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FUNCTIONAL CHARACTERIZATION OF GIBBERELLIC ACID RELATED GENES FROM OIL PALM IN Arabidopsis thaliana FOR POTENTIAL ROLE HEIGHT REGULATION

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By

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Master of Science

FUNCTIONAL CHARACTERIZATION OF GIBBERELLIC ACID RELATED GENES FROM OIL PALM IN Arabidopsis thaliana FOR POTENTIAL ROLE IN HEIGHT REGULATION

By

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December 2017

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Oil palm is the most important commodity crop in Malaysia with a total planted area of 5.74 million hectares. In general, the economic life of the oil palm is associated with the stature of the tree. At maturity, oil palm trees commonly reach over 15 meters in height making harvesting a challenge as fruit bunches may weigh over 20 kg and become damage as the bunches fall to the ground hence reduce the quality of fresh fruit bunch (FFB). Height regulation in plant is commonly associated with gibberellic acid (GA), therefore study of genes related to GA biosynthesis and signaling will improve our understanding on height regulation mechanism in oil palm. Thus, the main objective of the research was to isolate GA-related genes from the oil palm (Elaeis guineensis) and characterize their functions in order to study height regulation in oil palm. Due to oil palm long life cycle, it is difficult to study the gene function in vivo, therefore functional characterization of the genes was conducted in heterologous system using model plant Arabidopsis thaliana. Three GA-related genes, EgGA200x, EgGA2ox and EgGAI were isolated from leaf tissue of clonal oil palm treated with paclobutrazol (GA inhibitor). EgGA20ox and EgGA2ox genes expression were affected by paclobutrazol treatment whereas EgGAI gene was not affected by the paclobutrazol application. EgGA20ox gene was constitutively expressed in most tissues tested except for kernel. EgGA2ox gene was highly expressed in young root of the oil palm. On the other hand, EgGAI gene expression was presence in most tissues except for root and kernel. Prior to genes functional study, six expression constructs were generated consisting of three overexpression (pH2OE-EgGA20ox, pH2OE-EgGA2ox, pH2OE-EgGAI) and three RNAi (pH7RNAi-EgGA20ox, pH7RNAi-EgGA2ox, pH7RNAi-EgGAI) constructs. The constructs were transformed into Arabidopsis via Agrobacterium-mediated transformation using floral dip method. Phenotypic characterization analysis of the transgenic Arabidopsis showed that EgGA20ox gene promotes vegetative and reproductive growth. Up regulation of EgGA20ox gene increased the height of transgenic Arabidopsis and length of leaf, root and silique. Flower formation of this line was also improved. Down regulated of EgGA200x gene reduced the height of Arabidopsis and the length of leaf, root and silique. In addition, less flower formation was observed. On the contrary, up regulation of EgGA2ox gene reduced Arabidopsis height, increased leaf length and delayed in flowering. It was found that there was no effect in terms of flower formation, root and silique. Down regulation of EgGA2ox gene generated taller transgenic Arabidopsis, increased root and leaf length, early flowering but produced normal flower and silique formation. Transgenic Arabidopsis lines carrying oil palm GA-Insensitive (EgGAI) gene were also affecting the vegetative and reproductive growth. Overexpressed of EgGAI gene in transgenic Arabidopsis resulted in shorter plant and reduced root and leaf length. Delayed in flowering was also observed however there was no effect on flower and silique formations. Down regulation of EgGAI gene increased the transgenic Arabidopsis height but reduced the root and leaf length. In terms of reproductive growth, fewer flowers were generated but silique length remain similar to control plant. Based on our findings, EgGA20ox, EgGA2ox and EgGAI genes may play an important role in the plant growth and development. This study has shown that Arabidopsis can be utilized for gene functional studies especially genes involve in oil palm height regulation.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk Ijazah Sarjana Sains

PENCIRIAN FUNGSI GEN BERKAITAN ASID GIBERELIK DARIPADA SAWIT DALAM Arabidopsis thaliana UNTUK PENGATURAN KETINGGIAN SAWIT

