

*Review article*

## **Salt Tolerance Research in Sago Palm (*Metroxylon sagu* Rottb.): Past, Present and Future Perspectives**

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### **ABSTRACT**

The sago palm (*Metroxylon sagu* Rottb.) is one of the underdogs in the food crop planting industries for its potential which is extremely vast but the community appreciating it is scarce. Its capabilities to thrive well in undesirable environmental conditions, salt tolerance and high starch yield are one of the many advantages it possesses over other food crops like wheat, corn and rice. One important factor to look into for crop plantation is none other than its salt tolerance. The salt tolerance researches on this unique palm have commenced since 1977 and the pace of research was unbelievably slow in progression. Nevertheless, it was not until recently that this palm was being placed in the limelight once more. In this review, we are focusing on salt tolerance research and further detailed on the past, present and future of this research line. It is anticipated that consolidation of talents and resources can come in time and in tandem for the utilization of this cash palm to end world hunger.

*Keywords:* Food crop, food security, sago palm, salt tolerance, starch yield

### **INTRODUCTION**

The sago palm (*Metroxylon sagu* Rottb.) is a true palm Calamidae subfamily member categorized under the order Arecales and

family Areaceae. This palm is native to Southeast Asia countries like Malaysia, Philippines, Papua New Guinea and Indonesia, thriving well in tropical rain forests as well as low-land freshwater swamps (Johnson, 1977). The sago palm is a hapaxanthic (only flowers once per stem) multiple-stemmed type of palm and its flowers emerge from the upright terminal of its 10 to 15 metres stem (Kiew, 1977; Kueh, 1977).

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The sago palm undergoes a period of stemless vegetative growth with 175 cm leaf blades extending from its base (Lim, 1991). Upon elongating its stem up to its maximum height, its once-per-lifetime inflorescence develops where spirally arranged flower pairs emerge from the third-order branches encompassing a male and hermaphrodite flower prior to fruiting (Kueh et al., 1987; Lim, 1991). The palm reaches the end of its lifecycle upon bearing fruit and usually the best time to harvest the heavily starch-packed trunk is before the flowering stage in which the starch content is maximal (Hamanishi et al., 1999; Lim, 1991; Pei-Lang et al., 2006). The trunk of the sago palm is not the only plant organ with high economic value (Ehara, 2009; Husaini et al., 2016; Karim et al., 2008), the list goes from the leaf petioles, fronds, pith, sap and down till the fibrous residue ("*hampas*"), all of them playing major roles in industries like renewable energy, textile, pharmaceutical, food as well as polymer (Ishiaku et al., 2002; Nuttanan et al., 1995; Purwani et al., 2006; Radley, 1976). In the field of research, the sago palm is one palm that is progressively moving into the limelight, tapping into fields like microbiology, plant biology, sago waste management, bioprocess technology, computational biology, genetics and phenotypic studies (as reviewed by Lim et al., 2019c).

One of the most famous investigations in the fields of plant biology, physiology and genetics is no other than the salt tolerance research. Salt tolerance research, or widely known as salinity test or salt

stress investigations, is one important field of research to determine the survivability of plants (especially essential food crops) against salt-inducing environment. Under salt stress, plants generally tend to cease in terms of water and essential elements absorption as well as photosynthesis due to the sudden plummet in water potential in soil and turgor pressure in cells (Kaku, 1996). Almost all crops suffer from mortality at a threshold NaCl level of 100 mM and beyond, however halophytic plants like the sago palm is vastly known to have the capability to withstand this salt stress using its exclusively equipped mechanisms (Matoh, 1999). Some halophytic plants like the sago palm can uptake salts from the root system to prevent metabolic interruptions via the cancelling of osmotic pressure gradient between cytoplasm and vacuoles as a result of high salt level (Matoh, 1999). Osmoregulating compounds, at this time, play their roles in restoring the osmotic pressure gradient and those who do not disrupt the metabolic activities when present in high concentrations are known as compatible solutes and they are usually low in molecular weight (Nakamura & Takabe, 1999). Some of the well-known compatible solutes are proline, sugar alcohols, glycine betaine and inorganic ions (Wada, 1999). Besides,  $K^+$  absorption mechanism is also found in the sago palm, although it is rarely found in other crops, facilitating it in terms of selective  $K^+$  absorption (Tadano, 1986; Yoneta et al., 2006). These mechanisms involve various metabolic pathways and genes in the sago palm, in which our

knowledge on these are very much limited and still in its infancy. In this review, we place-focus on salt tolerance research and further detailed on the past, present and future of this research line in hope to consolidate talents and resources in the utilization of this cash palm to end world hunger.

