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Review Article

Sago Palm (*Metroxylon sagu* Rottb.): Now and Beyond

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ABSTRACT

The sago palm (*Metroxylon sagu* Rottb.) is one of the underutilized food crops that has the promising potential to strengthen food security program especially in Sarawak, Malaysia. Thriving well in harsh environments such as the freshwater swampy area, the sago palm is also unique for its ability to store starch within its trunk, compared to other types of starch storage organs. With its superb high starch yield as compared to commonly found starch sources such as the corn, rice and wheat, it is deemed as the palm of many uses. Researches sprouting from this unique palm come from various fields of study, namely microbiology, food technology, polymer synthesis, bioprocess technology and most recently, computational biology. In this review, we presented a survey of recently published results from each field and further provided future recommendations and knowledge gaps to be filled. It is hoped that with the consolidation of research talents and funding from around the world, the sago palm industry will be matured in time to equip mankind with the solutions to combat the oncoming global food scarcity issues.

Keywords: Food crop, food security, industry, starch yield, underutilized

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INTRODUCTION

The sago palm (*Metroxylon sagu* Rottb.) is a true palm classified under the order Arecales, family Palmae and subfamily Calamideae. This palm can thrive well in low-land freshwater swamp and tropical rain forests and it is native to Southeast Asia including Papua New Guinea, Malaysia and

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Indonesia (Johnson, 1977). It is one-of-its-kind underutilized crop that stores starch in its trunk instead of legumes, cereals and tubers. With the capability to yield starch three- to four-fold to that of corn, rice and wheat as well as 17-fold to that of cassava (Karim et al., 2008), it has the potential to strengthen food security program (Husaini et al., 2016; Ehara, 2009).

The sago palm can grow up to the height of 10 to 15 metres with diameter of trunk reaching 35 to 75 centimetres (Kiew, 1977; Kueh, 1977). Photosynthesis are carried out throughout the seven to fifteen years of vegetation phase where nutrients generated from the leaves are channelled to the trunk for long term starch storage, filling the trunk with starch (Lim, 1991). Flowering occurs at palm's full maturity after eight to twelve years and the fruiting process follows. The palm death is foreshadowed by the event of the mature fruit falling off (Kueh et al., 1987). In Sarawak, the growth stages of sago palm are characterized into five stages: "*Plawei*" where the palm at maximum vegetative growth, "*Plawei Manit*" where the emergence of inflorescence occurs, "*Bubul*" where the development of inflorescence takes place, "Angau Muda" where flowering happens and "*Angau Tua*" where fruiting ensues (Lim, 1991) as depicted in Figure 1. While the "*Plawei*", "*Plawei Manit*" and "*Bubul*" stages show no significant differences in terms of starch yield (Lim, 1991), the "*Angau Muda*" stage is the only stage where the greatest starch yield per trunk can be found at 39% to 41% on dry weight basis (Lim, 1991; Pei-Lang et al., 2006) among all other stages, producing 216 to 219 kg of starch (Hamanishi et al., 1999).

The sago palm is a cash crop with high economic value as different parts such as frond, leaf petioles, sap, pith and even the "*hampas*" (fibrous residue) are valuable raw materials for various industries (Singhal et al., 2008). The sago starch is one of the highly utilized part of the palm in polymer, pharmaceutical, food and textile industries (Ishiaku et al., 2002; Nuttanan et al., 1995; Purwani et al., 2006; Radley, 1976).