Oleh

MUHAMAD AFIQ BIN ABDUL HALIM

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Sawit merupakan tanaman komoditi penting di Malaysia yang meliputi kawasan seluas 5.74 juta hektar. Umumnya, jangka hayat ekonomi sawit berkait rapat dengan ketinggian pokok. Sawit yang matang mampu mencapai ketinggian lebih daripada 15 meter menyebabkan proses penuaian mencabar kerana berat buah sawit boleh mencecah 20 kg dan rosak apabila jatuh ke tanah seterusnya mengurangkan kualiti buah sawit. Pengaturan ketinggian pokok sering dikaitkan dengan asid giberelik (AG), oleh hal yang demikian kajian gen berkaitan biosintesis dan pengisyaratan AG akan meningkatkan kefahaman terhadap mekanisme pengaturan ketinggian sawit. Sehubungan dengan itu, kajian ini dijalankan untuk mengkaji gen yang berkaitan dengan pengaturan ketinggian sawit. Tujuan utama penyelidikan ini adalah untuk memencilkan gen berkaitan AG daripada sawit (Elaeis guineensis) dan mencirikan fungsinya. Disebabkan hayat sawit yang panjang, kajian tentang fungsi gen secara in vivo adalah sukar, oleh hal yang demikian, pencirian fungsi gen telah dijalankan dalam sistem heterologus menggunakan pokok model Arabidopsis thaliana. Tiga gen berkaitan AG, EgGA20ox, EgGA2ox dan EgGAI telah dipencilkan daripada genom sawit. Gen tersebut dipencilkan daripada tisu daun yang dirawat paclobutrazol (perencat AG). Ekspresi gen EgGA20ox dan EgGA2ox dipengaruhi oleh rawatan paclobutrazol. Namun, ekspresi gen EgGAI tidak dipengaruhi oleh kehadiran paclobutrazol. Gen EgGA20ox diekspres dalam hampir kesemua tisu yang diuji kecuali tisu isirung. Gen EgGA2ox diekspres tinggi dalam tisu akar muda sawit. Manakala, ekspresi gen EgGAI ditemui dalam hampir kesemua tisu kecuali tisu akar dan isirung. Lanjutan dari itu, enam konstruk ekspresi telah dihasilkan mengandungi tiga konstruk ekspresi melampau (pH2OE-EgGA20ox, pH2OE-EgGA2ox, pH2OE-EgGAI) dan tiga konstruk RNAi (pH7RNAi-EgGA20ox, pH7RNAi-EgGA2ox, pH7RNAi-EgGAI). Konstruk tersebut ditransform dalam Arabidopsis melalui perantaraan Agrobacterium menggunakan kaedah rendaman bunga. Analisis pencirian fenotip pokok Arabidopsis transgenik menunjukkan gen EgGA20ox menggalakkan pertumbuhan vegetatif dan reproduktif. Pengawalaturan tinggi gen EgGA20ox menambah ketinggian Arabidopsis transgenik dan kepanjangan daun, akar dan silikua. Perkembangan bunga juga dipertingkatkan. Pengawalaturan rendah EgGA20ox mengurangkan ketinggian Arabidopsis dan kepanjangan daun, akar dan silikua. Tambahan pula, pertumbuhan bunga berkurangan. Berbeza dengan EgGA2ox, pengawalaturan tinggi merendahkan Arabidopsis, memanjangkan daun dan melewatkan pengeluaran bunga. Namun demikian, tidak mempengaruhi perkembangan bunga, akar dan silikua. Pengawalaturan rendah gen EgGA2ox menghasilkan Arabidopsis transgenik vang tinggi, memanjangkan akar dan daun, mempercepatkan pembungaan namun menghasilkan bunga dan silikua yang normal. Arabidopsis transgenik melibatkan gen EgGAI mempengaruhi perkembangan vegetatif dan reproduktif. Pengawalaturan tinggi gen EgGAl merendahkan Arabidopsis transgenik dan mengurangkan kepanjangan akar dan daun. Pembungaan menjadi lewat namun tiada perubahan terhadap perkembangan bunga dan silikua. Pengawalaturan rendah gen EgGAI menambah ketinggian Arabidopsis transgenik tetapi mengurangkan kepanjangan akar dan daun. Tambahan pula, penghasilan bunga berkurang namun kepanjangan silikua adalah sama seperti pokok kawalan. Sebagai rumusan, gen EgGA20ox, EgGA2ox dan EgGAl berperanan penting dalam pertumbuhan dan perkembangan pokok. Kajian ini menunjukkan bahawa Arabidopsis boleh diolah untuk kajian fungsi gen terutama gen yang terlibat dalam pengaturan ketinggian sawit.

