

UNIVERSITI PUTRA MALAYSIA

ISOLATION AND MOLECULAR CHARACTERIZATION OF EgCBF3 ENCODING OIL PALM CBF/DREB TRANSCRIPTION FACTOR AND EFFECTS OF ITS ECTOPIC EXPRESSION IN TOMATO (Solanum lycopersicum cv. MT1)

MORTAZA EBRAHIMI

FP 2015 79



ISOLATION AND MOLECULAR CHARACTERIZATION OF EgCBF3 ENCODING OIL PALM CBF/DREB TRANSCRIPTION FACTOR AND EFFECTS OF ITS ECTOPIC EXPRESSION IN TOMATO (Solanum lycopersicum cv. MT1)

By

MORTAZA EBRAHIMI

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Doctor of Philosophy

February 2015

COPYRIGHT

All material contained within the thesis, including without limitation text, logos, icons, photographs and all other artwork, is copyright material of Universiti Putra Malaysia unless otherwise stated. Use may be made of any material contained within the thesis for non-commercial purposes from the copyright holder. Commercial use of material may only be made with the express, prior, written permission of Universiti Putra Malaysia.

Copyright © Universiti Putra Malaysia

C



Specially Dedicated

To my wife, children and parents

For their Love & Supports

C

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Doctor of Philosophy

ISOLATION AND MOLECULAR CHARACTERIZATION OF *EgCBF3* ENCODING OIL PALM CBF/DREB TRANSCRIPTION FACTOR AND EFFECTS OF ITS ECTOPIC EXPRESSION IN TOMATO (*Solanum lycopersicum* CV. MT1)

By

MORTAZA EBRAHIMI

February 2015

Chairman: Professor Datin Siti Nor Akmar Abdullah, PhD

Faculty: Agriculture

One of the well understood mechanisms in plants to overcome biotic and abiotic stresses is mediated through transcription factors. The APETALA2/Ethylene Response Factor (AP2/ERF) is one of the plant specific transcription factors. They are categorized into three families, termed AP2, RAV and ERF. ERF family is divided into two major subfamilies; the Ethylene Responsive Factors (ERF) and the C repeat-binding factor/dehydration responsive element-binding factor (CBF/DREB). In this study, a new member of the *CBF/DREB* was isolated from oil palm (*Elaeis guineensis* var. Dura × Pisifera) ripening fruit and designated as *EgCBF3*. Bioinformatics analysis revealed that *EgCBF3* belongs to A-1 subgroup of CBF/DREB subfamily. The transcripts of *EgCBF3* were detected ubiquitously, in oil palm's root, leave and mesocarp tissue. This gene was responsive to the cold, ethylene, abscisic acid, NaCl and polyethylene glycol treatments. The *EgCBF3::mGFP* fusion protein was localized to the nucleus of onion epidermal cells. Using in vitro and in vivo DNA-protein binding assays it has been shown that E_gCBF3 was able to bind with DRE/CRT element. Expression pattern of polygalacturonase (SlPG) and SlE8 two fruit ripening related genes were affected under transient overexpression of EgCBF3 in tomato fruits at four different developmental stages. Two carotenoid biosynthesis-related genes phytoene desaturase (SIPDS) and phytoene synthetase (SIPSY) showed upregulation at four studied stages. Same result was observed for 9-cisepoxycarotenoid dioxygenase (SINCED1). The ethylene biosynthesis related genes demonstrated an expression pattern related to the fruit developmental stages. These results predict that EgCBF3 can mediate abiotic stress response in ripening fruits and regulates the ripening process through modulation of ethylene and abscisic acid biosynthesis. Functional characterization of EgCBF3 was further performed using stable transformation of tomato cv. MT1. An in vitro technique was developed for efficient regeneration of transgenic tomato. Seed pretreatment with Thidiazuron (TDZ, 1 mg/l) enhanced organogenesis of the cotyledonary leaf with abaxial side down on MS medium supplemented with 2 mg/l Benzyl Amino Purine (BAP) and 0.02 mg/l Indole Acetic Acid (IAA). The EgCBF3 tomatoes demonstrated dwarfism for the first few weeks, delayed leaf senescence and flowering time, increased chlorophyll content (~0.085 mg/cm²) and abnormal morphology compare to wild type. In vitro studies of the transgenic lines confirmed that overproduction of EgCBF3 can enhance drought, salt and cold tolerance in tomato. Expression of ethylene biosynthesis-related genes encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and 1aminocyclopropane-1-carboxylic acid oxydase (ACO) were down-regulated in transgenic lines. Also, the studied pathogenesis-related genes showed altered expression in wounded leaves of transgenic plants compared to wild types. These findings were consistent with the hypothesis that *EgCBF3* can modulate plant growth and development, as well plant biotic and abiotic stress tolerance through direct regulation of related regulons, and partly via ethylene regulatory pathway.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

