Data in Brief

First high-quality genome assembly data of sago palm (*Metroxylon sagu* Rottboll)

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A R T I C L E   I N F O

Article history:
Received 18 November 2021
Accepted 4 January 2022
Available online 6 January 2022

Keywords:
*Metroxylon sagu*
Sago palm
Genome annotation
Starch synthesis

A B S T R A C T

The sago palm (*Metroxylon sagu* Rottboll) is a tropical halophytic starch-producing, economically important crop palm mainly located in Southeast Asian countries. Recently, a genome survey was conducted on this palm using the Illumina sequencing platform, with a very low (21.5%) BUSCO genome completeness score, and most of them (~78%) are either fragmented or missing. Thus, in this study, the sago palm genome completeness was further improved with the utilization of the Nanopore sequencing platform that produced longer reads. A hybrid genome assembly was conducted, and the outcome was a much complete sago palm genome with BUSCO completeness achieved at as high as 97.9%, with only ~2% of them either fragmented or missing. The estimated genome size of the sago palm is 509,812,790 bp in this study. A sum of 33,242 protein-coding genes was revealed from the sago palm genome and around 96.39% of them had been functionally annotated. An investigation on the carbohydrate metabolism KEGG pathways

**Abbreviations:** aa, amino acid; bp, base pair; BUSCO, Benchmarking Universal Single Copy Orthologs; KEGG, Kyoto Encyclopedia of Genes and Genomes; SDS, Sodium dodecyl sulfate.

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https://doi.org/10.1016/j.dib.2022.107800
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also unearthed that starch synthesis was one of the major sago palm activities. The genome data obtained from this work is indispensable for future molecular evolutionary and genome-wide association studies on the economically important sago palm.

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Specifications Table

| Subject                      | Biological Sciences |
|------------------------------|---------------------|
| Specific subject area        | Genomics            |
| Type of data                 | Sequencing raw reads, Table and Figure |
| How data were acquired       | Sequencing          |
| Data format                  | Raw Reads (fastq), Assembly (fasta) |
| Parameters for data collection| Total DNA was collected from Metroxylon sago planted in the living germplasm of Universiti Malaysia Sarawak East Campus (1°27′52.3″N, 110°27′04.7″E). |
| Description of data collection| About 5 μg of unfragmented genomic DNA libraries were prepared using LSK110 kit according to the manufacturer's protocols. The resultant libraries were sequenced on the Oxford Nanopore PromethION platform. Reads were basecalled employing high-accuracy mode in Guppy version 4, and only passed reads were uploaded to the NCBI SRA database. The minimum cutoff length was set at 500 bp. |
| Data source location         | Institution: Universiti Malaysia Sarawak City/Town/Region: Kota Samarahan, Sarawak, Malaysia Latitude and longitude for collected samples/data: (1°27′52.3″N, 110°27′04.7″E). |
| Data accessibility           | With the article. The sequencing reads used in assembly analysis of Metroxylon sago are available under the NCBI BioProject PRJNA769197 (https://www.ncbi.nlm.nih.gov/bioproject/769197) |

Value of the Data

- First complete genome dataset for the eco-economic important sago palm (Metroxylon sago Rottboll).
- High completeness of the sago palm genomic dataset will facilitate future research, such as genome-wide association studies.
- The data is useful in pioneering sago palm genetic landscape investigations which in turn unmask the mystery behind its high starch yield, salinity tolerance and disease resistance.

1. Data Description

The sago palm genome was estimated at 509,812,790 bp in this study. The sago palm genome sequencing from this study had greatly improved the genome completeness in an unprecedented manner. A previous report on BUSCO genome completeness of sago palm by [1] revealed 21.5% single-copy complete genes and 1.1% duplicated complete genes, whereas 32.2% and 45.2% are fragmented and missing, respectively. In this study, the nanopore approach coupled with the Illumina method has yielded 97.9% complete genes (89.8% single-copy and 8.1% duplicated), 1.1% is fragmented, and only 1% is missing (Table 1). The total number of contigs in this study is 2025, which is minuscule compared to the 739,583,200 contigs reported on the sago genome survey [1]. However, the overall contig lengths in this study is higher than that reported by [1], with 1801 contigs documented in this study to have at least 50,000 bp length in contrast to
Table 1
Genome statistics of the sago palm (*Metroxylon sagu* Rottboll) genome.