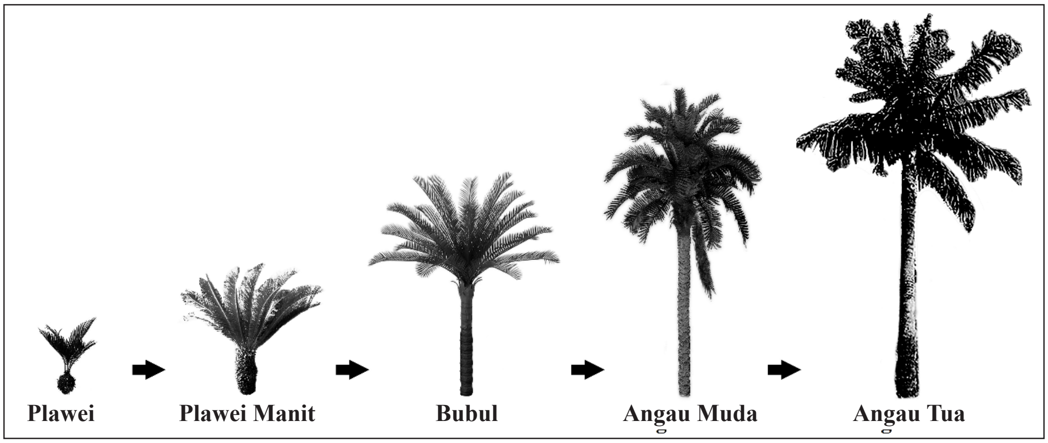

Figure 1. The five developmental stages of sago palm, namely: Plawei, Plawei Manit, Bubul, Angau Muda and Angau Tua

Besides, the papermaking and thatching are perfected with the use of sago fronds as raw materials due to its high durability (Jamaludin et al., 1995). The sago "*hampas*" is not wasted as it has been utilized widely as biosorbent, animal feed, fermentable sugar and microbial conversion agent via solid state fermentation (Awg-Adeni et al., 2010; Bujang et al., 1996; Kumaran et al., 1997; Vickineswary et al., 1994). With many more on-going researches in the fields of microbiology, genetics, bioprocess technology, population studies, food technology, sago waste management, computational biology and phenotypic variations, the undiscovered potential of the sago palm is limitless. In this review, we will highlight on the current sago palm research progress in the respective fields and further provide future directions and potentials.

Microbiology

The microbiotas exist within and surrounding the sago palm are getting into the limelight of sago-related research as the microbial activities within the palm affects the quality of the starch and the surrounding microbiota interactions affects the palm growth greatly (Toyota, 2018). The cultivation of the sago palm is generally under unfertilized conditions, the acquisition of nitrogen of this palm is greatly dependent on the nutrient-furnishing ability of soil which is driven by the decomposition of soil organic matter by animals and soil microbiota (Toyota, 2018).

The nitrogen-fixing microbiota exploration in sago palm has successfully isolated a myriad of nitrogen-fixing bacteria such as *Enterobactor cloacae*, *Klebsiella pneumoniae*, *Bacillus megaterium*, *Pantoea agglomerans* and *Klebsiella oxytoca* from various parts of the palm, namely root, trunk, bark, midrib and starch (Shrestha et al., 2006). Further investigation on the microbial interactions between these nitrogen-fixing bacteria and different indigenous bacteria that were both isolated from the same sago palm sources showed higher nitrogen-fixing activities in almost all amalgamations tested than single culture of these nitrogen-fixing bacteria (Shrestha et al., 2007). At the end of these study, they left an open window for isolation of anaerobic, uncultivated or slow-growing bacteria that are believed to have beneficial roles in nitrogen-fixing interactions (Shrestha et al., 2007).

Shipton et al. (2010) attempted to isolate nitrogen fixers particularly diazotrophic bacteria in pith and rhizosphere of the sago palm. Nitrogen fixers were found in moist starch compared to that in pith, suggesting that these bacteria might have been originated from the soil. They further suggested that fixed nitrogen was the key element in sustaining the growth of numerous toxigenic and pathogenic microbiota in sago. A study on bacterial pathogens and mycological screening of the traditionally prepared sago starch in Papua New Guinea found that three quarter of the sample was high in faecal coliforms and filamentous fungi from the genera *Scytalidium*, *Acremonium*, *Penicillium* and *Aspergillus* (Greenhill, 2006). It is believed that a more detailed study on the haemolytic metabolites released by fungi found in sago starch can aid in garnering further understanding on the aetiology of sago haemolytic disease that has caused foodborne illness to the people of Papua New Guinea.