PEMENCILAN DAN PENCIRIAN MOLEKUL EgCBF3 PENGEKOD FAKTOR TRANSKRIPSI CBF / DREB KELAPA SAWIT DAN KESAN PENGEKSPRESAN EKTOPIKNYA DI DALAM TOMATO (Solanum lycopersicum cv. MT1)

oleh

MORTAZA EBRAHIMI

February 2015

Pengerusi: Profesor Datin Siti Nor Akmar Abdullah, PhD

Fakulti: Pertanian

Salah satu mekanisma yang difahami secara mendalam adalah perantaraan melalui faktor transkripsi. 'APETALA2/Ethylene Response factor' (AP2/ERF) adalah salah satu faktor transkripsi khusus tumbuhan. Mereka dikategorikan kepada tiga famili iaitu AP2, RAV dan ERF. Famili ERF dibahagikan kepada dua subfamili utama: 'Ethylene Responsive Factors' (ERF) dan 'repeat-binding factor/dehydration responsive element-binding factor' (CBF/DREB). Dalam kajian ini, ahli baru CBF/DREB telah dipencilkan daripada buah kelapa sawit (Elaeis guineensis var. Dura \times Pisifera) masak dan dinamakan sebagai EgCBF3. Analisis bioinformatik mendedahkan EgCBF3 adalah kepunyaan subfamili CBF/DREB kumpulan A-1. Traskrip EgCBF3 dikesan merata dalam akar, daun, dan tisu mesokarp. Gen ini responsif pada rawatan sejuk, etilina, asid absisik, NaCl dan polietilina glikol. Protein gabungan GFP EgCBF3 tersasar dalam nukleus sel epidermis bawang. Asai pengikat DNA-protein in vitro dan in vivo menunjukkan bahawa EgCBF3 mengikat elemen DRE/CRT. Corak pengekspresan polygalacturonase (SIPG) dan SIE8 dua gen kemasakan buah responsif etilina menunjukkan perubahan pengekspresan dalam pengekspresan transien EgCBF3 dalam buah tomato pada empat peringkat perkembangan berlainan. Dua gen berkaitan biosintesis karotenoid, phytoene desaturase (SIPDS) dan phytoene synthetase (SIPSY) menunjukkan peningkatan tahap pengekspresan dalam keempat peringkat yang dikaji. Keputusan yang sama telah dilihat untuk 9-cisepoxycarotenoid dioxygenase (SINCED1). Gen biosintesis etilina menunjukkan corak pengekspresan bertalian dengan peringkat perkembangan buah. Keputusan ini mencadangkan EgCBF3 menjadi perantara tindakbalas tekanan abiotik pada peringkat kemasakan buah dan mengawal proses peranuman melalui modulasi biosintesis etilina dan asid absisik. Pencirian kefungsian EgCBF3 selanjutnya dibuat melalui transformasi kekal menggunakan tomato cv. MT1. Teknik in vitro telah dibangunkan untuk kecekapan dalam pertumbuhan semula tomato transgenik. Prarawatan biji benih dengan TDZ (1 mg/L) meningkatkan organogenesis daun kotiledon dengan bahagian abaksial di bawah di dalam media MS yang ditambah dengan 2 mg/L BAP dan 0.02 mg/L IAA.. Tomato EgCBF3 menunjukkan sifat kerdil untuk beberapa minggu, penangguhan senesens dan pembungaan, peningkatan kandungan klorofil (~0.085 mg/cm²) dan morfologi bunga yang tidak normal berbanding tomato liar. Kajian in vitro ke atas lajur transgenik mengesahkan bahawa penghasilan berlebihan EgCBF3 boleh meningkatkan toleransi terhadap kekeringan, kemasinan dan kesejukan dalam tomato. Ekspresi gen biosintesis etilena yang mengekodkan 1-aminocyclopropane-1-carboxylic acid synthase (ACS) dan 1-aminocyclopropane-1-carboxylic acid oxidase (ACO) telah menurun. Juga gen pengekspresan gen patogenesis yang dikaji menunjukkan perubahan dalam tisu daun transgenik yang cedera berbanding jenis liar. Penemuan ini adalah konsisten dengan hipotesis yang EgCBF3 boleh mengawal pertumbuhan dan perkembangan tumbuhan, juga toleransi terhadap tekanan biotik dan abiotik melalui kawalan terus regulon dan sebahagiannya melalui tapak jalan peagawalaturan etilina.

iv

ACKNOWLEDGEMENTS

Here by, I would like to express my utmost appreciation to my supervisor, Professor Datin Dr. Siti Nor Akmar Binti Abdullah, who gives me constructive comments and great support.

I would also like to express my deepest thanks to my beloved wife, for her endless kindness, support and love, infinite patience and understanding, and my dearest children Paria and Mohammad Hossein.

Last but not least, very special thanks to my loving father, father-in-law, mother and mother-in-law for their endless love and support, and sincere thanks to all of my family members and friends. I certify that a Thesis Examination Committee has met on to conduct the final examination of Mortaza Ebrahimi on his thesis entitled " **ISOLATION AND MOLECULAR CHARACTERIZATION OF OIL PALM CBF/DREB TRANSCRIPTION FACTOR, EGCBF3 AND EFFECTS OF ITS ECTOPIC EXPRESSION IN TOMATO** (*Solanum lycopersicum* cv. MT1)" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Pertanian Malaysia [P.U. (A) 106] 15 March 1998. The Committee recommends that the student be awarded the relevant degree of Doctor of Philosophy.

