced diabetes rats (STZ) due to the inhibition of glucose-6-phosphatase as well as stimulation of the activity of hepatic glucose-6-phosphate dehydrogenase (Lawrence *et al.*, 2009). In addition, an aqueous extract of raw ginger (*Zingiber officinale*) was shown to have a significant effect in lowering serum glucose, hypolipidemic potential of STZ-induced diabetic rats compared to the control group after 7 weeks (Amin *et al.*, 2006). Moreover, the effect of fenugreek (*Trigonella foenum graecum*) ethanolic extract was examined after 2 weeks. The result was a significant reduction in weight loss in diabetic rats. From that, the serum glucose, cholesterol profile was reduced, whereas the insulin level was increased only in diabetic rats, $p < .05$ (Akram *et al.*, 2007).

The purpose of this research is to review existing evidence of the role of selected underutilised species in controlling T2DM. Promising species will be selected for *in vitro* studies to determine the effect on the GI value of a rice based diet, thus creating a GI profile for the underutilised species. The species selected for study are bitter melon, ginger, fenugreek, and turmeric.

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Initial studies will include the development of an *in vitro* method to simulate digestion and absorption. Boiled white rice will serve as the control. The effect of adding the species under investigation at various concentrations will be studied.

Time and ethics permitting, the second phase of the study will include *in vivo* measurement of blood glucose in a range of subjects following consumption of rice and mixed meals containing the species being investigated.

VALUE ADDED BIOFUELS AND BIOCHEMICALS PRODUCTION FROM UNDERUTILISED CROPS VIA A BIOREFINING STRATEGY (BioP1-001)

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Abstract

In order to meet objectives outlined by CFF and to diversify the source of biomass used for the production of renewable energy, this PhD project proposes that a biorefining process will be established to develop the use of an underutilised crop for the production of value added products. The underutilised crops will be used as a biomass substrate to produce enzymes, bioethanol and biogas, developing the market potential for this crop. To avoid the food-versus-fuel controversy, only the non-food part or post-processing waste of each crop is used as the biomass. Currently six crops – Bambara, Napier, nipah palm, sago palm, leucaena, and oil palm – have been screened for cellulase production during a solid-state fungal fermentation (SSF) process. Different fermentation conditions for the production of cellulolytic enzymes were explored to optimise the process. Several aspects were explored including the use of two different fungi – *Aspergillus niger* and *Trichoderma reesei*, addition of nutrients (starch and yeast extract), use of two different mineral solutions, and incubation period. Cellulase activity for the six crops ranged from 1.442 U/g to 16.702 U/g, with Napier producing the highest cellulase activity. Optimisation of SSF conditions was done using Napier as the substrate. The addition of mineral solution I improved cellulase production when using *A. niger*; however, the addition of mineral solution II was best for cellulase production when using *T. reesei*. Overall, the use of *A. niger* resulted in higher cellulase production compared with *T. reesei*. The addition of yeast extract and mineral solution improved the cellulase activity from Napier from 16.702 U/g to 22.561 U/g, a 1.35 fold increase. From this initial research, two of the six crops will continue to be used for further analysis – Napier and sago. Sago hampas, the waste material remaining after the starch extraction process, produced little cellulase activity. However, it proves an interesting crop for further analysis as our results showed it is still very high in starch ($51.43\% \pm 2.38$ (w/w) dry wt basis) even after starch extraction processing. Another fungus, *Aspergillus awamori*, is currently being cultured and used in the solid state fermentation process, using sago. Experiments will be carried out to optimise conditions (as above) to maximise gluco-amylase activity. Liquid media fermentation will also be carried out to compare enzyme production with the production from SSF process.

PYROLYSIS OF NAPIER GRASS TO BIO-OIL AND SUBSEQUENT UPGRADING TO COOKING AND HEATING GRADE FUEL (BioP-005)