Genetics and Omics

There are not many molecular studies conducted on sago palm to date, and the ones being reported are in the field of genetics, transcriptomics and proteomics. In terms of genetics, a number of genes has been isolated from the genome of the sago palm, including the GA20-oxidase, ADP-glucose pyrophosphorylase, xylanase, fructose-1,6-bisphosphate, chloroplast petD and chitinase gene (Jamel et al., 2011; Roslan & Anji, 2011; Wee & Roslan, 2012b). With a total of 1465 nucleotide sequences (1053 nucleotide entries and 412 EST entries) being deposited to the GenBank database to date, this number is merely 0.028% of that available for the maize plant with a total of 5,200,499 nucleotide sequences deposited despite the huge potential of sago palm to emerge as future cash crop in future for its disease-free superior characteristics (Sasaoka et al., 2014).

In terms of the transcriptomics of the sago palm, Wee and Roslan (2012a) had performed transcriptome analysis via the construction of cDNA library to discover the expressed sequence tags (ESTs) from young leaves of sago palm. Upon functional annotation, there were 49 ESTs found to have stress tolerance functions in which reactive oxygen species (ROS)-combating enzymes such as glutathione S-transferase, alcohol dehydrogenase class III and ascorbate peroxidase were found (Wee & Roslan, 2012a). Besides, defence-related enzymes such as class I chitinase, cytosolic ascorbate peroxidase and cysteine protease are discovered, and they are believed to have contributed to the strong disease defence mechanism found in young sago palm allowing it to thrive in harsh conditions (Wee & Roslan, 2012a). Wee and Roslan (2012a) concluded that 5.38% of ESTs studied were novel to sago palm and that this palm was a great reservoir for the study of defence- and stress-related proteins.

The proteomics aspect of the sago palm has only been explored at the tip of an iceberg only as it is only used as a comparison tool to distinguish trunking from non-trunking sago palm to date (Hussain et al., 2012a). This aspect will be discussed in detail in the phenotypic variation studies section below. Apart from transcriptomics and proteomics, another approach is currently being employed in sago palm study is based on metabolomics analysis (Hussain et al., 2012b). The metabolites in leaf of sago palms are analysed using nuclear magnetic resonance spectroscopy (NMR) and gas chromatography-mass spectrometry (GC-MS) (Hussain et al., 2012b). These are to determine differential metabolites in non-trunking and trunking sago palm. Current study shows several metabolite groups such as haloalkanes, sulfite esters and phosphonates which are differently expressed between trunking and non-trunking sago palm (Hussain et al., 2012b).

The genomic research of the sago palm is on-going with the plans on the study of trunk formation and starch biosynthesis pathways (Roslan, 2012). The sequencing of the nuclear genome as well as the organellar genome (mitogenome and plastogenome) which would help us understand more on the mechanisms behind the ability of sago palm to adapt to harsh environment and stresses. Furthermore, genome-wide enhancer studies can also be conducted to aid in the understanding of the contributors towards the high adaptability of this palm at the molecular level, emulating researches that have been done onto some plant model organisms like *Zea mays* and *Arabidopsis thaliana* (Lim et al., 2018a; Lozano et al., 2018; Marand et al., 2017; Weber et al., 2016; Zhu et al., 2015; Zicola, 2017).

Bioprocess Technology

The sago starch is the one of the most utilized part of the palm in the field of bioprocess technology to produce bioethanol, lactic acid and sugar. The research involving the simultaneous saccharification and ethanol fermentation of sago starch started back in the year 1986 by Lee et al. (1986) using amyloglucosidase and immobilized *Zymomonas mobilis*. Since then, the goals in this field of research were always targeting at high ethanol yield in terms of both quantity and quality via the optimization of various parameters such as starch concentration, pH, enzyme and nitrogen concentration (Bujang et al., 1996; Mel et al., 2010; Niyong, 2012).