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TABLE OF CONTENTS

			Page
ABSTR			i
ABSTR		GEMENT	iii
APPRC		JEWENI	v vi
		N	vi
	FTABL		xiv
	F FIGUE		XV
		VIATIONS	xviii
СЦАРТ	-ED		
CHAPT	EK		
1	INTRO	DUCTION	
	1.1	Research background	1
	1.2	Problem statement and objectives	2
2	LITER	ATURE REVIEW	
-	2.1	The origin and development of oil palm	4
	2.2	Classification and morphology of the oil palm	4
	2.3	Oil palm industry and distribution in Malaysia	10
	2.4	Challenges in the industry	12
	2.5	Height regulation in plant	14
	2.6	Phytohormone: Gibberellic Acid (GA)	15
		2.6.1 GAs inhibitors	17
		2.6.2 GAs biosynthesis pathway	20
		2.6.3 Gibberellins (GAs) oxidase genes	22
		2.6.4 Gibberellin 20-oxidases (GA20oxs) genes	24
		2.6.5 Gibberellin 2-oxidases (GA2oxs) gene	25
		2.6.6 GAs signaling pathway2.6.7 Gibberellic Acid-Insensitive (GAI) gene	25 26
	2.7	Gene functional studies in plant	20 27
	2.8	Model plant: Arabidopsis thaliana	29
3	RESPC	HOLOGICAL AND PHYSIOLOGICAL CHANGES IN DNSE TO PACLOBUTRAZOL (PBZ) TREATMENT XPRESSION PROFILING OF GA-RELATED GENES	
		NAL PALM	
	3.1	Introduction	32
	3.2	Materials and Methods	34
		3.2.1 Plant material and growth condition	34
		3.2.2 Treatments	34

Morphological measurement	35
Physiological measurements	35
Statistical Analysis	36
Identification and analysis of putative GA-	36
	Physiological measurements Statistical Analysis

related genes 3.2.7 RNA extraction 37

(C)

	3.2.8 3.2.9 3.2.10	RNA purification cDNA synthesis Isolation of the <i>EgGA20ox</i> , <i>EgGA2ox</i> and	38 39 39
3.3	3.2.11 Results	<i>EgGAI</i> genes coding regions Real-time PCR (qPCR)	40 41
	3.3.1	Oil palm growth and PBZ treatment	41
	3.3.2	Impact of PBZ treatment on chlorophyll index and photosynthetic rate of clonal oil palms	44
	3.3.3	Isolation and sequence analysis of putative <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGAI</i> genes from the oil palm tissues	50
	3.3.4	<i>In-silico</i> analysis of putative <i>EgGA20ox</i>	55
	3.3.5	In-silico analysis of putative EgGA2ox	61
	3.3.6	In-silico analysis of putative EgGAI	67
	3.3.7	Expression profiling of putative <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGA1</i> genes in different	75
		tissues of the oil palm using RT-PCR	
	3.3.8	Expression profiling of putative <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGAI</i> genes in PBZ treated	77
o 4		clonal oil palm using qPCR	~ 4
3.4	Discus		81
	3.4.1	Oil palm growth pattern after PBZ treatment	81
	3.4.2	Impact of PBZ on chlorophyll index and photosynthetic rate of the clonal oil palm	82
	3.4.3	<i>In-silico</i> analysis of putative <i>EgGA200x</i> , <i>EgGA20x</i> , and <i>EgGA</i> /from the oil palm tissues	84
	3.4.4	Expression pattern of putative <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGAI</i> genes in different tissues of the oil palm	87
	3.4.5	Expression pattern of putative <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGAI</i> genes in PBZ treated tissues	88
3.5	Conclus		90
0.0	Conorad		00
GENES PALM	6 (<i>EgGA</i> USIN		
	KDOWN		
•	•	thaliana)	
4.1	Introduc		92
4.2	Materia	Is and Methods	94
	4.2.1	Generation of expression constructs	94
		4.2.1.1 Entry clones construction4.2.1.2 Plasmid extraction	96 96