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Abstract

Fossil fuel is currently the major source of energy supply globally. With increase in population and energy demand, the consumption rate per annum of crude oil continues to rise which in turn causes depletion of the known reserves. Fear of energy insecurity in the near future and environmental and sociopolitical issues associated with fossil oil has led to searching of alternative renewable energy sources such as biomass, wind, solar and mini-hydro. Among the renewable resources, biomass is the only renewable resource that has carbon in its building blocks which can be processed to liquid fuel. This study is focused on biomass based liquid fuel technology development. There are various pathways to produce liquid fuel from the biomass: biochemical and thermochemical. Our interest is in thermochemical processes and subsequent upgrading. A literature search in the area has been performed and thermochemical conversion through fast pyrolysis was found to be appropriate for high yield of liquid bio-oil with fewer processing steps and complexities. Literature has elucidated poor characteristics of bio-oil produced from pyrolysis, and therefore the need for upgrading to fuel grade. Different unit operations and unit processes in the bio-oil upgrading have been examined. The later approach with the aid of catalysts is gaining recognition. However, from the current reviews and the experimental works, none has been able to establish fully an upgrading process to produce refinery-ready intermediates. Issues regarding reaction mechanisms, kinetics, catalyst deactivation and sustainable sources of hydrogen are not fully understood. Therefore, focus is on development of a robust process to upgrade bio-oil to heating and cooking grade fuel for rural applications.

In our studies, locally grown Napier grass was collected from CFF field and assessed as received, characterized and preserved for further treatment and analysis. Proximate analysis of the biomass on dry basis (moisture content, ash content, volatile matter, fixed carbon and higher heating values-HHV) and ultimate analysis (carbon, hydrogen, nitrogen, sulfur and oxygen) on dry basis were carried out. Prior to pyrolysis, pretreatment of the biomass materials was carried out

with neutral, acid and alkaline solvents to remove extractives and inorganic components that will otherwise retard conversions, yield and selectivity during pyrolysis. Increasing severity factor during pretreatment with neutral solvent increased the removal of ash and its alkaline and alkaline earth metal components. Improvement in the higher heating value of the pretreated biomass was also recorded. Similar observations in the heating value and ash extraction were also noted with acid solvent as the concentration increased. On the other hand, decrease in heating value of pretreated biomass was recorded with alkaline solvent. Pyrolysis of raw Napier was performed in a fixed bed reactor at heating rate 30°C/min under nitrogen atmosphere. Effects of nitrogen flow rate and reaction temperature were investigated. Optimum bio-oil yield was recorded at reaction temperature between 558-600°C and 30-40mL/min nitrogen flow rate. Further productions were carried out at this optimum condition. Physicochemical characteristics of bio-oil such as pH, water content and HHV were determine using microcomputer pH meter, Karl Fischer titration and oxygen bomb calorimeter respectively. Chemical composition of the oil was also carried out with GC-MS. Bio-char was analyzed using EDX and SEM. Composition of non-condensable gas was determined with Draeger gas analyzer. Bio-oil contains significant volume of water and oxygen rich molecules that requires separation and catalytic upgrading to liquid fuel. Four different types of catalysts (zeolite based) were collected and characterized and will be used for the upgrading of bio-oil.

SYNTHESIS OF SUSTAINABLE SAGO STARCH VALUE CHAIN (BioP1-003)

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Abstract

Sago palm is one of the underutilised crops that can be found in South East Asia countries and Papua New Guinea. Sago palm has a strong ability to sustain and thrive in swampy areas and acidic peat soil. Once the sago palm has matured, sago starch is extracted from the sago trunk. Such starch is one of the major carbohydrate sources for humans. It can be converted into food products (e.g., noodles, cakes, biscuits, etc.) and non-food products (e.g., ethanol, sugar, kojic acid, etc). In order to produce sago starch, essential processes such as plantation, harvesting, starch processing as well as transportation of raw material (sago logs) and sago starch are involved. These series of processes form a sago starch value chain. Note that this value chain has caused several environment issues (e.g., river and air pollution) especially during the sago starch processing. This is because huge volumes of biomass (sago fibres, sago bark, etc.) and wastewater are generated during the starch processing. In current practice, sago wastewater and sago fibre are combined and discharged into river without any treatment. Meanwhile, sago bark is left in sago mills as flooring material. In cases where there is an excess of sago bark in the sago mill, the bark will be burned off. These practices cause serious river and air pollution. Therefore, it is important to enhance the sustainability of sago starch value chain with minimum environmental impacts and maximum economic performance. On the other hand, since a large amount of water is required in sago palm plantations and sago starch processing, it is vital that the water footprint (WFP) is considered in synthesising sustainable sago starch value chain. Besides, it is noted that significant amounts of greenhouse gases such as carbon dioxide (CO₂) are emitted to the environment in the sago starch value chain. Therefore, carbon footprint (CFP) is another important criterion to be considered. Additionally, the number of workers involved in sago starch value chain must also be taken into consideration; this workplace footprint (WFPF) can be divided into three levels of risks: death risk (D), non-permanent disability (NPD) risk and permanent disability (PD). In order to consider WFP, CFP, WFPF and total profit (TP) of sago starch value chain simultaneously, a Fuzzy Multi-Footprint Optimisation (FMFO) approach is presented. FMFO extended the use of fuzzy optimisation approach to trade off the conflicts between the optimisation objectives using a fuzzy degree of satisfaction, λ so that optimum logistic network and processing facilities can be located. Based on the proposed approach, an optimum pathway of sago starch value chain with maximum λ of 0.616, minimum CFP of 0.2389×10^8 kgCO₂/year, WFP of 0.4250×10^9 m³/year, death risk of 0.0388 D/year, NPD risk of 0.3166 NPD/year and PD risk of 0.0120 PD/year as well as maximum TP of 0.4477×10^8 MYR/year is determined.