In 2010, two pre-production stages were introduced prior to the bioethanol synthesis, namely the hydrolysis and fermentation (Mel et al., 2010). The enzymes used are glucoamylase and α-amylase for the saccharification and liquefaction step respectively (Mel et al., 2010). This study has determined the optimal conditions for the hydrolysis step in bioethanol production in terms of glucoamylase enzyme concentration, sago starch concentration and time of saccharification (Mel et al., 2010). For the bioethanol fermentation step, factors such as agitation, pH, and inoculum concentration are optimized (Mel et al., 2010). Not long after, Niyong (2012) attempted the “Ishizaki Process” in the continuous fermentation of bioethanol and had determined the optimal nitrogen concentrations from three different sources: corn steep liquor, yeast extract and Mieki. In 2017, several strains of solvent-tolerant *Clostridium* sp. were employed for biobutanol synthesis directly from sago waste residues and the NSW strain was found to be the most suitable candidate that had the potential to replace *Bacillus coagulans* (Johnravindar et al., 2017).

The lactic acid fermentation is another prominent and indispensable role of sago starch in the bioprocess field, employing lactic acid bacteria such as *Lactococcus lactis IO-1* and *Enterococcus faecium* (Hipolito et al., 2000; Shibata et al., 2007). The amylolytic lactic acid bacterium, *E. faecium* that was identified and utilized by Shibata et al. (2007) on sago starch yielded productivity comparable to that of glucose and the lactic acid yield was the top among all other starches tested. Hipolito et al.

(2012) further improved the lactic acid yield from sago starch by using the repeated batch fermentation approach, which was proven to be much more effective than continuous fermentation and simple batch mode in terms of lactic acid concentration. Interestingly, Bujang et al. (2018) utilized abundantly found sago frond sugar (SFS) as a cheaper raw material alternative to produce lactate, achieving 85% fermentation efficiency in which the lactic acid amount produced was similar to that produced by the Standard Medium.

The current view is to produce sugars directly from both sago starch and sago "*hampas*", without the fermentation into bio-ethanol or lactic acid (Bujang, 2015). Production of sugars have been performed in 1 L lab-scale vessels for the hydrolysis of sago starch and the optimal parameters for enzymatic hydrolysis of sago starch has been comprehensively determined (Bujang et al., 2000a). The enzymatic hydrolysis of sago starch involves the utilization of Termamyl-12OL (a thermostable -amylase from *Bacillus licheniformis,* 120 KNU/g) for liquefaction (0.5µl/gram of starch), followed by incubation at 90^{o}C for 2 hours (Bujang, 2015). Next, Dextrozyme (a mixture of pullulanase from *Bacillus acidopullulyticus* and glucoamylase from *Aspergillus niger*, 225 AGU/ml) are employed for saccharification (0.6µl/gram of starch), before incubation at 60^{o}C for another four to six hours to yield hydrolysed sago sugars (Bujang et al., 2000b [as cited in Bujang, 2018, p. 300]; Bujang & Jobli, 2002) which generates a 100% glucose recovery from sago starch (Bujang, 2015). It has also been previously established that the optimum starch concentration is at 20% (w/v) sago starch (Bujang et al., 2000a; Bujang et al., 2004), harvested from best pH of 6.5 for liquefaction as well as pH 4.5 for saccharification (Bujang, 2015). Future research in this field will be focusing on improving the reusability of cells to withstand higher fermentation cycles (Hipolito et al., 2012) as well as establishing more cost-effective approaches to lower the production expenditures.

Pest Management

The cultivation of sago palm is affected by the invasion of 40 insect species known to have adverse effects on the health of the palm (Smith, 2015). For instance, the trunk of sago palm is the host for larvae of *Oryctes rhinoceros* and *Graphosoma rubrolineatum* (Kimura, 1979) whereas the leaves of sago palm are often infested by the *Psychidae* and *Monema flavescens* (crickets and locusts) (Jong, 2006; Kimura, 1979). Particularly, termites, sago beetles and hispid beetle larvae are pests vastly found in sago palm cultivation in Sarawak and Indonesia (Smith, 2015). Besides, fungal infections such as the white root diseases has been reported in young palms, but this is not lethal to the palm as there is no life-threatening disease reported to date on sago palm (Smith, 2015).