Members of the Thesis Examination Committee were as follows:

Mohd Rafii bin Yusof, PhD Professor Institute of Tropical Agriculture Universiti Putra Malaysia (Chairman)

Halimi bin Mohd Saud, PhD

Associate Professor Faculty of Agriculture Universiti Putra Malaysia (Internal Examiner)

Ho Chai Ling, PhD

Associate Professor Faculty of Biotechnology and Biomolecular Science Universiti Putra Malaysia (Internal Examiner)

Carol Wagstaff, PhD

Associate Professor Faculty of Sciences University of Reading United Kingdom (External Examiner)

BUJANG KIM HUAT, PhD

Professor and Deputy Dean School of Graduate Studies Universiti Putra Malaysia

Date:

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfillment of requirement for degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

Siti Nor Akmar Abdullah, PhD Professor Faculty of Agriculture Universiti Putra Malaysia (Chairman)

Maheran Abdul Aziz PhD

Associate Professor Faculty of Agriculture Universiti Putra Malaysia (Member)

Parameswari Namasivayam, PhD

Associate Professor Faculty of Biotechnology and Biomolecular Sciences Universiti Putra Malaysia (Member)

BUJANG BIN KIM HUAT, PhD

Professor and Dean School of Graduate Studies Universiti Putra Malaysia

Date:

Declaration by graduate student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any other institutions;
- intellectual property from the thesis and copyright of thesis are fullyowned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be obtained from supervisor and the office of Deputy Vice-Chancellor (Research and Innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials as stated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software.

Signature:

Date:

Name and Matric No.: Mortaza Ebrahimi (GS26901)

Declaration by Members of Supervisory Committee

This is to confirm that:

- the research conducted and the writing of this thesis was under our supervision,
- supervision responsibilities as stated in the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) are adhered to.

Signature:

Name of

Chairman of

Supervisory

Committee: Siti Nor Akmar Abdullah, PhD

Signature:

Name of

Member of

Supervisory

Committee: Maheran Abdul Aziz, PhD

Signature:

Name of

Member of

Supervisory

Committee: Parameswari Namasivayam, PhD

TABLE OF CONTENTS

ABSTRACTiABSTRAKiACKNOWLEDGEMENTSyAPPROVALyDECLARATIONyLIST OF TABLESxLIST OF FIGURESxLIST OF APPENDICESxx			Page i iii v vi viii xiii xivi xxiv xxiv
1	INT	RODUCTION	1
2	LIT	ERATURE REVIEW	3
	2.1	Oil Palm	3
	2.2	The Oil Palm Fruit	3
	2.3	Ethylene-Regulated Fruit Ripening	5
	2.4	Ethylene Perception and Signal Transduction	9
	2.5	Transcription Factors Involved in Transcriptional Regulatory	10
		2.5.1 Transcription Factors	10
		2.5.2 Fruit Ripening-Related Transcription Factors	13
	2.6	AP2/ERF (APETALA2/Ethylene Response Element) Superfamily	14
		2.6.1 Structure, Classification and Function	14
		2.6.2 The DREB/CBF (Dehydration Responsive Element- Binding	17
3	BIN	LATION AND CHARACTERIZATION OF A COLD DING FACTOR FROM OIL PALM'S (<i>Elaeis guineensis</i>) SOCARP TISSUE	21
	3.1	Introduction	21
	3.2	Materials and Methods	22
		3.2.1 Plant Materials	22
		3.2.2 Genomic DNA Extraction	22
		3.2.3 Total RNA Extraction	23
		3.2.4 Gene Isolation from cDNA and DNA	23
		3.2.5 Gene Cloning	23
		3.2.6 Transformation of <i>Escherichia coli</i>	24
		3.2.7 Bioinformatics analysis	26

G

		3.2.8	Preparation of Expression Clone	27
		3.2.9	Transformation of <i>Agrobacterium tumefaciens</i> Strain <i>LBA4404</i>	27
		3.2.10	Subcellular Localization:	28
		3.2.11	1 5 5 6	29
		3.2.12	In-Vivo Transactivation Assay using Yeast One-	32
			Hybrid System	
		3.2.13	Characterization of <i>EgCBF3</i>	36
	3.3	RESUL	LTS	39
		3.3.1	Isolation and In Silico Analysis	40
		3.3.2	Subcellular Localization	44
		3.3.3	In Vivo DNA-Protein Binding Assay	45
		3.3.4	In Vitro DNA-Protein Binding Assay	45
		3.3.5	Expression Profile of <i>EgCBF3</i> in Oil Palm Tissues	47
		3.3.6	EgCBF3-Mediated Transient Expression of Ripening-	51
		1.1	Related	
	3.4	Discuss	sion	53
4	IMP	ROVEN	IENT OF THE ORGANOGENESIS AND	57
	AGI	ROBAC	FERIUM-MEDIATED TRANSFORMATION OF	
	TON	AATO (S	Solanum lycopersicum cv. MT1)	
	4.1	Introdu	ation	57
	4.2		als and Methods	58
	7.2	4.2.1	Plant Materials	58
		4.2.2	Regeneration Media	58
		4.2.3	Root Induction Medium	58
		4.2.4	Hardening	59
		4.2.5	Agrobacterium- Mediated Transformation	59
		4.2.6	Data Analysis	61
	4.3	RESUL		61
		4.3.1	Effect of TDZ	61
		4.3.2	Effect of Explant	63
		4.3.3	Effect of Growth Regulators	64
		4.3.4	Agrobacterium-Mediated Transformation and	72
			Verification of	
	4.4	Discuss	sion	72
5	FUN	ICTION	AL ANALVSIS OF E-CRE2 ENCODING AN OH	76
3			AL ANALYSIS OF <i>EgCBF3</i> ENCODING AN OIL /DREB IN TRANSGENIC TOMATO (<i>Solanum</i>	70
			e cv. MT1)	
				_
	5.1	Introdu		76
	5.2		als and Methods	77
		5.2.1	Plant Materials, Total RNA Extraction and RT-PCR	77
		5.2.2	Cloning Method	77