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COMMUNITY BASED REMEDIATION OF LLACHU AND TOTORA FODDER CROPPING SYSTEM AT TITIHUE LAKE PERU

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Abstract

On December 2013, the Peruvian Ministry of Agricultural and Irrigation received a request from the rural community of Titihue to analyze and solve the environmental issue affecting the natural resources of Titihue Lake, which is located in the district of Huancané in Puno, Peru, at northern part of Titicaca Lake. The Titihue community lives around the lake and uses indigenous aquatic plants like Llachu and Totora as fodder crops for their livestock. Recently, farmers have addressed their concern about the poor quality of Llachu (*Elodea potamogeton*, *Myriophyllum elatinoides*, and *Potamogeton strictus*) and Totora (*Schoenoplectus californicus*), which has been progressively decaying with the years. Farmers have observed changes in water colour, fish size and quantity; this has led to increasing concerns in the community that changes in their environment are having a negative impact on the lake. It is widely perceived that these changes are associated with mining activity in the upstream of Ramis watershed, conducted by small-scale illegal miners. Mining activities on abandoned mining sites has been depositing heavy metals such as mercury, arsenic and cyanide in small ponds, which end up in the streams of Ramis River and later in Titihue Lake. In the rainy season, Ramis river flows into Titihue Lake which then unites with Arapa lake, this allows the deposition of heavy metals in the boundary area of the lakes. The conditions noted by farmers, associated with the continued presence of illegal mining activities in the watershed, suggest that heavy metal toxicity may be affecting the complete lake ecosystem composed of sediments, plants, water, llachu, totora, fish and other aquatic species.

BIODIVERSITY LOSS ASSOCIATED WITH OIL PALM PLANTATIONS IN MALAYSIA: SERVING THE NEED VERSUS SAVING THE NATURE (BioP1-011)

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Abstract

Oil palm is considered one of the most important crops for the future in serving the global food and biodiesel needs. Oil palm also serves as an important source of rural employment and plays a major role in poverty alleviation in Malaysia. The increasing need for palm oil has resulted in the rapid expansion of oil palm plantations in the last few decades, which has become the biggest cause of deforestation in Malaysia. The Google deforestation map for the year 2000-2012 shows that Malaysia has the highest deforestation rate of all the countries in the world. Malaysian forests are home to numerous endemic species, which are threatened. Some oil palm promoting corporations have claimed that oil palm plantations support a healthy biodiversity. This research assesses the biodiversity value of oil palm in comparison with primary forests and secondary forests. The biodiversity value of secondary forests are overly underestimated and are readily converted into plantations. Using species richness data of vertebrates and invertebrates from previous publications, this research argues that conversion of either primary or secondary forest to oil palm plantation would adversely affect biodiversity. The oil palm plantations are filled with non-native invasive species or generalist species of low conservation interest. The review results, compiling numerous species richness surveys in Malaysia, show that there is a 34.9% reduction in species richness in oil palm compared to forest habitats, and 79.6% of the species found in forest habitats were not found in oil palm habitats. The primary cause of the reduction of species richness is found to be poor ground vegetation, lack of structural complexity and poor microclimate in oil palm plantations. In order to sustain the biodiversity in Malaysia, it is recommended that future expansion of plantations in primary or secondary forests should be strictly prohibited. It is also recommended that the oil palm management regime should focus on improving the structural complexity and ground vegetation of oil palm plantations.