The widespread cultivation of the *Cycas* plant like the sago palm had also led to the rapid expansion of unwanted alien pests such as *Chilades pandava* on a global scale (Donaldson, 2003). Wu et al. (2010) investigated the outbreak of this pest in 50 different localities in Taiwan and had identified the source of outbreak using COII gene as marker. A total of 29 haplotypes were discovered despite the record of high haplotype diversity and this study further highlighted the importance of monitoring within the horticultural plantation field to avoid the threatening of the native species (Wu et al., 2010). Future work will involve the investigation of other gene markers to further tap into the demographic backgrounds of the introduced alien species as well as their native counterparts and it is hoped that the pest management issues can be addressed in a sustainable manner.

Population Studies

The variations within the sago palm populations were studied using markers such as isozymes, DNA methylation profiles, random amplified polymorphism DNA (RAPD), amplified fragment length polymorphism (AFLP) and chloroplast DNA markers. Boonsermsuk et al. (1995) had succeeded in distinguishing sago palm harvested from 15 populations in three different provinces in southern Thailand from the other ten palm species via zymogram techniques. From the isozyme profiles (zymogram) of esterase, sorbitol dehydrogenase, peroxidase and acid phosphatase obtained via polyacrylamide vertical slab gel electrophoresis (PAGE), low isozyme variations were detected, depicting the closely associated genetic background and very limited ancestry (Boonsermsuk et al., 1995). The AFLP (Kjær et al., 2004) and RAPD (Ehara, 2009) analysis that follows, have all come to the same conclusion, which is in line with the observations done by Rauwerdink (1986): regardless of the spiny and non-spiny phenotypes, there is only one species of sago palm across Mindanao, Philippines, Indonesia and Malaysia.

The genetic diversity of the sago palm was also explored in Indonesia employing the chloroplast DNA markers (Abbas et al., 2010). In this study, a sum of 97 individuals have contributed to the discovery of ten haplotypes and eleven alleles across Sulawesi, Papua and Kalimantan (Abbas et al., 2010). With the individuals from Papua scoring the highest in both specific haplotypes and haplotype numbers, Papua was crowned as the origin centre of sago palm diversities in Indonesia (Abbas et al., 2010). Besides, DNA methylation profiling of sago palm was conducted by Novero et al. (2012) in an attempt to distinguish spiny from non-spiny plants. Using high performance liquid chromatography (HPLC), the methylated (5dmC) and non-methylated cytosine (dC) were used as benchmark for DNA methylation patterns investigation. As a result, the significant difference in methylation percentage between spiny and non-spiny palms suggested that spine formation was indeed an age-dependant epigenetic event, accounted by the environmental conditions (wet or dry) they thrive in.

In 2017, Abbas et al. (2017) studied the sago palm genetic variations in a whole new aspect: progenies produced from natural pollination. Interestingly, RAPD genetic variations as well as morphological dissimilarities were detected, indicating the natural cross-pollination event occurring among the sago palms. This phenomenon was believed to have resulted from the genetically differing seeds and fruits of the sago palm. While the RAPD approach lacks reproducibility, it is recommended to conduct DNA fingerprinting investigations such as the sequence characterized amplified regions (SCAR) analysis onto the sago palm as a more sensitive and reproducible way to identify polymorphisms undetected by other approaches (Bhagyawant, 2016).

Food Technology and Polymer Synthesis

The food technology that evolves around the sago palm is mainly focused on the sago starch as it has the potential to channel into food security program as products such as noodles, vermicelli and sohun (Ahmad, 2013). In fact, the quality of the noodles made from sago starch were examined under the effects of heat moisture treatment and as a result, excellent elasticity and firmness as well as less cooking loss were found to be strong points of this newly emerged sago noodle (Purwani et al., 2006).