### **Impact of Soil Salinity on Sago Palm**

The sago palm naturally inhabits along the banks of rivers, swamps and lakes, is equipped with strong adaptability towards land from sea level up to 1.2 km elevation (Schuiling, 2009). The optimal growth habitat for this palm is below 0.4 km elevation where its growth performance (speed and yield) starts to decline at elevations exceeding the abovementioned altitude (Djoefrie, 1999). A much more miniature trunk diameter and diminished height (6 metres difference) was observed on sago palm trees planted at above 0.6 km elevation (Schuiling & Flach, 1985).

A vast variety of soil can support the growth of the sago palms and they are divided into developed and undeveloped soils (Notohadiprawiro & Louhenapessy, 1992). Developed soils like tropohemists and sulfihemists, trophaquepts, thaptohisthic fluvaquents as well as troposaprists of peatlands are proven conducive for sago palm growth (Notohadiprawiro & Louhenapessy, 1992). The psammaquents, hidraquents, fluvaquents, sulfaquents and trophaquents are undeveloped soils that can sustain optimal sago palm growth (Notohadiprawiro & Louhenapessy, 1992). Under swampy

conditions, sago palms can thrive well in concentrated levels of organic matter and mineral nutrition, without pneumatophores being submerged, as well as marginally acidic brownish stagnant water, all in which favours the propagation of microbiota benefiting sago palm development (Bintoro et al., 2010). In swampy areas situated in close proximity to the ocean, these palms are hardy towards salinity, especially sodium ions where excess sodium ions are stored in the root organ. The photosynthetic activities of the sago palms are not affected up to the salt concentration of 0.2 M (Yoneta et al., 2006).

Moreover, soils with podzolic, alluvial, volcanic, hydromorphic and grumusol properties are all suited to the growth betterment of the sago palms (Djoefrie, 1999); provided that the optimal amount of microbiota and nutrients (potassium, phosphorus and magnesium) are abundantly available (Haryanto & Pangloli, 1992). On the side note, starch synthesis can be easily halted under over-waterlogged environmental conditions (Haryanto & Pangloli, 1992). The peatlands, consisting of great level of organic matter (C-organic > 18%) and more than half a metre organic matter depth, are also supportive of the sago palm optimal growth (Agus & Subiksa, 2008). Majority of sago palms in Malaysia are planted on peatlands but their productivities are very much affected by the lack of minerals in soil. For instance, the time of harvest can be shortened by 2.9 years if the palm was planted in mineral soil as compared to peat soil (Kueh et al., 1991).

Besides, the leaf amount of sago palm is 4% to 35% fewer when it is planted in peat soil than those planted in mineral soil (Bintoro, 2008; Flach & Schuling, 1991). Indirectly, the dry starch content of sago palm is found to have diminished by 29.6% to 82.1% when planted in peat soil in comparison to mineral soil (Sim & Ahmad, 1991).

The period for the initiation of maturity phase (rosette phase) in sago palm tends to be lengthy than usual when it is being subjected to suboptimal growth conditions, delaying the emergence of new leaves and starch synthesis (Flach et al., 1986). According to Bintoro et al. (2018), the high salt and hydrological tolerance of the sago palms have granted them great economic advantage over other food crops beside the high yield as they can literally thrive in almost all harsh environments where other plants can hardly survive.

### **Salt-adaptation Capacity of Sago Palm**

The sago palms, like other halophytic plants, are naturally equipped with specific mechanisms to orchestrate salt uptake and strengthen their immunity against adverse salt effects, enabling them to thrive with brackish waters (Okazaki & Sasaki, 2018). Back in the year 1977, Flach et al. (1977) was one of the first to initiate investigations on the salinity of sago palms and it was found that this palm can survive in solutions with up to 12.5% to 14.3% of electrical conductivity (which corresponds to salinity) to that of seawater where any concentrations beyond had declined in the growth of sago palms.