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TOWARDS A USER-CENTRIC APPROACH FOR ASSESSING QUALITY OF CROWD-SOURCED DATA, APPLICATIONS IN UNDERUTILISED CROPS (CropB1-011)

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Abstract

Recent years have been witnessing the rapid development of crowdsourcing or volunteered geographic information (VGI). Supplementing traditional government programmes, crowdsourcing recently has become the new trend for generating geospatial data due to its strengths such as: low-cost, large numbers of data producers, time-efficient for individual data producers, and near real-time data collection. Foremost in these developments is the increasing power and ubiquity of mobile smart phones with precision positioning capabilities, high-quality cameras, large memories, fast processing and broad-band communications. These devices can also be wirelessly linked to search engines, cloud-computing services, sensors and sensor networks and even low-cost unmanned air vehicles for associative data collection and analysis. However, unlike traditional authoritative data, crowdsourcing has no assurance of data quality. Therefore, there is a need for a range of assessment algorithms which can validate, control, and ensure the quality of submitted crowd-sourced data. In this research, we propose a user-centric approach where relative majority defined from flexible thresholds can assure high, moderate or outlier crowd-validity of each possible answer of the crowdsourcing experiment. Depending on this first qualification, an interactive mechanism allows to test if, for example, outlier crowd-qualified data are local rare but valid events or true outliers due to user variations. How data collected by non-specialists and volunteers, i.e. "the crowd", can be assessed for credibility and quality through a client-server based framework is the generic framework of our research. In particular, the framework specifically adopts the potentially iterative triggering of requests back to the crowd for location and topic specific confirmatory or associative information so that a credibility ranking or confidence rating can be assigned to the data and, where appropriate, quality and error-bounds calculated. A trusted ranking system of the volunteers is also to be developed in order to assist the data quality assessment process, and to motivate the contribution of volunteers.

ONTOLOGY-DRIVEN CROPBASE KNOWLEDGE SYSTEM (CropB1-001)

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Abstract

Knowledge representation in the field of AI (Artificial Intelligence) involves the use of principles and structures to model and present information in a way that facilitates inference. However, due to inconsistencies in nomenclature of domain concepts and the diversity of modeling structures involved, comparable knowledge can appear to be entirely different. These ambiguities results in obstacles to knowledge-sharing especially among interdisciplinary researchers, such as those in the Crops for the Future Research Centre (CFFRC). Thus, a standard vocabulary (Ontology) of a given research domain needs to be shared and adhered to by researchers in order to effectively interface correlated research goals. To achieve the project goal, different research activities have so far been accomplished, including formulating the research question and surveying the state of the art in crops ontologies and extending ontologies with Rules. In the early experiments, we develop the first version of UC-ONTO using the Web Ontology Language (OWL), which at present contains more than 500 underutilised crop-related concepts and extended with some set of LP rules written in the Semantic Web Rules Language (SWRL). In developing the UC-ONTO, we employ the *Collaborative ontology development methodology*, where domain experts work closely with knowledge engineers during ontology development. In a nutshell, the current version of UC-ONTO comprises a total of 24, 701 OWL axioms, with 111 classes, 397 individual assertions, 94 object properties, and 133 data properties.

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OPTIMISING CANOPY ARCHITECTURE AND PHOTOSYNTHESIS FOR BIOMASS PRODUCTION (BioP1-006)

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Abstract

There is wide variation in plant architecture both between and within species. This is particularly relevant to biomass production as the shape, size and orientation of plant material within a canopy will, in part, determine light acquisition and therefore the productivity and photosynthesis of the plant as a whole. This project uses a novel method created at the University of Nottingham, UK, to reconstruct plants in 3-dimensions to a high degree of accuracy. The method is a fully automatic approach to image-based 3D reconstruction that can be achieved using a single low cost camera on any plant species. Each reconstructed plant is represented as a series of small planar sections that together form a mesh that models the more complex architecture of the whole plant. Such reconstructions can then be used to populate whole canopies. A forward ray tracing algorithm can then be applied to the 3D structural data to determine the light environment at each section of leaf using a number of changeable parameters including day number, latitude and time of day etc. Light history can be used to predict photosynthetic response in plants using variety of applications including both empirical and mechanistic models. One application of the technique has been realized through the creation of an empirical model assessing the effects of photoinhibition (i.e. a lowering of quantum efficiency caused by too much light) on photosynthesis and carbon gain. Within this project, the imaging and modeling technique, as well as a field trial, is being used to assess the productivity of intercrop canopies of Bambara Groundnut and Proso Millet; two crops exhibiting high water use efficiency.