Furthermore, the sago starch oligosaccharides were employed in the growth enhancement of lactic acid bacteria in homemade yogurt with a bright potential to be developed as prebiotic health food in the near future (Shima et al., 2012). Apparently, sago sugar (glucose) has numerous health benefits, compared to consumption of sugar (sucrose) from cane sugar (Bujang, 2015). Purified (white) sago sugar, which can be harvested from both sago starch and "*hampas*" (Janggu & Bujang, 2009; Monib, 2015), was found to encompass 94% glucose content and it is a much healthier (50% less in sweetness test) alternative to sugar cane sucrose (Bujang, 2015; Monib, 2015). Due to its high carbohydrate contents, Che Jusoh et al. (2016) foresaw the feasibility of the sago starch, in terms of its chemical and physical characteristics, as one of the underutilized supplement sources in the peri-exercise period for sustaining performance and enhancing recovery.

Besides, sago frond sugar (SFS) containing 16% to 18% cellobiose and 9% to 11% glucose, has been synthesised from enzymatic hydrolysis of sago frond (as dried powder) where these prebiotic cellobiose are employed in the fermentation of dairy products associated with bifidobacteria (Ahmad, 2015; Awg-Adeni et al., 2018). Gunawan et al. (2018) had recently succeeded in increasing the nutritive value of sago flour in terms of amylose and protein content by 20% to 33% and 1.4% to 4.1% respectively by optimizing bacterial count and fermentation time. The sago food technology field will be further placing major focus onto presenting the sago starch as a cheaper carbohydrate alternative to currently available starch products and shifting the consumer base paradigm towards the acceptance of this dark horse of the food industry.

In the field of polymer synthesis involving the sago palm, Muljana et al. (2016) had pioneered the transesterification approach of sago starch and waste palm cooking oil in the production of thermoplastics starch using densified carbon dioxide as a solvent. The end product was found to have improved thermal stability and hydrophobicity compared to native sago starch and this study serves as a green movement in plastics synthesis towards the utilization of biodegradable compounds, safer solvent as well as renewable feedstocks for the environment (Muljana et al., 2016).

Sago Waste Management

The sago waste comes in two forms: sago solid waste ("*hampas*") and sago wastewater. The sago "*hampas*" encompassing 60 to 70% starch on dry weight basis (Vickineswary et al., 1994) is very useful in various applications such as animal feed, production of laccase by solid state fermentation, biosorbent, particle board production, fermentable sugars and compost for mushroom cultivation (Awg-Adeni et al., 2010; Kumaran et al., 1997; Linggang et al., 2012).

Recent sago "*hampas*" research has been moving towards bioethanol synthesis via fermentation (Awg-Adeni et al., 2013; Bukhari et al., 2017). Awg-Adeni et al. (2013) attempted to hydrolyse sago "*hampas*" via three enzymatic treatment cycles and had achieved improved glucose yield and greater conversion yield in which these substrates will be fed into bioethanol synthesis process. Bukhari et al. (2017) further optimized the conditions for acid hydrolysis and enzymatic digestion to make sago "*hampas*" feasible for bioethanol production. They had also proven that 98% ethanol harvest was achievable in the absence of nutrients and nitrogen as higher yield and conversion rate was determined in acid hydrolysis compared to that of the enzymatic hydrolysis.

The sago wastewater is also a valuable resource for cultivation. The cultivation of *Rhodopseudomonas palustris* strain B1 in 50% sago wastewater had not only produced useful biomass supplement for prawn feed, but also reduced chemical oxygen demand (COD) by 77% (Vickineswary et al., 1997). Phang et al. (2000) had successfully cultivated *Spirulina platensis* (Arthrospira) in sago wastewater with an upflow packed bed digester. They had accomplished 98%, 99.4% and 99.9% reduction of COD, phosphate level and ammoniacal-nitrogen level in digested effluent respectively (Phang et al., 2000). Moreover, various treatments had been proposed to treat sago wastewater before disposal into the environment. For instance, Saravanane et al. (2001) had attempted a fluidized bed reactor approach and attained maximum efficiency of 82% with the digested sludge being vital for agricultural utilization. Banu et al. (2006) proposed to treat sago wastewater with Hybrid Upflow Anaerobic Sludge Blanket (HUASB) reactor and had resulted with the success of 87 to 91% COD reduction and 67 to 70% total solid removal. Priya et al. (2015) further improved the HUASB reactor with the addition of effective microorganisms and the outcome was promising with 88% and 77% reduction in COD and total suspended solids respectively. Using response surface methodology, Sangeetha and Sivakumar (2016) converted sago wastewater into biogas, resulting in 91.61% BOD reduction and 81.85% COD reduction as well as 99.4 ml/day biogas yield. Further directions in this field will be in the discovery of conditions to increase product yield and the design of low-cost treatment system with short retention periods.