 \mathbf{G}

		5.2.3	Plant Transformation	11
		5.2.4	Morphological Characterization of Transgenic	78
			Tomato	
		5.2.5	Relative Water Content	78
		5.2.6	Cell Membrane Stability	78
		5.2.7	Leaf Chlorophyll Content	78
		5.2.8	Abiotic Stress Assessment	79
		5.2.9	Gene Expression Analysis	79
		5.2.10	Transient Assay	80
		5.2.11	Data Analysis	80
	5.3	RESUI	LTS	82
		5.3.1	Verification of Transgenic Tomatoes Harboring	82
			EgCBF3 Gene	
		5.3.2	Morphological and Physiological Characterization of	82
			the	
		5.3.3	Stress Assessment	86
		5.3.4	Ethylene Biosynthesis-Related Genes Expression	89
		5.3.5	Pathogenesis-Related Gene Expression	90
	5.4	Discuss	sion	95
6	SUM	IMERY	, CONCLUSION AND RECOMMENDATIONS	98
	FOR	R FUTUI	RE RESEARCH	
REFERENCE 10			101	
APPENDICES			123	
BIODATA OF STUDENT			141	
LIS	LIST OF PUBLICATIONS 142			142

 (\mathbf{G})

LIST OF TABLES

Table		Page
2.1	Different classes of eukaryotic transcription factors and their distribution in plant and animal kingdom.	12
2.2	Comparison of several plant transcription factor databases	13
2.3	Categories of plant transcription factors and the structural features of their conserved domains.	15
3.1	The oligonucleotides were designed with two overhangs at 5' and 3' sides to clone the oligoes directionally in pAbAi vector. 5'-HindIII:AAGCTT and 3'-XhoI: CTCGAG. The cis-elements and their mutants are shown in bold and underlined format.	33
3.2	Results of the Minimal Inhibitory Concentration of Aureobasidin A for Bait-Reporter Yeast Strains. As indicated in the table, AbA with 100 ng/ml is the optimum minimal inhibitory concentration to screen the yeast colonies for Prey-Bait interaction.	35
3.3	List of primers were used in real-time PCR analysis in tomato (Solanum lycopersicum)	38
5.1	List of primers used in real-time PCR analysis	81
5.2	Mean comparison of different morphological and physiological parameters between transgenic EgCBF3 plants (T1, T2 and T3) and wild type tomato. The parameters were recorded in plants with same condition in transgenic greenhouse.	83

LIST OF FIGURES

Figure

2.3

- 2.1 Schematic representation of the main structures in oil palm fruit (Poku, 2002).
- Hormonal regulation of fruit ripening in various phases of 2.2 tomato fruit development. (A) Fruit developmental stages. I. floral development and fruit set; II, cell division during early fruit development; III, cell expansion and fruit maturation, and IV, fruit ripening. (B) Schematic representation of hormonal fluxes. (C) Sigmoidal growth curve, mitotic index and growth rate. (D) Some of the genes with altered expression is associated with hormonal changes in different phases of developing fruit. The downpointing arrow represents the downregulation of a gene. Le20ox-1, Le20ox-2 and Le20ox-3 (GA20 oxidase 1, 2 and 3, respectively); GAD3 (similar to non-metallo short-chain alcohol dehydrogenase); Lin5, Lin7 and Lin6 (invertase isoenzymes); LeACS2, LeACS4, LeACS6 and LeACS1A (1aminocyclopropane-1-carboxylic acid (ACC) synthase-2, 4, 6 and 1A, respectively); Le3OH-2 (GA 3bhvdroxylase); CDKA1 (cyclin-dependent protein Kinases- type A-1); CDKA2 (cyclindependent protein Kinases- type A-2); CDKB1:1 (cyclindependent protein Kinases- type B-1:1); CDKB1:2 (cyclindependent protein Kinases- type B-1:2); CDKC:1 (cyclindependent protein Kinases- type C:1); LeCycD3:1, LeCycD3:2 and LeCycD3:3 (D3 cyclins); LeCPS (copalyl diphosphate synthase); DR12 (an auxin response factor); LeExp2 and LeExp4 (Expansin 2 and 4); LeEXT1 (xyloglucan endotransglycolase); Cel7 (endo-1, 4-b-glucanase); LeSNF4 (sucrose non-fermenting 4); LeNOR (non-ripening); LeMADS-RIN (a MADS-box transcriptional factor); LeETR1-6 (ethylene receptor 1-6) and LeCTR1 (Constitutive Triple Response 1) (Srivastava and Handa. 2005).

(A and B) Differential expression of *ACSs* and *ACOs* during fruit development and ripening associated with two systems of ethylene biosynthesis in tomato. Ethylene production in autoinhibitory system (system I) is mediated by a reduction in *LeACS1A* and 6 expression. Expression of *LeACS2* and 4 and *LeACO1* and 4 at the onset of fruit development and ripening mediate autocatalytic ethylene synthesis (system II) (Barry and Giovannoni, 2007; Argueso et al., 2007).