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A MULTI-SCALE MATHEMATICAL MODEL FOR PREDICTING CROP GROWTH (Bam1-008)

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Abstract

We introduce a basic multi-scale mathematical model for modeling crops. Our work is concerned with the canopy interactions between neighbouring plants. It is a challenge in science to explain findings at the crop scale in terms of the physiological processes at the plant scale. As a community we are beginning to bridge the gap between these pieces of knowledge, however our understanding in these areas are often qualitative and do not explain the more subtle processes of plant morphology and biochemistry. Utilising a non-linear system of ordinary differential equations to describe the development of an individual plant trunk and canopy we investigate the growth of a plant as a function of intercepted radiation from sunlight. Included in this system of equations is the loss of intercepted radiation due to neighbouring plants. We then move on to consider how individual canopy interactions between two plants, planted rows and simple arrays of plants affects the overall yield of biomass of the planted crop. We discuss the results of a series of numerical investigations of our model and discuss future developments we plan to apply to the model. In doing this, we hope to investigate how processes and interactions at plant scale affect the yield at the crop scale.

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DEVELOPING A QUALITATIVE FRAMEWORK THROUGH WHICH TO ASSESS AND ENHANCE THE QUALITY OF TRANS-DISCIPLINARY COMMUNICATION IN MULTIFACETED AGRICULTURAL RESEARCH ORGANISATIONS (B1-005)

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Abstract

Nature and society is complex and the world is full of confrontations between people, groups, nature and nations who think, feel and act differently. Agriculture represents a class or expression of complexities which researchers need to look at because of its immense contribution to rural development and poverty reduction. Developing ways of meeting the societal needs that are productively and environmentally sustainable requires an approach capable of linking a range of perspectives to solving complex challenges especially for the agricultural sector.

This study specifically at this point focuses on Crops for the Future Research Centre (CFFRC) working as a global research leader for underutilised species with a plethora of different researchers and disciplines. CFF is a multidisciplinary research agricultural organisation with an objective to solving complex real life problems of hunger and food insecurity by developing underutilised species as alternative crops to the existing major crops. This objective will contribute to the nutritional requirements of man, contribute to the global food security state, and serve as a coping mechanism to climate change adversities and as an alternative to crop failures. Achieving this task resulted in formulating transdisciplinary teams of researchers, with diverse backgrounds and perspectives, to work together. If this is to function effectively, then the skills and perspectives of different knowledge communities (themes, programmes and supporting units) must address those elements of the programme to which they are relevant and related. Equally, the extent to which the overall objectives of programmes are achieved is dependent on how effectively and efficiently these different knowledge communities are combined.

This project examines how socio cultural factors and knowledge perspectives influence the quality of communication between members of disparate knowledge communities of CFF and investigates how they can be improved. Combining these knowledge communities with different perspectives, different socio cultural elements and interest brings about communication challenges that can affect collaboration, teamwork, networks and general organisational outputs. This challenge then raises the question as to whether it is possible to formulate approaches of inter- and transdisciplinary concepts which are capable of reducing inefficiencies in communications within CFF.

In particular, the study examines how different themes and programmes define their own critical contribution to the organisation, and also on the types of knowledge inputs that specific knowledge communities are likely to seek from others. It is also developing a coherent

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methodological approach and framework to understand communication processes in complex scientific programmes like CFF. Added to these is the evaluation of the socio-cultural elements in relation to communication between different knowledge communities in complex research programmes and consortiums. Finally, it examines the appropriate multi perspective approach to solving complex research communication challenges.

As a method of this study, elements of an ethnographic and discourse analysis approach is used to examine the nature and quality of communication and interaction between knowledge communities involved in CFF themes and programmes. Observations, interactions and interviews with structured and non-structured questionnaires are used to generate data for the project with researchers within CFF. Researchers and staff from the supporting units are the respondents or objects of this study. Respondents are clustered in to three groups, namely: Senior Researchers (Directors and Coordinators), Programme Managers and Support Staff (Human resource, accounts, communication, business development and field research centre). These actors constitute the core working groups of CFF.