| Organism | *Metroxylon sagu* |
|----------|------------------|
| SRA      | SUB10461460      |
| Bioproject | PRJNA769197    |
| Biosample | SAMN15953627    |
| Accession number | JACVBY000000000 |
| BUSCO completeness | 97.9% complete (89.8% single-copy; 8.1% duplicated); 1.1% fragmented, 1% missing |
| # contigs (>= 0 bp) | 2025 |
| # contigs (>= 1000 bp) | 2025 |
| # contigs (>= 5000 bp) | 2024 |
| # contigs (>= 10,000 bp) | 2022 |
| # contigs (>= 25,000 bp) | 2002 |
| # contigs (>= 50,000 bp) | 1801 |
| Total length (>= 0 bp) | 509,812,790 bp |
| Total length (>= 1000 bp) | 509,812,790 bp |
| Total length (>= 5000 bp) | 509,810,926 bp |
| Total length (>= 10,000 bp) | 509,794,905 bp |
| Total length (>= 25,000 bp) | 509,389,047 bp |
| Total length (>= 50,000 bp) | 501,302,081 bp |
| Largest contig | 4,418,102 bp |
| Genome size | 509,812,790 bp |
| GC (%) | 36.50 |
| N50 | 453,371 bp |
| N75 | 220,193 bp |
| L50 | 341 bp |
| L75 | 742 bp |
| # N’s per 100 kbp | 0.00 |

**Genome annotation**

| # protein-coding genes | 33,242 |
|------------------------|--------|
| # functionally annotated proteins | 32,041 |
| Mean protein length | 313 aa |
| Longest protein | 3768 aa (titin protein) |
| Shortest protein | 23 aa (TIGR01906 family membrane protein) |
| Mean exon length | 276 bp |
| Longest exon | 8579 bp (heavy metal-associated isoprenylated plant protein 3) |
| Shortest exon | 2 bp (uncharacterized gene) |
| Mean intron length | 926 bp |
| Longest intron | 25,685 bp (putative eukaryotic translation initiation factor) |
| Shortest intron | 5 bp (pyruvase kinase isozyme A) |

the Illumina short sequencing reads whereby majority of them are 100 to 2000 bp long [1]. On a side note, the GC content of this improved sago palm genome assembly is 36.5%, which is a little lower than that reported by [1] (37.31%).

A total of 33,242 protein-coding genes were discovered from the sago palm genome in this study. Around 96.39% (32,041) of these protein-coding genes have been successfully annotated in terms of functionality. The mean protein length reported in this study is 313 aa. The largest protein found within the sago palm genome in this study is the titin protein with an amino
Fig. 1. The breakdown of the KEGG carbohydrate metabolism pathways the sago palm genes are involved in.

acid length of 3768 aa whereas the smallest protein is only 23 aa, namely the TIGR01906 family membrane protein. The mean exon and intron lengths uncovered in this study are 276 bp and 926 bp correspondingly. The lengthiest exon is 8579 bp long, revealed within the heavy metal-associated isoprenylated plant protein 3 gene. An uncharacterized sago palm gene contains the shortest exon of 2 bp among all other exons within the genome. The longest sago palm genome intron belongs to that of the putative eukaryotic translation initiation factor gene, with 25,685 bp in length. The shortest intron (5 bp) was unearthed within the pyruvase kinase isozyme A gene of the sago palm.

All protein-coding genes of sago palm were subjected to functional annotation. The focus was placed on the carbohydrate metabolism KEGG category as this is one of the most imperative yet untapped aspects of the sago palm, contributing to its high starch yield. Under the carbohydrate metabolism category, there are 15 metabolic pathways described, namely glycolysis/gluconeogenesis, citrate cycle (TCA cycle), pentose phosphate pathway, pentose and glucuronate interconversions, fructose and mannose metabolism, galactose metabolism, ascorbate and aldarate metabolism, starch and sucrose metabolism, amino sugar and nucleotide sugar metabolism, pyruvate metabolism, glyoxylate and dicarboxylate metabolism, propanoate metabolism, butanoate metabolism, C5-branched dibasic acid metabolism, as well as inositol phosphate metabolism. A total of 2221 protein-coding genes were unveiled to be closely related to the 15 aforementioned carbohydrate metabolism pathways (Fig. 1). Majority of them (260 or 12%) are related to amino sugar and nucleotide sugar metabolism. Almost an equal number of genes (256 or 11%) were associated with glycolysis/gluconeogenesis and starch and sucrose metabolism pathways. Only 1% (22) of them are involved in the C5-branched dibasic acid metabolism. This phenomenon shows that starch production is the major limelight among all other carbohydrate metabolism pathways in the sago palm genome context [2,3].