- 4.2.1.3 Validation of entry clones 4.2.1.4 Preparation of competent *E.coli* 97 98
- 4.2.1.5 Expression clones construction 98

99

Generation of transgenic Arabidopsis 4.2.2 homozygous lines carrying the expression constructs

 \mathbf{G}

	4.2.2.1 Preparation of competent Agrobacterium tumefaciens (C58)	99
	4.2.2.2 Transformation of competent A.	99
	tumefaciens (C58)	
	4.2.2.3 Preparation of <i>Arabidopsis</i> and growth condition	100
	4.2.2.4 Transformation of <i>Arabidopsis</i> with overexpression and RNAi constructs	101
	4.2.2.5 Screening of transgenic <i>Arabidopsis</i> carrying overexpression and RNAi constructs	101
	4.2.2.6 Genomic DNA extraction from Arabidopsis	102
	4.2.2.7 Validation of putative transgenic Arabidopsis	103
	4.2.2.8 Generation of homozygous transgenic Arabidopsis	103
	4.2.2.9 Phenotypic characterization analysis of the homozygous transgenic <i>Arabidopsis</i>	103
	4.2.2.10Expression profiling of the homozygous transgenic <i>Arabidopsis</i>	104
Results		105
4.3.1	Generation of entry clones	105
4.3.1 4.3 <mark>.2</mark>	Generation of overexpression and RNAi	103
4.0.2	constructs	107
4.3. <mark>3</mark>	Mobilization of expression constructs into <i>A.</i> tumefaciens (C58)	110
4.3.4	Generation of putative transgenic Arabidopsis	113
4.3.5	Overexpression and RNAi homozygous lines generation	116
4.3.6	Phenotypic characterization analysis and expression profiling of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA20ox</i> and pH7RNAi- <i>EgGA20ox</i> constructs	116
	4.3.6.1 Morphology comparison of leaves, siliques and flowers of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA20ox</i> and pH7RNAi- <i>EgGA20ox</i> constructs	124
4.3.7	Phenotypic characterization analysis and expression profiling of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA2ox</i> and pH7RNAi- <i>EgGA2ox</i> constructs	126
	4.3.7.1 Morphology comparison of leaves, siliques and flowers of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA2ox</i> and pH7RNAi- <i>EgGA2ox</i> constructs	133

4.3

6

		4.3.8	Phenotypic characterization analysis and expression profiling of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGAI</i> and pH7RNAi- <i>EgGAI</i> constructs	135
			4.3.8.1 Morphology comparison of leaves, siliques and flowers of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGAI</i> and pH7RNAi- <i>EgGAI</i> constructs	141
	4.4	Discus		144
		4.4.1	Generation of pGW-EgGA20ox, pGW-	144
			EgGA2ox and pGW-EgGAI entry clones	
		4.4.2	Generation of pH2OE- <i>EgGA20ox</i> , pH2OE- <i>EgGA2ox</i> , pH2OE- <i>EgGAI</i> , pH7RNAi-	144
			EgGA20ox, pH7RNAi-EgGA2ox and	
			pH7RNAi-EgGAI expression constructs and	
			transformation into A. tumefaciens	
		4.4.3	Transformation of Arabidopsis by A.	147
			tumefaciens (C58) carrying expression	
			constructs via floral dip and generation of	
			homozygous lines	
		4.4.4	Phenotypic characterization of transgenic Arabidopsis carrying pH2OE-EgGA20ox and pH7RNAi-EgGA20ox constructs	148
		4.4.5		150
		4.4.5	Phenotypic characterization of transgenic Arabidopsis carrying pH2OE-EgGA2ox and pH7RNAi-EgGA2ox constructs	100
		4.4.6	Phenotypic characterization of transgenic Arabidopsis carrying pH2OE-EgGAI and pH7RNAi-EgGAI constructs	152
	4.5	Conclu	-	154
5	CLIMANA	ADV CO	NCI USION AND FUTURE STUDY	
5	5.1		DNCLUSION AND FUTURE STUDY	156
	5.1 5.2		ary of the study	156
	5.2	Genera	I conclusion and future study	159
REFERENCES APPENDICES BIODATA OF STUDENT			161 180 198	
LIST OF PUBLICATIONS 19			199	

