Protein Induced as Salinity Stress in *Elaeis guineensis* Jacq.

Dolly Sojuangan Siregar[1], Mohammad Basyuni[2] and Rahmah Hayati[3]
[1]*Department of Agrotechnology, Faculty of Agriculture, Universitas Samudra, Meurandeh, Langsa City, Aceh, Indonesia*
[2]*Department of Forestry, Faculty of Forestry, Universitas Sumatera Utara, Jl. Tri Dharma Ujung No. 1 Medan, North Sumatera 20155, Indonesia*
[3]*Graduate School of Agrotechnology, Faculty of Agriculture, Universitas Sumatera Utara, Jl. Dr. A Sofyan No. 3 Medan, North Sumatera 20155, Indonesia*

Keywords: Oil Palm, Plasma Membrane, Salinity.

Abstract: Palm oil plants (*Elaeis guineensis*) are oil-producing plants grown in the tropics. Palm oil is sensitive to low temperatures but high tolerance to salinity stress and drought. The present work evaluates of the bioinformatics on the NCBI database as well as expected the physicochemical of protein salinity. There is three protein salinity induced from *E. guineensis* deposited in NCBI. Length of genes was between 525 to 633 bp. The same Molecular weight at X1 and X2 was 5945.24, but it is different from X3 which was 18052.17. Chloroplast transit peptide ranged from 0.142 and 0.445. Reactive oxygen species (ROS) plays a crucial role in promoting mitochondrial peptide targets in plants induced by salinity, ranging from 0.022 to 0.110. These results d variations and roles of different physical and chemical characteristics of amino acids in protein due to salinity stress in oil palm plants.

1 INTRODUCTION

Salinity is a major problem that affects the world's agricultural output and ecosystems. In latest decades, elevated soil salinity has transformed global farming barriers (Rengasamy, 2006; Munns and Tester, 2008). About 50% of the world's land will become salt by the 21st century (Mahajan and Tuteja 2005).

One of the most notable concerns of osmotic stress in plants is the production of high quantities of reactive oxygen species (ROS), followed by oxidative damage, e.g. protein, lipid, pigment, and DNA degradation. (Das and Roychoudhury 2014).

Palm oil (*Elaeis guineensis*) is susceptible to low temperatures but has a high tolerance to salt stress and drought (Cao et al., 2011). By identifying and validating genes associated with salinity stress responses in oil palm, it will help through molecular breeding.

The first sensory mechanism that senses salt stimulation is two elements that are seen during salinity stress circumstances, namely hyperosmotic stress and Na+ ion toxicity. As a result of salinity stress, plants produce Ca_2 + and ROS which are secondary messengers. The main organ of the plant that feels the salinity stress is the root. Plasma membranes and cytoplasmic proteins, G proteins, Ca2 + binding proteins, phosphoproteins and ethylene receptors intermediate the process. (Ghosh and Xu 2014).

At present, it is indispensable to recognize the nature of the mechanism of salt adaptation in oil palm plants to advance future oil palm varieties that are tolerant of salinity. The discovery of salt-tolerant genes will help breeders select parent species (germplasm) and progenies using marker aid. The results of the physiological and multi-OMICS analysis may deliver responses to the subsequent major questions:

1. Are some existing oil palm varieties adaptive to salt stress?
2. What is the mechanism for the adaptation of salt stress to oil palm plants?
3. Are there differences between sporogenous tissue in roots and leaves during salt stress?
4. Does the oil palm salinity gene affect the phenotype?
5. What is related to the modification of posttranslational salinity tolerance in oil palm plants?

The present study, therefore, evaluates of the bioinformatics on the NCBI database as well as expected the physicochemical of protein salinity from *E. guineensis.*

Siregar, D., Basyuni, M. and Hayati, R.
Protein Induced as Salinity Stress in Elaeis guineensis Jacq..
DOI: 10.5220/0008526301120115
In *Proceedings of the International Conference on Natural Resources and Technology (ICONART 2019)*, pages 112-115
ISBN: 978-989-758-404-6

2 MATERIAL AND METHOD

2.1 Materials

Three salinity genes on oil palm acquired from NCBI. The DNA and amino acid references used in the research follow:

1. XM_019850660.1 GI: 1130661850 Salt stress-induced hydrophobic peptide ESI3-like [*E. guineensis*]; NCBI Reference Sequence: XP_019706219.1
2. XM_019846899.1 GI: 1130626415 Salt stress-induced hydrophobic peptide ESI3-like [*E. guineensis*]; NCBI Reference Sequence: XP_019702458.1
3. JZ142439.1 GI: 527498159 EgFLSTP6 *E. guineensis* cDNA similar to salt tolerance protein 6, mRNA sequence 525 bp linear mRNA

2.2 Physicochemical Features of the Salinity Protein of Oil Palm

Online Protparam (web.expasy.org/protparam/) has been used to control the composition, physicochemical features of oil palm plants ' protein salinity. The calculated factors are the length of genes/bp, molecular weight, theoretical isoelectric values points, a total number of atoms, total negatively charged residues, total number of positively charged residues, instability coefficient, aliphatic index, and grand mean of hydropathicity as prior described (Basyuni et al., 2017)

2.3 Peptide Transfer and Subcellular Localization of Protein-induced Salinity Proteins in Oil Palm Plants

Peptide predictions transit through the online P1.1 target server (www.cbs.dtu.dk/services/targetp/). Peptide chloroplast transit, mitochondrial target peptide, the signal peptide of the secretory pathway, reliability indicator were found. Online PSORT (predictive tool for subcellular localization of proteins) (psort.hgc.jp/form.html) is used to analyze the subcellular of protein dehydration which is induced by salinity stress in oil palm plants as earlier shown (Basyuni and Wati, 2017).