To date, there are only 20 representative full monocot genomes with complete records of coding sequences and proteins found within the GenBank public database. The maximum like-
Fig. 2. The maximum likelihood whole genome phylogenetic tree constructed based on BUSCO genes across all the available full monocot genomes (with complete records of coding sequences and proteins) found within the GenBank public database, with 1000 bootstrap replications. The species targeted in this study were highlighted in a black box.

Maximum likelihood phylogenetic tree was constructed based on single-copy proteins across the full genomes of 21 monocots (including sago palm) and two dicot outgroups (Fig. 2). Five major clades were found within the tree plotted and each of them represents an order, namely Dioscoreales, Poales, Arecales, Zingiberales, and Asparagales. Most clades are backed with strong bootstrap ratio of 1, indicating high bootstrap confidence. In this study, the sago palm was grouped under the order Arecales along with two other palm members, the oil and date palm. The Arecales order was underrepresented due to the lack of available full genome sequences [4–6]. More informative branching can be observed among the palm members when more full genomes are sequenced in the future as seen in the sago palm phylogenetic trees constructed based on chloroplast genome and ITS2 region [1,7]. In a nutshell, this sago palm complete genome would be a valuable resource for future molecular evolutionary studies as well as genome-wide association studies.

2. Experimental Design, Materials and Methods

2.1. Whole genome sequencing

Fresh sago palm leaves were harvested from the tree chosen by [6] for whole chloroplast sequencing in which this tree has been previously verified by our plant expert team from the living germplasm of Universiti Malaysia Sarawak East Campus (1°27'52.3"N, 110°27'04.7"E). The Illumina reads of sago palm were obtained from [1] which was sequenced using Illumina HiSeq X.

In order to produce Oxford Nanopore long reads, the genomic DNA was first extracted from fresh sago palm leaves using high-salt SDS approach. About 5 μg of unfragmented genomic DNA libraries were prepared using LSK110 kit according to manufacturer’s protocols. The resultant libraries were sequenced on Oxford Nanopore PromethION platform. Reads were basecalled employing high-accuracy mode in Guppy version 4 and only passed reads were uploaded to the NCBI SRA database. The minimum cutoff length was set at 500 bp.
2.2. Hybrid genome assembly and genome annotation

The Maryland Super-Read Celera Assembler v.3.2.2 was utilized to perform the *de novo* hybrid genome assembly of the sago palm. The sago palm hybrid genome assembly was conducted emulating that of [8,9].

The prediction of all protein-coding genes was conducted using Augustus. A BUSCO analysis was performed on the annotated sago palm genome dataset utilizing the embryophyta-specific dataset as reference. TransDecoder v5.5.0 was employed to extract the protein coding sequences prior to the clustering at 98% similarity of protein using cdhit v4.7 (-g 1 -c 98). The functional annotation was done using eggNOGmappr (evolutionary genealogy of genes: Non-supervised Orthologous Groups) with a 0.001 minimum E-value.

2.3. Phylogenetic analysis

All available full monocot genomes (with complete records of coding sequences and proteins) found within the GenBank public database were downloaded, totaling to 20 monocots and two dicot outgroups (only one representative was selected for each duplicated species). BUSCO analysis was conducted to all full genomes downloaded to extract all single-copy proteins. These proteins were aligned using Muscle prior to the maximum likelihood phylogenetic tree plotting using iqtrees with 1000 bootstrap replications. The tree was visually improved using FigTree software.

Ethics Statement

The collection of plant material was carried out in strict accordance with the guidelines outlined by the germplasm committees of Universiti Malaysia Sarawak, Malaysia.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have influenced the work reported in this article.

CRediT Author Statement

Leonard Whye Kit Lim: Data curation, Writing – original draft; Melinda Mei Lin Lau: Data curation; Hung Hui Chung: Conceptualization, Funding acquisition, Writing – review & editing; Hasnain Hussain: Writing – review & editing; Han Ming Gan: Methodology, Conceptualization, Writing – review & editing.

Acknowledgments

This work was fully funded by UNIMAS Tun Openg Sago Chair Research Grant F07/TOC/2068/2021 awarded to H. H. Chung.

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