 \bigcirc

LIST OF TABLES

Table		Page
2.1	Oil palm fruit forms and types	7
2.2	Characterized GA oxidases from different plant species	23
2.3	<i>Arabidopsis</i> growth stages for the plate and soil-based phenotypic analysis platforms for Colombia ecotype	31
3.1	Plant height, stem thickness and number of leaf after the application of PBZ on clonal oil palms	44
3.2	BLAST analysis of the isolated putative <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGAI</i> genes with highest similarity	54
3.3	BLAST analysis of deduced amino acid sequence of putative <i>EgGA200x</i> gene from oil palm with GA20-oxidases from other plant species	56
3.4	BLAST analysis of deduced amino acid sequence of putative <i>EgGA2ox</i> gene from oil palm with GA2-oxidases from other plant species	62
3.5	BLAST analysis of deduced amino acid sequence of putative <i>EgGAI</i> gene from oil palm with DELLAs protein from other plant species.	67

G

LIST OF FIGURES

Figure		Page
2.1	Typical oil palm tree	6
2.2	Fruit forms and its morphology	9
2.3	Oil palm planted area in Malaysia from 1960 until 2016.	11
2.4	General chemical structure of bioactive GAs	16
2.5	Paclobutrazol (PBZ) chemical structure	19
2.6	Inhibition point of plant growth retardant in GAs biosynthetic pathway	19
2.7	GAs biosynthesis pathway in plant	22
2.8	GAs signaling pathway in plant	26
2.9	Model plant Arabidopsis thaliana	30
3.1	Effect of PBZ treatment on clonal oil palms (Clone 8A/PL233/5/9AP-1/4/S/R) at Week 12	42
3.2	Effect of PBZ on plant height.	43
3.3	Effect of PBZ on leaf structure, coloration and growth at Week 18	45
3.4	Effect of PBZ on relative chlorophyll content index	46
3.5	Photosynthetic rate (PN) of the PBZ treated clonal palms	47
3.6	Stomatal conductance (g_s) of the PBZ treated clonal palms	48
3.7	Transpiration rate (E) of the PBZ treated clonal palms	49
3.8	Water use efficiency (WUE) of the PBZ treated clonal palms	50
3.9	Total RNA integrity tested on 1 % (w/v) agarose gel	51
3.10	PCR amplification of putative <i>EgGA20ox</i> , <i>EgGA2ox</i> , and <i>EgGA1</i> genes from oil palm tissue	53
3.11	Multiple sequence alignment of deduced amino acid of GA20ox from various plant species	59
3.12	Phylogenetic tree of GA20ox protein sequences from different plant species	60
3.13	Multiple sequence alignment of deduced amino acid	65
	of GA2ox from various plant species	
3.14	Phylogenetic tree of GA2ox protein sequences from different plant species	66
3.15	Multiple sequence alignment of deduced amino acid of DELLA from various plant species.	73
3.16	Phylogenetic tree of DELLA protein sequences from different plant species	74

