Journal of Applied Biology & Biotechnology Vol. 10(02), pp. 21-34, February, 2022
Available online at http://www.jabonline.in
DOI: 10.7324/JABB.2022.100204

Identification of differentially expressed transcripts for trunk formation in sago palm using annealing control primer GeneFishing technique

Hasnain Hussain[1]*, Anastasia Shera Edward-Atit[1], Norzainizul Julaihi[2], Rina Tommy[2], Mehvish Nisar[1], Nurhazlina Hamdan[1], Hiroshi Ehara[3]

[1]Centre for Sago Research, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Sarawak, Malaysia.
[2]PELITA Mukah Sebakong Sago Plantation Sdn Bhd, Mukah, Sarawak.
[3]International Center for Research and Education in Agriculture, Nagoya University, Nagoya, Japan.

ARTICLE INFO

Article history:
Received on: March 9. 2021
Accepted on: August 3. 2021
Available Online: February 15, 2022

Key words:
Differential display, differentially expressed transcripts (DET), nontrunking, trunking, sago palm

ABSTRACT

In the state of Sarawak, Malaysia's vast peatland cultivated with sago palm (*Metroxylon sagu*), a considerable amount of cases involving stunted, nondeveloped trunk of sago palms was observed. Molecular-level understanding of the mechanism or pathway involved in the trunking (T) process leading to storage starch accumulation in the trunk of the sago palm is yet to be fully understood. A Polymerase Chain Reaction-based differential display analysis using Annealing Control Primer based GeneFishing technique on leaf samples of normal T compared to the nontrunking (NT) palm showed distinct differentially expressed transcripts pattern with differences in intensity between 35% and 123%. The translated sequence identified functions that are grouped under energy metabolism, nutrient regulation, biosynthetic reactions, defense mechanism, and stress tolerance. Transcripts from T showed higher expression of redox-regulating functions, while NT samples had proteins actively involved in the respiratory chain and chloroplast regulation. In nutrient regulation, the T sample showed higher transcript levels of nitrogen utilization and regulation of phosphate and cobalt, whereas NT showed activities of nitrogen uptake and regulation of calcium, magnesium, and zinc. This study identified different levels of transcripts in two physiologically different sago palms, and the formation and the development of the trunk are induced by these enzymes.

1. INTRODUCTION

Sago palm is found growing across South East Asia, in the regions of Thailand, Philippines, Indonesia, Malaysia, and Papua New Guinea. The different varieties of the sago palm in the different regions displayed varying degrees in growth duration and starch yield [1,2]. The starch formed in the trunk of the sago palm can be harvested and used as a source of carbohydrate and it remains among the highest-yielding starch yield crops in the world [3]. The palm can be found growing in various types of soil, including peat soil. It is estimated that there were 43,448 hectares of land cultivated with sago in Sarawak by smallholder and commercial plantations. The export of sago starch is valued at almost RM62 million in 2019. Japan is one of the largest importers of raw sago starch, estimated to be around 20,000 mt from Malaysia and Indonesia for more than 20 years [4].

Generally, the growth duration of sago palms varies for different varieties of the palm, with some species taking up to 16 years for completion for the trunk-formation stage alone [2,5]. For *Metroxylon sagu* (Rottb.) palm, the formation of the trunk is generally expected after 4–6 years of planting. However, for a sago palm cultivated in a plantation, there are instances where the trunk failed to form even after 10 years and stay in the rosette stage which can be considered an abnormality. The nontrunking (NT) sago palm has been highlighted as one of the major production limitations [6]. Reasons for this abnormality

*Corresponding Author
Hasnain Hussain, Centre for Sago Research, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Sarawak, Malaysia.
E-mail: hhasnain @ unimas.my