Some interviews were recorded with respondents' consent and prior approval and adherence to strict ethical considerations. Available official documents of the organisation relevant to the study were used in addition to the observed data generated. Observations and other forms of data collection from the organisation were largely guided by the ethical regulations and requirements of UNMC and CFF as a research organisation. NVIVO software will be used to compute and analyse the data collated for write up. The findings of the study are expected to contribute to the outputs of CropBase programme of CFF and agricultural research projects at large.

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Abstract

The goal of this study is to integrate, interrelate and interlink disparate data assets. This effort is an approach to hyper-data, attempting to offer; minimal barriers of entry for preexisting stored and modeled information enabled by current mainstream technologies, a framework that provides value in simple implementations. This makes a case for its adoption and at the same time allows for scaling in collaborative iterations, increasing value along with increased complexity, and a simple enough interface for the interrogation and discovery of the interlinked data model that it represents. At this stage this work is focused on making a generalisation for modeling data assets (regardless of their current format or underlying technology with which they are stored) as a set of annotations that is referred to as an observation. Observations are published on different servers and are interlinked through hyper links that establish a relationship between them. Observations can be driven from data stores such as relational database management systems or can be driven from processing such as statistical models that normalise underlying data views or even be generated on the fly entirely. Three relation types have been identified, namely a conjoin which maps to one to one relationships, an extension mapping to one to many and a similarity mapping to many to many relations. This model is designed to be distributed but interlinked with the goal of providing a framework through which the interrogation of the superset of interlinked published models is possible and fairly simple and the entire network is viewed as one integrated data source. For this purpose a special query language is being developed to enable users to interact with this published interwoven web of data assets. For the sake of adoptability care is being given to making this language not too different from the widely used SQL language (though it is not necessarily only for accessing relational databases per se). We are also designing this language with the aim of making knowledge of the meta-structure of the models minimal or transparent to the user. The pathways from one observation to the other shall be automatically discovered when the query is processed and the load of writing own join conditions is lifted from the user as much as possible. To enable this automatic discovery a crawler has been developed that seeks to identify how an annotation being sought in a query for any one observation is linked to that observation; this may span chains of linked observations across multiple servers. The involved servers then pass on messages among each other to supplement the information that was provided in the query such that the information required is retrievable.

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IDEA RECOMMENDER SYSTEM (CropB1-007)

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Abstract

Ideas exist in text corpus. Identifying ideas is important to understand the meaning of a piece of text and to make connections between multiple documents. Creating new ideas is crucial for researchers to come up with new solutions to solve problems in a specific knowledge domain. To help researchers to conduct scientific research via novel hypothesis generation, we present an ideas recommender system. There are many challenges associated with the automated extraction of ideas from texts. For example, there is no formal definition of idea from reading comprehension perspective. Another issue is that it is much more difficult to extract ideas from long articles, or multiple documents, than it is from a single sentence or paragraph. Text mining techniques have developed substantially in recent years, and it is now possible to automatically detect topics and make summarisations from textual information. However, there are very few studies on automated ideas identification, and the generation of new ideas. Our ideas recommender system functions by extracting noun-phrases from the abstracts of scientific papers across a range of domains, before subsequently identifying solution-phrases and problem-phrases within that set. Scientific publications are input into the ideas recommender system. Publications are then preprocessed for the purpose of labeling different parts of the publication, such as the title or abstract. After the extraction and categorisation of noun phrases, a bag of ideas (idea-set) is formed. The idea values are computed, and together with the pair < p-phrase, s-phrase> they are input into the recommender system. Using a collaborative filtering (CF) algorithm, potential new ideas are then generated. Noun-phrases are detected from the titles and abstracts of publications using the Part-Of-Speech tagging (POS) technique. We classify noun-phrases by comparing the phrases with a bag of trigger words, which can explicitly identify solution-phrases. Examples of trigger words are method, approach and solution. We have collected 14 trigger words by crowd sourcing. From these noun-phrases, candidate idea pairs are then constructed (<solution-phrases, problem-phrases>), and each of these is assigned an estimated value via a term frequency-inverse document frequency (tf-idf) score. Sets of these <solution-phrases, problem-phrases, value> are then input into a collaborative filtering based recommender system, the output of which is a set of dynamically generated idea recommendations. These have potential to provide cues to researchers with the necessary background knowledge and skills to integrate them into their hypothesis generation process. We have evaluated our system using a subset of publications from the journal of Science using a bisociation scheme, with precision and recall results indicating that our ideas recommender system can produce useful new ideas.