3.17	Gene expression of EgGA20ox, EgGA2ox, EgGAI	76
3.18	genes in different tissues EgGA20ox gene expression profile of PBZ treated oil	78
3.19	palm tissue using qPCR <i>EgGA2ox</i> gene expression profile of PBZ treated oil	79
3.20	palm tissue using qPCR EgGAI gene expression profile of PBZ treated oil	80
4.1	palm tissue using qPCR Schematic diagram of workflow on functional characterization of <i>EgGA20ox</i> , <i>EgGA20x</i> and <i>EgGA1</i> genes in <i>Arabidopsis</i>	95
4.2	Verification of entry clones carrying <i>EgGA20ox</i> , <i>EgGA2ox</i> and <i>EgGA1</i> genes.	106
4.3	Validation of overexpression constructs (pH2OE- EgGA20ox, pH2OE-EgGA2ox and pH2OE-EgGAI)	108
4.4	Validation of RNAi constructs (pH7RNAi-EgGA20ox, pH7RNAi-EgGA2ox and pH7RNAi-EgGAl)	109
4.5	Validation of transformed A. tumefaciens (C58) carrying overexpression constructs (pH2OE-	111
4.6	EgGA20ox, pH2OE-EgGA2ox and pH2OE-EgGAI) Validation of transformed A. tumefaciens (C58) carrying RNAi constructs (pH7RNAi-EgGA20ox, pH7RNAi EgGA2ox and pH7RNAi-EgGA20ox,	112
4.7	pH7RNAi- <i>EgGA2ox</i> and pH7RNAi- <i>EgGAI</i>) Validation of putative transgenic <i>Arabidopsis</i> of	114
4.8	overexpression constructs from leaf tissue Validation of putative transgenic <i>Arabidopsis</i> of RNAi constructs from leaf tissue	115
4.9	Phenotype of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA20ox</i> construct	118
4.10	Measurement of growth parameters of transgenic Arabidopsis carrying pH2OE-EgGA20ox construct	119
4.11	Expression of <i>EgGA20ox</i> gene in transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA20ox</i> construct in	120
4.12	different tissues with relative band intensity Phenotype of transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGA20ox</i> construct	122
4.13	Measurement of growth parameters of transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGA20ox</i> construct	123
4.14	Expression of <i>EgGA20ox</i> gene in transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGA20ox</i> construct	124
4.15	in different tissues with relative band intensity Morphology of leaf, silique and flower of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA20ox</i> and pH7RNAi- <i>EgGA20ox</i> construct	125

 \bigcirc

4.16	Phenotype of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA2ox</i> construct.	127
4.17	Measurement of growth parameters of transgenic Arabidopsis carrying pH2OE-EgGA2ox construct	128
4.18	Expression of <i>EgGA2ox</i> gene in transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA2ox</i> construct in different tissues with relative band intensity	129
4.19	Phenotype of transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGA2ox</i> construct.	131
4.20	Measurement of growth parameters of transgenic Arabidopsis carrying pH7RNAi-EgGA2ox construct	132
4.21	Expression of <i>EgGA2ox</i> gene in transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGA2ox</i> construct in different tissues with relative band intensity	133
4.22	Morphology of leaf, silique and flower of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGA2ox</i> and pH7RNAi- <i>EgGA2ox</i> constructs	134
4.23	Phenotype of transgenic Arabidopsis carrying pH2OE-EgGAI construct	136
4.24	Measurement of growth parameters of transgenic Arabidopsis carrying pH2OE- <i>EgGAI</i> construct	137
4.25	Expression of <i>EgGAI</i> gene in transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGAI</i> construct in different tissues with relative band intensity	138
4.26	Phenotype of transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGAI</i> construct	139
4.27	Measurement of growth parameter of transgenic Arabidopsis carrying pH7RNAi-EgGAI construct.	140
4.28	Expression of <i>EgGAI</i> gene transgenic <i>Arabidopsis</i> carrying pH7RNAi- <i>EgGAI</i> construct in different tissues	141
4.29	Morphology of leaf, silique and flower of transgenic <i>Arabidopsis</i> carrying pH2OE- <i>EgGAI</i> and pH7RNAi- <i>EgGAI</i> constructs.	143
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LIST OF ABBREVIATIONS