Generally, terrestrial plants experience salt stress when exposed to a salt level of 0.1% (around 20 mmol L<sup>-1</sup>) and growth ceases significantly when the level is beyond 0.3% (Matoh, 2002). However, it was discovered that sago palm seedlings depicted the best growth pattern at salt concentration of 0.05% (around 10 mmol L<sup>-1</sup>) NaCl solution, especially when compared to 0% NaCl solution (Yoneta et al., 2004, 2006). It was not until the salt concentration of around 50 to 200 mmol L<sup>-1</sup> (0.25% to 1.0 %) that the growth performance started to deteriorate (Yoneta et al., 2004, 2006). There are two types of salt stress, namely ionic stress and osmotic stress (Okazaki & Sasaki, 2018). The ionic stress is the primary factor of salinity stress where it involves the excess mutilation induced by salt-composing ions that pose specific physiological adverse effects (Okazaki & Sasaki, 2018). On the other hand, osmotic stress refers to the hindrance of water uptake induced by the osmotic pressure due to the presence of high salt level from the environment (Okazaki & Sasaki, 2018).

The sago palm is a special food crop with incredibly high salt tolerance and the following are some of the known mechanisms against salt stress. Sago palm tends to transport excess Na<sup>+</sup> ions from the roots to the leaflets and petioles when being subjected to 0% to 0.2% NaCl solution but it is not the case for sago palm seedlings as seedlings prefer to stockpile Na<sup>+</sup> ions within the roots and progressively transporting these ions to the lower leaves (Ehara et al., 2006). The transpiration rate of the sago

palm was also found to decrease with the elevating levels of NaCl in the treatment solution and at the same time the level of potassium ions in the petiole rises (Ehara et al. 2008). In order to sustain the high osmotic pressure of the cytoplasm, sago palm employs a brilliant strategy to surge the uptake of compatible solutes like glycine betaine, potassium ion and proline to function as orchestrator of osmotic pressure (Yoneta et al., 2006). Furthermore, the sago palm was also discovered to have a unique way to halt the absorption of excess Na<sup>+</sup> ions via its special barriers (Ehara et al., 2003, 2006).

### The Past

The past researches involved the investigations on salt tolerance capability of the sago palm in terms of plant biology and physiology. In other words, the sago palm is tested on their response to NaCl physically and chemically. One of the first salinity investigations on sago palm was that by Flach et al. (1977) where they discovered that the growth of the sago palm was not halted in a Hoagland solution with six to seven millisiemens (mS) per cm electrical conductivity. This electrical conductivity unit is equivalent to around one eighth to one seventh to that of seawater (Flach et al., 1977). A study by Hirotsu et al. (2002) unravelled that proline and glycine betaine were produced in both *Metroxylon* genus counterparts, namely *M. sagu* and *M. warburgii* when they were subjected to salt stress. Similarly, it was discovered that *M. sagu* tended to synthesise 0.16 to 3.0 mg kg<sup>-1</sup>

dry weight of glycine betaine when induced by salt concentration ranging between 0 to 200 mM (Yoneta et al., 2003).

In the year 2006, Yoneta et al. (2006) performed a NaCl stress investigation by immersion of sago palm seedlings grown in 5 L plastic pots into 6 L plastic pots at various salt concentrations, namely 0, 10, 50, 100, 200 and 400 mM. The greatest growth of sago palm was in the ones being subjected to 10 mM NaCl and growth was stunted at concentrations beyond 50 mM (Yoneta et al., 2006). In this study, the highest glycine betaine was found in the 200 mM NaCl treatment set, and overall there was no correlation between glycine betaine and NaCl level (Yoneta et al., 2006). Ehara et al. (2006) compared the salt accumulation in different organs of the sago palm seedlings, namely root, petiole and leaflet, between treated (86 mM or 0.5% NaCl) and non-treated samples. The Na<sup>+</sup> accumulation in the roots was found to be 5.3 to 6.6 times that of the negative control whereas the petioles were discovered to store 1.7 to 8 times more Na<sup>+</sup> than the negative control (Ehara et al., 2006). Generally, the lower positioned petioles stored more Na<sup>+</sup> than the upper positioned petioles in both negative control and treated samples (Ehara et al., 2006). The leaflets Na<sup>+</sup> accumulation was found to be 4 times higher in treated samples as compared to negative controls and they were all had lower levels of Na<sup>+</sup> in comparison with petioles in all positions (Ehara et al., 2006). However, the K<sup>+</sup> level tended to be higher in upper positioned petioles and leaflets than the lower ones.