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BIOMASS SUPPLY CHAIN OPTIMISATION: CONSIDERATION OF UNDERUTILISED BIOMASS VIA BIOMASS CHARACTERISTIC (BioP1-007)

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Abstract

Worldwide development has to move toward sustainability to minimise usage of non-renewable resources. One of the highly anticipated approaches is the development and utilisation of bio-resources into higher value downstream product. Exploration in bio-resources has led to the success of implementation in few bio-resources, such as palm oil. However, this development is yet to be considered mature and systematic, for instance biomass is yet to be feasible in industrial scale implementation due to high logistic cost. Many works only focus on specific species of upstream biomass generated from plantation due to huge data availability and better understanding of the resources. For example, the palm oil industry has gone through major revolution from its original state, especially in establishment of palm biomass technologies at the laboratory scale. However, this creates an issue such that less research is conducted on other biomass, leading to underutilisation of potential resources. Less work has been done on downstream biomass generated from processes, which could potentially be another alternative resource. From an optimisation point of view, the current biomass system is yet to be optimum as the whole system is not properly analysed and many biomass types have yet to be exploited. In this study, a mathematical supply chain model is constructed to optimise regional biomass supply chain network and fully utilise biomass available within the system. The Novel Element Targeting Approach is being used to integrate resources and demand via biomass elemental properties and characteristics. Biomass characteristics considered include cellulose, hemicellulose, lignin, heat value, moisture, ash, fixed carbon, volatile matter, C, H, N, O and S content. Integration of elements is inspired from the fact that some technologies are element sensitive, such as moisture content in pyrolysis and combustion. This approach also breaks through the species barrier in biomass selection as biomass selection will be based on elements instead of its species. Element Targeting and biomass selection is based on a hypothesis that if the element properties of biomass mixture are similar to the original feedstock, there will be no major changes in the technology yield. Element Targeting reflected in Biomass Demand-Resources Value Targeting (DRVT) will be modelled with a theoretical case study. The model shows a significant improvement of biomass utilisation and overall profit by using the DRVT approach. This approach is further refined by using Biomass Element Life Cycle Analysis (BELCA) which includes the consideration of downstream biomass. One of the main gaps in this study is to verify the hypothesis in a variety of technologies to prove the accuracy of the modelling result. Preliminary verification of the hypothesis is conducted with semi batch pyrolysis at the laboratory scale. However, more work will need to be done with other potential technologies. Collaboration with different disciplines from different biomass technologies is essential to generalise the hypothesis for all technologies. Aside from using laboratory equipment, collaboration with experts in simulation software such as HYSIS could be another alternative approach.

VEGETATION CLASSIFICATION USING GOOGLE MAPS IMAGERY: A CASE STUDY IN MALAYSIA (CropB1-009)

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Abstract

Emerging from the demand for continuous food supply, agriculture is considered one of the most basic and important economic sectors throughout human history. However, with more than 7 billion people living in the world today, the demand has become higher than ever before. In order to meet these demands while only having limited resources at hand, agriculture producers have had to develop efficient crop management practices capable of controlling and directing crop growth. During the past decades, agriculture has been transformed a great deal, thanks to the rapid development of technologies. In particular, the most significant movement is the shift towards precision, or so called site-specific management. Technological advances have provided us with useful information for monitoring crop growth as well as detecting different plant stressors that may result in reduced productivity. There are a large variety of analytical approaches ranging from the identification of spectral signatures of plant species, water or soil to the measurement of their thermal radiation. Among them, vegetation classification (VC) has been an active research area for the past three decades. However, remote sensing data is not always available nor is its quality always guaranteed, as rural and developing areas are generally not profitable enough to justify the required coverage. Due to the high cost of remote sensing resources, VC has typically been restricted to a limited number of areas and plant species. The lack of information is also a main driver to the current unbalance in cultivation. Over 7000 plant species are being grown by humans for food and yet only three of these (i.e. maize, wheat and rice) supply half of the world's daily demand. Current food security is extremely dependent on these main crops and any yield loss may lead to a dramatic consequence. By studying the potential of underutilised crops, Crops for the Future Research Centre (CFFRC) believes that it is possible to find alternative supplies that can satisfy world demand, providing more flexible solutions to ensure food security. Therefore, as a part of CFF's CropBase project, we aimed to tackle the VC problem by targeting underutilised crops and using Google Maps as an alternative data source. During our preliminary experiment, we sampled 5 Malaysian plant species (namely Coconut, Palm, Durian, Mango and Rubber) with contrasting criteria and reported the performance of 8 common classifiers on this new dataset. Overall, the results have shown the dominance of Deep Belief Networks despite its lengthy training time (more than 7000 seconds); the superiority of Random Forests over AdaBoost.M1 in terms of boosting by ensemble; as well as the issue of biased classification on noisy Google Maps images (detected in half of the classifiers).