Phenotypic Variation Studies

The sago palm can usually be harvested upon the 6th to 8th years of growth under normal growth conditions, however some palms tend to remain in its stunted growth state even after 10 to 14 years (Hussain et al, 2012a). The non-trunking phenotype of the sago palm (Figure 2) is deemed to have depreciation economic value to the sago palm planting industry. There are several researches that aimed to study the differences between the trunking and non-trunking sago palms in terms of proteomics, starch granule sizes and gene profiling.

In terms of proteomics, Hussain et al. (2012a) had identified that there were indeed differential protein expression profiles between trunking and non-trunking sago palms. Kamal (2014) further employed two-dimensional gel electrophoresis and matrix-assisted laser desorption/ionization-time of light/time of flight mass spectrometry (MALDI-TOF/TOF MS) analysis to discover the differential proteins originating from five different protein families. These proteins identified were postulated to have contributed towards the phenotypic makeup (physical characteristics) differences across trunking and non-trunking sago.

Figure 2. The sago palm tree on the right is one of the many trees that expresses the non-trunking phenotype whereas the sago palm tree on the left is its counterpart that depicts the trunking phenotype

Alias (2012) had studied the phenotypic differences between trunking and non-trunking sago palms in terms of their starch quality. The starch content and starch granule sizes did not show any significant differences between trunking and non-trunking sago palms. The starch granule size of both trunking and non-trunking sago palms were reported to be in the range of 10 µm to 20 µm from the trunk as well as 1 µm to 5 µm from the leaves (Alias, 2012). Moreover, distinct transcript patterns were also observed in leaf samples harvested from trunking sago palm in comparison to that of its non-trunking counterpart (Edward, 2013). Future researches in this field of study will be placing the limelight onto the genetic markers that can act as a diagnosis tool to distinguish trunking progenies from non-trunking ones at early stages of the palms to help reduce the economic loss in the industry.

Computational Biology

The utilization of computational biology on the sago palm is a brand new field to be explored in the future. With only one research published recently, to the best of our knowledge, it opens up vast possibilities in the future digital world. Based on the needs for near-real-time geospatial information on sago palm stands, Hidayat et al. (2018) had developed a semi-automated classification system in the sago palm mapping by the means of employing object-based image analysis outline with Pleiades-1A imagery.

Hidayat et al. (2018) considered various parameters such as spectral, textural, geometric and arithmetic characteristics to further improve the support vector system (SVM) classification accuracy up to 85%. The sago palm tree classification remains a daunting task, with the scattered distributions, similar spectral features it shares with nipa and oil palm as well as its ununiformed spatial patterns of the cultivation (Hidayat et al., 2018). Future directions of this field will be driven by the improvement of sampling approaches for more accurate measurement of segmentation, atmospheric and geometric corrections via multi-strip images (Hidayat et al., 2018).

CONCLUSION

The sago palm is one of the most promising food crops and cash crops in the future to cater to the increasing world demand for food each year. It is hoped that with the addition of new knowledge from this palm species from various fields, the research database for the endemic flora and fauna in Sarawak will be further enriched (Kadir et al., 2013; Lim et al., 2018b, 2019, in press; Ministry of Natural Resources and Environment [MNRE], 2016; Phillips, 2016; Soepadmo & Wong, 1995), adding data to enable for the study of biodiversity ecosystem in whole. With its utilization in various important fields are being realized throughout the years, it is essential that we consolidate all talents and funding towards the research of this underutilized food crop in the light of providing food security to the needy in time of world food scarcity.

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