Despite the differences, the correlation between  $K^+$  and  $Na^+$  concentrations was not significant (Ehara et al., 2006). In the same study, Ehara et al. (2006) tested the sago palm seedlings with different NaCl concentrations (0.5%, 1.0% and 2.0% NaCl) and yet the  $K^+$  concentration change was negligible. The transpiration rate of samples treated in 2.0% NaCl was also found to be 65% that of the negative control set (Ehara et al., 2006). They concluded that the sago palm exhibited avoidance salt tolerance mechanism in which it maintained low  $Na^+$  in the leaflets by stocking  $Na^+$  in the roots and petioles instead (Ehara et al., 2006).

Ehara et al. (2008) utilized sago palm seedlings at 8<sup>th</sup> or 9<sup>th</sup> leaf stage (9<sup>th</sup> or 10<sup>th</sup> leaf emerging) and subjected them to treatment of 342 mM (2.0%) NaCl for 31 days. Similar to previous investigation (Ehara et al., 2006), a low  $Na^+$  level was regulated in the sago palm leaflets and higher  $Na^+$  accumulations were uncovered in the roots and petioles (Ehara et al., 2008). The  $Na^+$  was found to be higher in the cortex than in the stele, in the large roots following NaCl treatment, and Ehara et al. (2008) suspected the role of endodermis in orchestrating the  $Na^+$  influx between the stele and cortex. They further examined the endodermis via X-ray micro-analysis and unveiled the fact that there was dense distribution of Na in close proximity to the large root endodermis (Ehara et al., 2008). It was also been revealed in the same study that the  $Ca^{2+}$  and  $Mg^{2+}$  changed in relation to that of  $Na^+$  were miniature (Ehara et al., 2008). Despite the slight postponement in

new leaves emergence and great decline in the rate of transpiration, the dry matter weight of all petioles and leaflets (regardless of position) had depicted no significant differences (Ehara et al., 2008). They further concluded that, apart from the avoidance mechanism previously proven in Ehara et al. (2006), the sago palm tended to impose constraint on transpiration by locking the water in the leaves (Ehara et al., 2008, 2011).

In the year 2011, Prathumyot et al. (2011) extended the salinity investigation further by conducting two cycles of diurnal NaCl concentration alterations (in the order of 224 mM, 0 mM, 224 mM and 0mM NaCl) for four months in a hydroponic system using four spiny sago palm seedlings (two treated samples and two negative controls). Interestingly, the amount of dead leaves in treated palms mirrored that of the control palms despite that the emergence of new leaves was much slower in treated samples (Prathumyot et al., 2011). They further tested on the phosphorus and nitrogen levels in the petioles and leaflets at all positions and unravelled that both phosphorus and nitrogen levels did not vary with NaCl treatments (Prathumyot et al., 2011). Moreover, the increment rate of chlorophyll level was found to be slower in the treated palms (measured in SPAD value) as compared to their control counterparts, together with the rate of photosynthesis, transpiration as well as stomatal conductance which declined by around 40% (Prathumyot et al., 2011). The  $Mg^{2+}$  levels were also tested, and a huge diminished level was observed in the

cortex, but the levels were not significant in leaflets, adventitious roots as well as petioles (Prathumyot et al., 2011). They concluded that the translocation of macronutrients like potassium, nitrogen and phosphorus was not affected by the induced NaCl stress in sago palm, and that chlorophyll synthesis was slowed down but not stunted, displaying the ability of sago palm to resist salt stress albeit the slower growth rate, without signs of mortality (Prathumyot et al., 2011).

### The Present

The present researches on salt tolerance of sago palm are more focused on the genetic and genomic field due to the booming of next-generation sequencing technologies. Roslan et al. (2017) had isolated and fully characterized the fructose-1,6-bisphosphate aldolase gene from *M. sagu* at the level of DNA, RNA and protein, which the protein of this gene was found to increase the salinity tolerance of *Escherichia coli*. On the other hand, Lim et al. (2020) had successfully sequenced the entire chloroplast genome of *M. sagu*, which provided huge insights on all salinity response genes from the chloroplast of the sago palm and opened new windows for their comparisons across other palms and food crops.