Page

4

6

- 2.4 Schematic representation of the ethylene biosynthetic pathway. Each step is catalysed by the enzyme noted above the arrow. AdoMet: S-adenosyl-methionine; Met: methionine; ACC: 1aminocyclopropane-1-carboxylic acid; MTA: methylthioadenine. Inputs that regulate the enzymes are shown above the pathway, either via a transcriptional or posttranscriptional mechanism (Argueso et al., 2007).
- 2.5 Representation of ethylene perception and signal transduction in tomato. Single copper ion (Cu) mediates the ethylene to bind to the ethylene receptors (*LeETR1*, *LeETR2*, *NR*, *LeETR4*, *LeETR5*, *LeETR6*). The signal transduction pathway is negatively regulated by binding of the ethylene to the receptors, mediated by interaction with *LeCTR1*, *LeCTR3* and *LeCTR4*. The MAPK cascade (*LeSIMKK* and *LeMPK6*) is released by inactivation of LeCTR protein(s) in the presence of ethylene; resulted in activation of ethylene signaling pathway. Downstream of the pathway, there are the other components like *LeEIN2*, *EIN3-like* and *LeEIL1–LeEIL4* transcription factors. Expression of the ERFs is mediated by these transcription factors, which in turn activate ethylene-responsive target genes (Adams-Phillips et al., 2004).
- 2.6 Schematic representation of DNA-binding domain and 16 oligomerization site in AP2/ERF transcription factors. Solid box representing the DNA-binding domain; dotted box, oligomerization site. In AP2 family there are two AP2 domain separated with a small conserved sequence (Liu et al., 1999).
- 2.7 Schematic representation of AP2 domain of AP2/ERF 16 transcription factors. Three β -sheets and an α -helix are indicated in the picture.
- 2.8 Schematic representation of different signatures and AP2 18 domain on a DREB/CBF member of Arabidopsis (*AtCBF3*: AT4G25480.1) (CLC genomics workbench ver. 3.6.5).
- 3.1 Schematic diagram of *pDONR/zeo* and the elements on this 25 vector.
- 3.2 Schematic diagram of *pMDC83* destination vector. The ORF of *EgCBF3* was cloned down-stream of 2x35S CaMV promoter and up-stream of mGFP as a reporter gene.
- 3.3 Schematic representation of constructs used for transformation 29 of A. *tumefaciens* strain *LBA4404*. The transformed bacteria

11

were used for subcellular localization assay.

- 3.4 Schematic map of the *pAbAi* Vector. This is a yeast reporter vector in which there is a multiple cloning site (MCS) up-stream of the yeast *iso-1-cytochrome C* minimal promoter for cloning of the Bait sequence. Deduced promoter runs an antibiotic resistance gene (*AUR1-C*) that confers resistance to *Aureobasidin* A (AbA). Interaction of the proteins with Bait as a target sequence is used to screen GAL4 AD/cDNA fusion libraries. Positive interaction of protein with target sequence drives the expression of *AUR1-C* and as a result, the yeast colonies are resistant to AbA.
- 3.5 Schematic illustration of homologous recombination of SMART 36 DNA (*EgCBF3*) in the yeast cells (B), and map of the *pGADT7-Rec* Vector (A). This vector is *Smal*-linearized provided by the kit and engineered to express a fusion protein (GAL4 AD and ectopic protein) in the yeast cells. Yeast transformation with the SMART DNA and *Smal*-linearized *pGADT7-Rec* is resulted in fully functional and circular vector. The yeast cellular *recombinases* will use the SMART DNA to repair the gap in *pGADT7-Rec*. This confers the yeast strain *Y1HGold* to survive and grow in –Leu medium.
- 3.6 Phylogenetic analysis of selected CBF-related proteins. 40 Phylogenetic tree constructed for *EgCBF3* gene. The tree was constructed from the amino acid sequences using MEGA6.06 software, by Neighbor Joining algorithm. The phylogenetic tree was prepared using bootstrap analysis with 1000 replicates. The substitutions type and model were amino acid and JTT (Jones-Taylor-Thornton), respectively.
- 3.7 Multiple sequence alignment of the deduced amino acid 41 sequences. Comparison of the deduced amino acid sequences of CBF-related proteins that have maximum sequence similarity with *EgCBF3* (Accession: KC312892.1; GI:460332880) with the other CBF proteins (*AtCBF1*: AT4G25490.1; *AtCBF2*: AT4G25470.1; *AtCBF3*: AT4G25480.1; *SlCBF1*: AAK57551; *SlCBF2*: AAS77821; *SlCBF3*: AAS77819; *EgCBF-like1*: DQ497736.1; *EgCBF-like2*: DQ497735.1).
- 3.8 (a) The schematic representation of different motifs and AP2domain in *EgCBF3*. The AP2 domain resides between amino acids 47-105 flanking with two signatures (ETRHP and DSAW). Three β -sheets and one α -helix were predicted in the AP2 domain. A Nuclear Localization Sequence (NLS) was detected at up-stream of AP2 domain. The deduced amino acid

sequence was analyzed using CLC Genomic Workbench ver. 3.6.5 software. (b) The predicted protein structure. The amino acid sequence was submitted to the Phyre2 software (http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index) (Kelley and Sternberg, 2009). Phyre2 uses the profile–profile matching algorithms to predict protein structure. The three β -sheets and one α -helix are indicated in the picture.