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ASSESSING THE ROLE AND THE CULTURAL VALUE OF UNDERUTILISED CROPS IN THE SMALLHOLDER SYSTEMS OF SRI LANKA (CropB1-sup1)

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Abstract

Sri Lanka, being an island in the tropical region, endowed with natural resources and diverse climatic conditions, is characterised by a dual economy with a commercial plantation crop sector and a subsistence, small farming sector, producing paddy and other subsidiary food crops. Cultivation of many varieties of crops with marked specialisation of production on the basis of agro ecological zones is prominent in its farming systems. However the nature of some of these crops, including underutilised cereal crops, suggest that the capacity of these farming systems to contribute to agricultural and rural development strategies, is worth investigating. While the assumption has long been that rural development activities benefit people, inadequate attention has been paid to the complexity of rural livelihoods. It is widely recognised that agricultural development disproportionately benefits the rural poor and many development programmes have focused on single household activities, neglecting the importance of external policy and institutional environment in overcoming poverty. Such approaches, overlooking existing smallholding and promoting larger scale monocultures, may not maximise the value of agricultural production in developing countries. The general objective of this study is to investigate whether appropriate strategies can be devised to improve the livelihood of small-scale farmers, based on the existing strengths of traditional farming systems.

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ECONOMIC VALUE PREDICTION SYSTEM FOR UNDERUTILISED CROP TO IMPROVE ECONOMIC GROWTH OF RURAL COMMUNITIES (CropB1-012)

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Abstract

The project deals with developing a model to predict the improved rural GDP through the use of renewable energy systems to cultivate suitable underutilised crops and commercialise related products. This effort not only reduces migration of young people to towns and cities for job opportunities, it also provides a methodology from which highly nutritious food (organic underutilised crops) can be produced at a cost level comparable to normal crops by using renewable energy. This can be done by training the SVM to recognise villages by significant variables that improve GDP through use of an economic model that can identify these variables and label them appropriately. For example, village "A" with characteristics that will allow profitable cultivation of underutilised crops using renewable energy systems is predicted using the designed model. Among the machine learning algorithms available, Support Vector Machine was selected to perform the prediction of economic growth in rural area in this project due to strong generalisation properties of SVM to perform well in modeling the complex, real world problems. Robustness of SVM in respond to uncertainty makes this machine learning technique superior in this project in comparison to other algorithms. In this project, high dimensional data set is acquired to perform the prediction in order to mimic the real world as much as possible. Knowledge based system is then formed as a decision making support system containing the crops database. Applying Case Based Reasoning cycle (Retrieve, Reuse, Revise and Retain) to the model assesses the chances of economic success of underutilised crops in the market. By proposing this hybrid data mining, case based reasoning and crop based modeling, this study aims to assess and optimise the economic value of underutilised crops to be economically comparative with the cash crops that have already achieved economic success. It is found that the four main economic factors that caused the underutilised crop to be neglected are gap between current economic value and potential economic value of underutilised crops, absence of output market for underutilised crops, market imperfections and market failures. Hence, the proposed technologies play the role of optimising the economic value of underutilised crops and the proposed model aims to assess economic value of the crops in order for neglected crops to be as competitive and successful as cash crops that are widely available on the market. The knowledge based system that will formed subsequently acts as a decision-making system for farmers to properly cultivate underutilised crops. All in all, this framework will be used to aid underutilised crop production by learning from existing crop model through exploring and understanding interactions between crop production and marketing and transferring this knowledge to underutilised crops.