°C L µl ml mg cm mm kg WAT FFB PBZ PCR GA ox IPP GGPP CaMV CPP CaMV CPP CaMV CPP CPS KS <i>g</i> bp kb cDNA DNA RNA RNA RT-PCR qPCR	degree Celsius litre microlitre milligram centimetre millimetre kilogram Week after treatment Fresh fruit bunches Paclobutrazol Polymerase chain reaction Gibbellin oxidase Isopentenyl diphosphate Geranylgeranyl pyrophosphate Cauliflower mosaic virus Copalyl diphosphate <i>ent</i> -copalyl diphosphate synthase <i>ent</i> -kaurene synthase <i>ent</i> -kaurene synthase gravity Base pair Kilo base Complementary DNA Deoxyribonucleic acid Ribonucleic acid Reverse transcription - polymerase chain reaction Real-time polymerase chain reaction
qPCR rpm EB TAE MPOB MPOC	Real-time polymerase chain reaction Rotatation per minute Elution buffer Tris-acetate-EDTA Malaysian Palm Oil Board Malaysian Palm Oil Council
\bigcirc	

CHAPTER 1

INTRODUCTION

1.1 Research background

Palm oil is the most traded oil in the world. The demand of the palm oil from the world's oils and fats market has been steadily increasing over the years (MPOB, 2017). Malaysia as one of the palm oil producing countries accounting for over one third of the total palm oil production in world export trade. The oil palm planted area across the nation covers almost 5.74 million hectares in 2016 (MPOB, 2017).

Despite vast plantation of the oil palm, the industry in Malaysia is facing the falling of fresh fruit bunches (FFB) productivity. The decrease of the yield and productivity are partly determined by the height of the oil palm tree. Management of tall oil palm tree is costly and will potentially damage the quality of the fruit upon harvesting. Current oil palm planting materials increase at the rate of 40-75 cm/year (Kushairi *et al.*, 1999). The palms will be too tall thus replanting programs after 25 to 30 years is required.

Plant height is often associated with gibberellic acid (GA). GA is one of the phytohormones that regulates many vital plant growth and developmental processes which includes seed germination, leaf expansion, induction of flowering and plant height (Yamaguchi, 2008). Previous studies showed that regulating gibberellins biosynthesis and signaling altered the height of many plants species (Li *et al.*, 2016; Liang *et al.*, 2014). Therefore, regulating plant height especially in oil palm by manipulating the gibberellins biosynthesis and signaling can be significant.

1.2 Problem Statements and Objectives

Numerous efforts have been done to study the height regulation in many plant species. Previous studies reported that manipulating GA-related genes affected the stature of various species of plant such as *Triticum aestivum* (Pearce *et al.*, 2015), *Oryza sativa* (Gebre *et al.*, 2013), *Solanum lycopersicum* (Chen *et al.*, 2016) and *Panicum virgatum* (Wuddineh *et al.*, 2015). Genes that are involved in height regulation in GA biosynthesis and signaling from the oil palm are yet to be revealed. Comprehensive researches which are related to the

characterization of the genes functions associated with GA is important to improve our understanding on height regulation mechanism in oil palm.

In planta characterization of genes function is often limited by time and cost constraints. Therefore, characterization of genes functions using heterologous system, *Arabidopsis thaliana* was opted to observe and evaluate the functions of the genes. The model plant *Arabidopsis* provides a convenient *in vivo* system for performing functional analysis of genes as better approach for cost and time efficiencies (Zubaidah *et al.*, 2017).

Thus, this research was conducted to study genes that are related to height regulation in oil palm. The main objective of the research was to isolate GA-related genes from the oil palm (*Elaeis guineensis*) and characterize their functions.

Therefore, the objectives of this study are:

- 1. To study the effects of PBZ on the growth pattern of clonal oil palm physiologically and morphologically.
- 2. To isolate and perform *in-silico* characterization of gibberellic acids related genes from clonal oil palm.
- 3. To profile the expression of gibberellic acids related genes in different oil palm tissues using RT-PCR and PBZ treated leaf tissue using qPCR.
- 4. To generate transgenic *Arabidopsis* lines (overexpression and RNAi) carrying GA-related genes and perform functional charaterization analysis.

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