2.4 Phylogenetic Analysis of Protein-induced Salinity in Oil Palm

Locus numbers of the sequence of the physical and chemical characteristic of oil palm protein induced salinity used this investigation in this manner: *E.guineensis* XM_019850660, XM_019846899, and JZ142439.1. Phylogenetic analysis of amino acid arrangement from of protein-induced salinity in oil palm was carried out with CLUSTAL W ver. 1.83 (Thompson et al., 1994) of the DNA Data Bank of Japan (Mishima, Shizuoka, Japan) accompanied by depicting with TreeView, ver. 1.6.6 (Page, 1996) according to a neighbor-joining method. Bootstrap analysis with 1000 repetitions was used to weigh the strong point of the knots in the tree (Felsenstein. 1995).

3 RESULT

3.1. Physicochemical Characteristics of the Protein Induced Salinity in *E. guineensis*

The physicochemical activities of a protein are analyzed by the similar properties of the amino acids in it. Each protein molecule contains of a long chain of amino acid residues and is connected by peptide bonds. Table 1 showed the several parameters of physicochemical protein induced salinity in *E.guineensis*. Length of genes between 525 to 633 bp. The same Molecular weight at X1 and X2 is 5945.24, but it is different from X3 which is 18052.17. Theoretical isoelectric points values at X1 and X2 are almost close to 4.65 and 4.0 but different from X3 which is 8.69. The total number of atoms at X1 and X2 is almost close to 8.64 and 8.71 three times different from X3 which is 2478.

The total number of negatively charged residues X1 and X2 which are 3 and 4 are different from X3 which is 11. The total number of positively charged residues on X1 and X2 is the same, namely 1, but different from X3, namely 14, Instability coefficient at X1, X2 and X3 between 27.15 and 31.66. Aliphatic indexes at X1 and X2 are 162.42 and 165.93 but are low at X3 which is 60.18. The hydrophobicity is a significant stabilization force in protein folding.

Grand average of hydropathicity on X1 and X2 is 1.604 and 1.491 while X3 is -0.443. Despite the availability of thousands of stress associated ESTs of in *E. guineensis* (Low et al., 2008), quantitative gene expression analysis of these genes is only recently attempted for the identification of candidate genes/factors that are contributing to salinity tolerance. With the advent of the qPCR technique, it is easier to quantify each gene and establish its relevance under the given stress situations.

Table 1: Physicochemical characteristic of the protein induced salinity in *E.guineensis.*

Variant	X1	X2	X3
Length of genes/bp	630	633	525
Molecular weight	5945.24	5945.24	18052.17
Theoretical isoelectric points values	4.65	4.00	8.69
Total number of atoms	864	871	2478
Total number of negatively charged residues	3	4	11
Total number of positively charged residues	1	1	14
Instability coefficient	27.15	31.66	27.54
Aliphatic index	162.41	165.93	60.18
Grand average of hydropathicity	1.604	1.491	-0.443

3.2. Potential Transfer of Peptide and Subcellular Location

The potential for a prospective transfer peptide in *E. guineensis* is shown in Table 2. Four reliability factors were identified: chloroplast transit peptide, mitochondrial target peptide, secretory path signal peptide, and prediction of reliability. Chloroplast transit peptide ranges from 0.142 and 0.445. ROS plays a crucial role in promoting mitochondrial peptide targets in plants that are gripped by salinity (Huang et al., 2016), ranging from 0.022 to 0.110.

The signal peptide of the secretory pathway can be found in terminal N and terminal C of protein and most cases stored in mature proteins with values ranging from 0.154 and 0.670. Reliability of X1, X2 and X3 predictions ranges between 3 and 5. These indicated that ROS-scavenging enzymes played crucial roles in salinity tolerance mechanism (Joseph et al., 2011).

Table 2: The promising of potential transit peptide induced salinity in *E. guineensis.*

Variant	Reliability			
	Chloroplast transit peptide	Mitochondrial target peptide	Signal peptide of secretory pathway	Reliability prediction
X1	0.142	0.022	0.670	3
X2	0.445	0.076	0.154	4
X3	0.291	0.110	0.170	5

Table 3 shows the subcellular location of protein-induced salinity in *E. guineensis*. There are two (2) variants (X1, X2) were located in the vacuole (Vac), Plasma (Plas), and extracellular (Extr). One variant (X1) in Endoplasmic Reticulum (ER), Golgi (Golg). One variant (X3) were located in Mitochondrial (Mito), Cytoplasm (Cyto), Nucleolus (Nucl) and Chloroplast (Chlo).