- 3.9 (a) Prediction of the biological process ontology of *EgCBF3*. The horizontal axis is demonstrated as % of reliability (https://www.predictprotein.org/). (b) Prediction of the subcellular localization EgCBF3. for (https://www.predictprotein.org/). In silico analysis showed that EgCBF3 is localized in the nucleus. Predictprotein uses a Metastudent predictator for gene ontology (GO). First a BLAST query is run for a given amino acid sequence. If the target protein hit a similar sequence, the output is used to calculate GO and there is no prediction with no similar amino acid sequence in the BLAST database. Metastudent uses F1 score to predict the reliability. The maximum F1 score achives in metastudent is 0.36 for the biological process ontology prediction. The F1 score is calculated using the following equation: F1= (2 × precision \times recall)/precision + recall. Where recall means: 'Precision corresponds to the number of correctly predicted GO terms divided by the number of all predicted GO terms'.
- 3.10 Subcellular localization of EgCBF3 protein fused to N-terminal of mGFP in the pMDC83 destination vector. Onion epidermal cells were transiently transformed with pEXP83:: 35SCaMV-mGFP (negative control), pEXP83::EgCBF3-mGFP and pEXP83::35S:EgAP2-1-mGFP (positive control) vectors. EgCBF3-mGFP fusion protein and control mGFP were detected with a fluorescent microscope (Nikon). Fluorescent images (left) and bright field images (right).
- 3.11 In vivo DNA-protein binding assay of EgCBF3 protein using 46 yeast one-hybrid system. The protein was fused to GAL4 AD of pGADT7-Rec vector. The first and second rows indicate the growth of different prey containing Bait-strains in SD/-Leu medium without antibiotic and with antibiotic, respectively. Petri dishes are 100mm×15mm.
- 3.12 Electrophoretic Mobility Shift Assay of *EgCBF3* with different 48 *cis*-elements: a DNA protein binding assay of *EgCBF3* protein with DRE/CRT *cis*-element and its mutant. b DNA protein binding assay of *EgCBF3* protein with GCC-box *cis*-element and its mutant. c nucleotide sequence of DRE/CRT, mutated

DRE/CRT (mDRE/CRT), GCC-box and mutated GCC-box (mGCC-box) probes.

- 3.13 (a) Expression profile of *EgCBF3* in oil palm's leaf, root and mesocarp tissue at different stages of development (waa: weeks after anthesis). Expression ratio of *EgCBF3* in mesocarp tissue under different treatments: (b) Cold (4°C) treatment, (c) PEG (20% PEG8000) treatment, (d) Ethylene (10% (w/v) ethephon) treatment, (e) ABA (100 μ M) treatment and f NaCl (300 mM) treatment. The expression ratio was calculated using the REST2009 software ver.2.0.13 (QIAGEN). Gene expression was normalized with *Elaeis guineensis* actine gene (accession number: AY550991.1) and *EgGAPDH* gene (accession number: DQ267444.1). The vertical axis for a, b and d are displayed in Log₁₀ scale.
- 3.14 Expression ratio of fruit ripening related genes (PG and E8), two carotenoid biosynthesis-related genes (PDS and PSY), ethylene biosynthesis-related (EBR) enzymes (ACS2, ACS4, ACO1 and ACO4) and ABA biosynthesis-related gene (NCED1) in a transient overexpression assay of EgCBF3 in tomato fruit in four distinct developmental stages (SG: small green, MG: mature green, BR: breaker and MR: mature red). WT series indicate the expression of deduced gene in normal fruit for each gene. Control series are the result of agro-injected fruit with empty vector. EgCBF3 series show the results of agroinjected fruit using EgCBF3 containing vector. Cell wall degrading polygalacturonase (PG), phytoene desaturase (SlPDS), phytoene synthetase (SIPSY), ethylene-responsive fruit ripening gene (SIE8), ACC synthase 2 (SIACS2), ACC synthase 4 (SlACS4), 1-aminocyclopropane-1-carboxylate oxidase 1 (SlACO1). 1-aminocyclopropane-1-carboxylate oxidase 4 (SIACO4), 9-cis-epoxycarotenoid dioxygenase (SINCED1). The expression ratio was calculated using the REST2009 software ver.2.0.13 (QIAGEN). Gene expression was normalized with Solanum lycopersicum elongation factor 1a (SlEF1 α) gene (accession number: X53043.1) and actin (SlAct) gene (accession number: U60480.1). The vertical axis for all figures is displayed in Log_{10} scale.
- 4.1 Schematic diagram of *pMDC32* destination vector. The ORF of 60 *EgCBF3* was cloned down-stream of 2x35S CaMV promoter.
- 4.2 A) Preparation of tomato explants for tissue culture by seed 62 germination on MS medium with different concentrations of TDZ (0, 1 and 2 mg/l). (B) Developments of the buds and early

50

stage of shoot regeneration on cotyledonary leaf of tomato cv. MT1, two weeks after culture. (C) Shoot development on cotyledonary leaf of tomato cv. MT1, three weeks after culture. (D) Subculture of the regenerated shoots to root induction medium after four weeks.

- 4.3 Effects of TDZ pretreatment (horizontal axis) on organogenesis of tomato (cultivar MT1). (A) Percentage of regenerated explant/replication. (B) Average number of bud(s) per regenerated explant(s)/ replication. (C) Average number of shoot(s) per regenerated explant(s)/ replication. (D) Mean of the explant weight (mg) after 4 weeks. In all Figures rep. is the abbreviation for replication. The values with the same letter are not significantly different (p \leq 0.05). Mean comparison using Duncan's multiple range test.
- 4.4 Effects of explant type (horizontal axis) on organogenesis of tomato (cultivar MT1). (A) Percentage of regenerated explant/replication. (B) Average number of bud(s) per regenerated explant(s)/ replication. (C) Average number of shoot(s) per regenerated explant(s)/ replication. (D) Mean of the explant weight (mg) after 4 weeks. In all Figures rep. is the abbreviation for replication. The values with same letter are not different significantly (p≤0.05). Mean comparison using Duncan's multiple range test.
- 4.5 Effects of different types of cytokinin (horizontal axis) on organogenesis of tomato (cultivar MT1). (A) Percentage of regenerated explant/replication. (B) Average number of bud(s) per regenerated explant(s)/replication. (C) Average number of shoot(s) per regenerated explant(s)/ replication. (D) Mean of the explant weight (mg) after 4 weeks. In all Figures rep. is the abbreviation for replication. The values with same letter are not different significantly (p≤0.05). Mean comparison using Duncan's multiple range test.
- 4.6 Effect of different culture media (horizontal axis) on percentage of regenerated explants per replication of tomato (cv. MT1). Rep. is the abbreviation for replication. Mean comparison with Duncan's Multiple Range Test (p≤0.05). In horizontal axis the growth regulator (GR) 1, 2 and 3 means BAP, Kin and ZR, respectively. The numbers in horizontal axis are in mg/l.
- 4.7 Effect of different culture media (horizontal axis) on average 66 number of bud(s) per regenerated explant(s)/replication of tomato (cultivar MT1). Rep. is the abbreviation for replication.

