ABSTRACT

HETHARIE. Abnormality of Flowers and Fruits in Oil Palm \((Elaeis\, guineensis\, Jacq)\) Clones Based on of Morphology, Biochemistry and Genomic analysis. Supervised by GUSTAAF A. WATTIMENA, MAGGY THENAWIJAYA S., HAJRIAL ASWIDINNOOR, and NURITA TORUAN-MATHIUS.

Phenomena of abnormal flowers found was around 0-17% among clones of oil palm, that reduce productivity. Previous research showed that abnormality of flower is related to DNA hipomethylation in calli and leaves tissues of the abnormality plant. The changes of DNA methylation correlates with gen expression in the specific tissue. In the case of oil palm abnormalities occur in flower and fruit tissues.

The objectives of this research were to characterize the morphology of flower and fruit, to determine the oil content in relation to malonyl-CoA and acetyl-CoA, to study changes of DNA methylation status and genomic DNA changes related with flower and fruit abnormality.

Eighty plants used in this research consisted of three clones, i.e MK152, MK 176, and MK 209. These were obtained from the collection of “Badan Pengkajian dan Penerapan Teknologi (BPPT) Ciampea”. Characterization of plant morphology was conducted visually, whereas the oil content of mesocarp was analyzed by extracting the oil with soxhlet system, determination of the malonyl-CoA and acetyl-CoA content by HPLC (High Performance Liquid Chromathography), the quantification of cytosine methylation by performance RP-HPLC, and detection of alteration of the DNA genome was analysed by RAPD technique (Random Amplified Polymorphic DNA).

The results showed that abnormalities of female and male flowers as well as fruits were found in tissue culture-derived plants. The rudimentary stamen in the female flower, and stamen of the male flowers were transformed into carpel-like structure. Fruit abnormality was categorized into five classes, i.e normal, light abnormal (AbR), heavy abnormal (AbB) and two types of severe abnormal, AbSB1 and AbSB2. The content of palm oil in immature fruit from the three type of fruits (normal, AbR and AbB) were similar. The normal fruit contained around 74.66 -77.26%, AbR 77.47-80.85%, and AbB 73.89-78.62%. The high palm oil content in the normal (MK 152), AbR (MK 209), and AbB (MK 176) were related to higher malonyl-CoA (0.069 0.085, dan 0.068 mg/ml respectively) than the acetyl-CoA (0.036, 0.021 dan 0.023 mg/ml respectively). On the contrary in the severe abnormal fruits, the acetyl-CoA was higher (0.066-0.087 mg/ml) and the malonyl-CoA lower (0.022-0.037 mg/ml). Compared to the normal plant, hypomethylation in leaves tissue was 1.31-4.01% and hypermethylation was 0.69-2.66% in flowers tissue of the abnormal plants. However, changes of DNA methylation status was not found in fruits tissue. Changes of the sequence of DNA genome in the plants within the same clone were detected using five random primers, i.e.OPC-08,OPD-15, W-15, OPC-09 and SC10-19. A band DNA of the normal plant was detected by OPC-08. Changes of the methylation status in leaf and fruit tissues was not directly related to the abnormality of the oil palm flowers. The difference of DNA bands were found among plants of the MK 152.

Key words : oil palm, abnormal flower, oil mesocarp, malonyl-CoA, methylation cytosine, DNA sequence