In the year 2017, Roslan et al. (2017) had successfully isolated full-length sequences of the fructose-1,6-bisphosphate aldolase gene via polymerase chain reaction (PCR). Furthermore, they also isolated the full-length cDNA of this gene via reverse transcriptase PCR (RT-PCR) and rapid amplification of cDNA ends PCR (RACE-

PCR) subsequently. In order to synthesise the protein of this gene, a pET41a(+) expression vector was chosen to be transformed into *E. coli* BL21 (DE3) strain (Roslan et al., 2017). The recombinant protein was then isolated via the nickel column which bound to the histidine affinity tag present at the fused target protein. Upon analysis, the gene was revealed to have 2322 bp in nucleotide length with five exons discovered (Roslan et al., 2017). The predicted protein of this gene has a molecular mass of 39.14 kDa and an isoelectric point of 6.49 (Roslan et al., 2017). They further characterized the fructose-1,6-bisphosphate aldolase protein via functional assay on *E. coli* (containing the recombinant pET41a(+) expression plasmid) treated with various NaCl concentrations, namely 0, 0.2, 0.4, 0.6, 0.8 and 1.0 M (Roslan et al., 2017). As a result, the survivability (in terms of colony count) of *E. coli* at 1.0 M NaCl as compared to 0 M NaCl in treated samples reduced by only 35% but the drastic reduction (85%) was observed in the negative controls (containing empty pET41a(+) plasmid) (Roslan et al., 2017). They concluded that this recombinant protein of fructose-1,6-bisphosphate aldolase gene had provided salinity immunity towards the tested *E. coli* cells (Roslan et al., 2017).

Recently, Lim et al. (2020) had sequenced and characterized the entire chloroplast genome of *M. sagu* (GenBank accession number: MN309778). Various genomic analyses such as codon usage, microsatellite, long repeats, inverted repeat structure (expansion and contraction), RNA

editing and phylogenetic analysis were conducted and reported in detail (Lim et al., 2020). The chloroplast genome of *M. sagu* was revealed to have high similarities to chloroplast genomes of other palms from the same family (Arecaceae) (Lim et al., 2020). The *M. sagu* closely resembles that of its genus counterpart, *M. warburgii* with high similarity over 98% (Barrett et al., 2016; Lim et al., 2020). To name a few, other palms with relatively high similarity to that of the *M. sagu* chloroplast genome includes *Phoenix dactylifera*, *Pigafetta elata*, *Mauritia flexuosa*, *Elaeis guineensis* and *Eugeissona tristis*.

### The Future

The future researches on salt tolerance of sago palm will surely be the upgrade of both past and present researches, which include the identification of new compounds responsible for salinity as well as characterization of more salinity response genes from the *M. sagu* genome, transcriptome and proteome.

**Genetic and Epigenetic Studies.** One of the most studied palm counterparts of *M. sagu* in terms of salt tolerance is the none other than *P. dactylifera* or widely known as the date palm. There are several aspects of salt tolerance researches that the *M. sagu* are lacking behind *P. dactylifera*, namely genome-wide miRNAome related to salinity, genome-wide salinity response expression profiling, growth improvement, antioxidant response to salinity, differential DNA methylation profile related to salinity,

identification of set of salinity response genes as well as salinity related proteome analysis (Al-Harrasi et al., 2018; Al Kharusi et al., 2019; Darwesh, 2013; El Rabey et al., 2016; Patankar et al., 2018; Yaish et al., 2017). Undoubtedly, with these efforts being implemented onto sago palm trees, it is not daunting to reveal the contributing factors towards the salinity tolerance of sago palm, be it in terms of novel salt-induced motifs, overexpression or downregulation of several salt stress genes as well as novel salt-detering protein products.

### Morphological and Variation Studies.

Most importantly, the core of these researches are to enable the deciphering of salinity adaptation mechanism of the sago palm. A good starting point and foundation would be the characterization of physical and morphological properties of the palm, encompassing histology, ion transport, growth rate, tissue content and many more (Faiyue et al., 2012; Gong et al., 2006; Yaish & Kumar, 2015; Yeo et al., 1999). This would help to first establish and identify salt-tolerant varieties to start with. For instance, there was a study conducted by Al Kharusi et al. (2019) which had tested on the antioxidant response of two varieties of date palms (“Umsila”, the salt tolerant variety and “Zabad”, the salt susceptible variety) towards salinity and as a result, the salt tolerant date palm variety was found to have higher reactive oxygen species (ROS)-scavenging metabolites and a balanced Na<sup>+</sup> and K<sup>+</sup> uptake. This type of experimentation can be easily inculcated on

the sago palm to further elucidate on this aspect of study for comparison purposes and knowledge enrichment. Furthermore, these characterization efforts of the sago palm variants would definitely provide a strong foundation and reservoir for further genetics, phylogenetics, taxonomical and genomics analysis.