65

64

63

66

xix

Mean comparison with Duncan's Multiple Range Test ($p \le 0.05$). In horizontal axis the growth regulator (GR) 1, 2 and 3 means BAP, Kin and ZR, respectively. The numbers in horizontal axis are in mg/l.

- 4.8 Effect of different culture media (horizontal axis) on average number of shoot(s) per regenerated explant(s)/replication of tomato (cultivar MT1). Rep. is the abbreviation for replication. Mean comparison with Duncan's Multiple Range Test (p≤0.05). In horizontal axis the growth regulator (GR) 1, 2 and 3 means BAP, Kin and ZR, respectively. The numbers in horizontal axis are in mg/l.
- 4.9 Effect of different culture media (horizontal axis) on mean of explant weight (mg) after 4 weeks. Mean comparison with Duncan's Multiple Range Test ($p \le 0.05$). In horizontal axis the growth regulator (GR) 1, 2 and 3 means BAP, Kin and ZR, respectively. The numbers in horizontal axis are in mg/l.
- 4.10 Effects of the best treatments from interaction of explant pretreatments with different growth regulators and explant type (vertical axis) on percent of regenerated explant per replication of tomato (cultivar MT1). Rep. is short for replication. Extracted from the table C-5 (Appendix C). The numbers in vertical axis are in mg/l.
- 4.11 Effects of the best treatments from interaction of explant pretreatments with different growth regulators and explant type (vertical axis) on average number of bud(s) per regenerated explant(s) per replicate of tomato (cultivar MT1). Rep. is the abbreviation for replication. Extracted from the table C-5 (Appendix C). The numbers in vertical axis are in mg/l.
- 4.12 Effects of the best treatments from interaction of explant pretreatments with different growth regulators and explant type (vertical axis) on average number of shoot(s) per regenerated explant per replicate of tomato (cultivar MT1). Rep. is the abbreviation for replication. Extracted from the table C-5 (Appendix C). The numbers in vertical axis are in mg/l.
- 4.13 Effects of the best treatments from interaction of explant pretreatments with different growth regulators and explant type (vertical axis) on mean of explant weight (mg) after 4 weeks of tomato (cultivar MT1). Extracted from the table C-5 (Appendix C). The numbers in vertical axis are in mg/l.
- 4.14 Regeneration of transgenic tomato cv. MT1. (A) Cotyledonary 73

leaves on selective medium containing appropriate antibiotics, after *Agrobacterium*-mediated transformation procedure. (B) Subculture of the regenerated explants on selective medium with same antibiotics. (C) Shoot regeneration on selective medium. (D) The regenerated shoot was transferred to root induction medium containing antibiotics. (E) Acclimatization of regenerated tomato plantlets in growth chamber. (F) Transplant of regenerated tomatoes cv. MT1 to the transgenic green house.

- 4.15 PCR mediated verification of transgenic plants. (A) A PCR product with ~990bp was observed in transgenic plants using a primer pairs from inside of 35S CaMV promoter to the end of *EgCBF3* coding region (lines 1-4). (B) There was no band with the same primers in wild type tomato (lines 5-9). GeneRuler (GR) (Thermo SCIENTIFIC #SM0331).
- 5.1 Verification of transgenic tomatoes and constitutive expression 84 of the *EgCBF3* in the root and leaves of transgenic tomatoes.
- 5.2 Morphological comparison of transgenic tomato harboring EgCBF3 with wild type. (A) Comparison of growth between transgenic tomatoes and wild type at three weeks and (B) 45 days after hardening, respectively. (C and D) Comparison of leaf development between EgCBF3 tomato and wild type, at 2 months and three weeks after hardening, respectively.
- 5.3 Comparison of rooting system development by ectopic 85 expression of *EgCBF3* in transgenic tomato (top row) and wild type (bellow). Transgenic lines produced a huge rooting system compared to wild type tomatoes under the same condition in the transgenic green house.
- 5.4 Comparison of the flowers among transgenic tomatoes 85 overexpression EgCBF3 and wild type. More abnormal flowers were produced in EgCBF3 tomatoes compared to wild type tomatoes. The transgenic plants showed altered petal morphology compare to wild type.
- 5.5 Longevity of individual leaves of *EgCBF3* overexpressing 86 plants and wild type tomatoes. (a) Time to leaf yellowing (days after hardening). Time to leaf senescence (days after hardening). Data are demonstrated in mean value \pm SE.
- 5.6 Effects of drought, salt and cold stresses on development of 88 rooting system and shoot growth of transgenic lines harboring *EgCBF3* and wild type tomato in *in vitro* condition. The stress treatments compared with control plants grown *in vitro*

condition without stress (termed normal, as untreated plants) (A) Effect of different stress treatments on root length (cm), (B) Effect of different stress treatments on root number, and (C) Effect of different stress treatments on shoot length (cm).