Table 3: Subcellular localization of protein-induced salinity in *E.guineensis.*

Var	Vac	ER	Plas	Golg	Extr	Mito	Cyto	Nucl	Chlo
X1	9	2	1	1	1	Nd	nd	nd	nd
X2	11	Nd	1	nd	2	Nd	nd	nd	nd
X3	nd	Nd	nd	nd	nd	1	2	2	9

Note: Vac: Vacuole, ER: Endoplasmic Reticulum, Plas: Plasma Golg: Golgi, Extr: Extracellular, Mito: Mitochondrial, Cyto Cytoplasm, Nucl: Nucleolus, Chlo: Chloroplast, nd: not detected

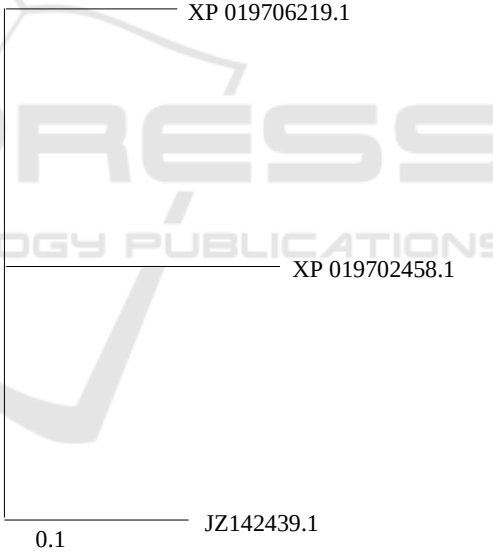

Figure 1: Phylogenetic tree among observed genes.

Figure 1 illustrates the phylogenetic among the gene observed. There are three branches representative by each gene. To further understand the genes, several additional genes related to salinity from *E. guineensis* are needed.

4 CONCLUSIONS

These findings stated differences and roles in salt-induced amino acids in oil palm of various physical

and chemical features. The promising prospective transit peptide, subcellular location of protein genes owing to the stress of salinity in *E. guineensis*.

ACKNOWLEDGEMENTS

This research was partially endorsed by a Penelitian Strategis Nasional Institusi (PSN Institusi 2019) (PSN Institusi 2019) from the Directorate for Research and Community Service, Ministry of Research, Technology and Higher Education, Republic of Indonesia.

REFERENCES

Basyuni, M., Wasilah, M., and Sumardi. 2017. Bioinformatics study of the mangrove actin genes *Journal of Physics Conference Series* 801, 012013

Basyuni, M. and Wati, R., 2017. Bioinformatics analysis of the oxidosqualene cyclase gene and the amino acid sequence in mangrove plants. In *Journal of Physics: Conference Series* 801, 012011.

Cao, H. X., Sun, C. X., Shao, H. B., and Lei, X. T. 2011. Effects of low temperature and drought on the physiological and growth changes in oil palm seedlings. *African Journal of Biotechnology*, 10(14), 2630-2637.

Das K, and Roychoudhury A. 2014. Reactive oxygen species (ROS) and response of antioxidants as ROS-scavengers during environmental stress in plants. *Frontiers in Environmental Science* 2:53.

Felsenstein, J., 1985. Confidence limits on phylogenies: an approach using the bootstrap. *Evolution*, 39(4), pp.783-791.

Ghosh, D. and Xu, J., 2014. Abiotic stress responses in plant roots: a proteomics perspective. *Frontiers in Plant Science* 5, 6.

Huang, S., Van Aken, O., Schwarzländer, M., Belt, K. and Millar, A.H., 2016. The roles of mitochondrial reactive oxygen species in cellular signaling and stress response in plants. *Plant physiology*, 171(3), 1551-1559.

Joseph, B., Jini, D. and Sujatha, S., 2011. Development of salt stress-tolerant plants by gene manipulation of antioxidant enzymes. *Asian Journal of Agricultural Research*, 5(1), 17-27.

Low, E.T.L., Alias, H., Boon, S.H., Shariff, E.M., Tan, C.Y.A., Ooi, L.C., Cheah, S.C., Raha, A.R., Wan, K.L. and Singh, R., 2008. Oil palm (*Elaeis guineensis* Jacq.) tissue culture ESTs: identifying genes associated with callogenesis and embryogenesis. *BMC Plant Biology*, 8(1), p.62.

Mahajan S, and Tuteja N. 2005. Cold, salinity and drought stress: an overview. *Archives of Biochemistry and Biophysics* 444,139-158.

Munns, R. and Tester, M., 2008. Mechanisms of salinity tolerance. *Annual Review of Plant Biology* 59, 651-681.

Page, R.D., 1996. Tree View: An application to display phylogenetic trees on personal computers. *Bioinformatics*, 12(4), pp.357-358.

Rengasamy, P., 2006. World salinization with emphasis on Australia. *Journal of Experimental Botany*, 57(5), 1017-1023.

Thompson, J.D., Higgins, D.G. and Gibson, T.J., 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic acids research*, 22(22), pp.4673-4680.