**Growth Improvement Studies.** Next, several growth improvement research can be conducted onto the sago palm to achieve the maximum growth and yield, like the one published by Darwesh (2013) on date palm where the author reported on the combinations of yeast and amino acids (40 and 50 mL/L yeast as well as 3.0 and 6.0 mL/L amino acids) that worked best in alleviating the adverse salt stress effects in date palm. With these growth improvement studies being initiated on sago palm in the future, it would greatly help sago palm cultivators to have confidence and grasp on the knowledge to yield maximum profit from the palm plantation as well as ways to curb salt invasion issues in sago palm trees.

**Genomics Studies.** With the advancement of the sequencing technology throughout decades, the genomics of higher plant species can be easily unravelled with much lower costs and processing time with higher throughput and quality. The chloroplast genome of the sago palm has been recently sequenced and characterized (Lim et al., 2020) but the sequences of the nuclear and mitochondrial genome remained unknown to date. As nuclear and mitogenomes are

crucial in terms of the comprehension of the salt stress mechanisms, these missing puzzle pieces are no qualms beneficial in explaining the superior salinity tolerance of this unique sago palm. With the booming of mitogenomes and nuclear genomes being published at an exponential rate to date, the focus of research has now moved towards the various non-model plant organisms such as the early flowering plant *Nymphaea colorata* (Dong et al., 2018), Norway spruce (Sullivan et al., 2020), *Chrysanthemum boreale* (Won et al., 2018), legume *Vicia faba* (Negruk, 2013), sugarcane (Evans et al., 2019) and many more. The information obtained from the complete sequences of nuclear and mitogenomes of sago palm will in turn aid in selective breeding, variation studies as well as salt stress mechanism pathways (Lim et al., 2019d).

**Transcriptomic and Proteomic Studies.** With the aid of the next generation sequencing technologies, the OMICS of these sago palm varieties will aid in yielding information on proteins or other compounds that orchestrate salt transport like the results achieved by El Rabey et al. (2016) on date palm where various proteins related to drought and salt resistance were discovered. The genome-wide expression profiling in leaves and roots of date palm exposed to salinity as reported by Yaish et al. (2017) was another interesting aspect of study to be implemented on the sago palm because a sum of 4687 and 2630 date palm genes were identified to be differently expressed under salt stress and the potential of sago

palm to be included into similar study like this is limitless. Recently, the differential methylome and transcriptome of date palm in response to salinity had been drafted by Al-Harrasi et al. (2018) and this will be highly reproducible in sago palm. Emulating the success of Patankar et al. (2018) in which a total of 24 salinity response genes were identified and functionally characterized in date palm, it is not impossible to produce a comparable gene list from that of sago palm. These would surely contribute to the salt related gene landscape formation of sago palm which will in turn help in the field of genetic engineering and selective breeding. The genome-wide identification of enhancers involved in salinity response mechanism in sago palm is also possible with the utilization of computational tools as reviewed by Lim et al. (2018a).

## CONCLUSION

The sago palm is one of the trees of life for its many uses ranging from food, textile, polymer, pharmaceutical, renewable energy and its role in the environment (carbon dioxide absorption and water conservation). Adding to its many advantages is that it is one of the most important food crops in future (yielding at least three-fold to that of our current established food crop), and it can be cultivated in order to achieve the ultimate goal of combating global food scarcity problems. The salt tolerance research on this palm is essential to improve our comprehension on what distinguishes it from other food crop in terms of genetic

aspect and physiology, besides providing us with the idea to incorporate these novel sago palm salinity resistant specific motifs in the field of genetic engineering to further improve the feasibility of other food crop to curb salt stress in future. These researches will also provide us with the knowledge and resources in time to establish its status and expand its cultivations worldwide, besides enriching the research database for endemic fauna and flora in Sarawak, Malaysia (Kadir et al., 2013; Lim et al., 2018b, 2019a, 2019b; Ministry of Natural Resources and Environment [MNRE], 2016; Phillips, 2016; Soepadmo & Wong, 1995), as well as in enabling the study of ecosystem wholly for aiding future conservation efforts. In short, as this cash crop is one expensive thing to be wasted and remain undiscovered, consolidated research efforts should start right now.

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## CONFLICT OF INTEREST

The authors declared no conflict of interest.

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