- 5.7 Comparison of the rooting system and shoot development of transgenic plants overexpressing *EgCBF3* and wild type tomato in normal *in vitro* condition. The transgenic tomato produced a huge and vigorous rooting system in *in vitro* condition compared to wild type tomato. The regenerated shoots demonstrated a dwarf phenotype. The lateral buds in *EgCBF3* tomato start to grow in *in vitro* condition.
- 5.8 Expression pattern of ethylene and ABA biosynthesis-related 92 genes in transgenic *EgCBF3* tomatoes compared to wild type. The bar on the graph representing the mean average of gene expression ratio \pm SE of three replicates in independent experiment. Expression ratio was evaluated by the Rest2009 software ver. 2.0.13 (QIAGEN). Gene expression was normalized with *SlAct* (U60480.1) and *SlEF1a* (X53043.1).
- 5.9 Expression profile of pathogenesis-related genes in transgenic 94 plants harboring EgCBF3 and transient assay compared to wild type tomato cv. MT1, using Real-time PCR. Each bar on the graphs representing the mean average of gene expression ratio±SE of three replicates in independent experiment. The gene expression ratio was calculated by REST2009 V.2.0.13 software (QIAGEN). Gene expression was normalized with SlAct (U60480.1) and SlEF1α (X53043.1).
- 6.1 Schematic diagram representing the effects of cold stress on 100 induction of CBF transcriptional activators in plants and possible mechanisms for enhancement of stress tolerance, growth and development and fruit ripening process. It has been shown that expression of the CBFs is positively regulated by the proteins like ICE and at the bigining of the cold stress there is a transient increase of the ethylene. So, it is predicted that CBFs can modulate plant stress tolerance, growth and developments and fruit ripening partly by direct regulation of related regulons or indirectly through regulation of ethylene biosynthesis-related genes and resulting in altered level of the ethylene. Also, it is proposed that CBFs can regulate expression of PRs (or AFPs) through ethylene signaling pathway or by direct interaction with regulatory elements on their promoter. CORs: Cold Regulated Genes; ICE (Inducer of CBF expression); PRs: Pathogenesis Related genes; AFPs: Anti-freeze Proteins and EBRs: Ethylene

89

xxii

Biosynthesis Related genes.

- B-1 Verification of *pBait-ABA* vectors for four target sequences 126 (GCC-box, m GCC-box, DRE/CRT and mDRE/CRT) using colony PCR. The predicted PCR product is ~1.6 kb. Gene ruler (GR), lines 1, 3 and 4 for GCC-box, 5, 6 and 7 for mGCC-box, 8, 9 and 10 for DRE/CRT, and 11 and 13 for mDRE/CRT containing *pBait-AbA* vector. GeneRuler 100 bp Plus DNA Ladder (Thermo SCIENTIFIC #SM0321).
- B-2 Verification of the yeast Bait-strains using Matchmaker Insert 126 Check PCR Mix 1. The predicted PCR product is ~1.4 kb. Gene ruler (GR). Lines 1, 4, 5, 9 and 11 indicating the positive yeast Bait-strain. GeneRuler 100 bp Plus DNA Ladder (Thermo SCIENTIFIC #SM0321).
- B-3 Verification of the yeast Bait-Prey strains containing (*EgCBF3*). 127 The predicted PCR product is 633 bp. Gene ruler (GR). Lines 1-6 and 13-14 indicating the positive yeast Bait-Prey strains. GeneRuler 100 bp Plus DNA Ladder (Thermo SCIENTIFIC #SM0321).
- B-4 Isolation of the *EgCBF3* from genomic DNA (lines 1-6) and cDNA (lines 7-9). GeneRuler (GR) (Thermo SCIENTIFIC #SM0331).

LIST OF APPENDICES

Appendix		Page	
А	Reagents and Buffers	123	
В	Complementary Images	126	
С	Complementary Results of Data Analysis	128	



 (\mathbf{G})

LIST OF ABBREVIATIONS

AP2/ERF	APETALA2/Ethylene Response Factor		
CBF/DREB	C-Repeat-Binding Factor/Dehydration Responsive Element-		
	Binding Factor		
RAV	Related to ABI3/VP1		
w.a.a	Week After Anthesis		
kb	Kilo Base-Pair		
bp	Base Pairs		
CDS	Coding Region		
cDNA	Complementary DNA		
CTAB	Hexacetyltrimethyl Ammonium Bromide		
DEPC	Diethyl Pyrocarbonate		
DNA	Deoxyribonucleic Acid		
RNA	Ribonucleic Acid		
DNase	Deoxyribonuclease		
RNase	Ribonuclease		
dNTPs	Deoxynucleotides		
SS	Single-Stranded		
ds	Double-Stranded		
LiCl	Lithium Chloride		
EDTA	Ethylene Diamine Tetra Acetic Acid		
EtBr	Ethidium Bromide		
DRE/CRT	Dehydration Response Element/C-Repeat		
TF	Transcription Factor		
rpm	Round per minute		
TE buffer	Tris-EDTA buffer		
PCR	Polymerase Chain Reactions		
RT-PCR	Reverse Transcriptase Polymerase Chain Reaction		
NaCl	Sodium Chloride		
SDS	Sodium Dodecyl Sulphate		
NaOH	Natrium Hydroxide		
LB	Luria-Bertani		
S.O.C	Super Optimal Broth		
OD	Optical Density		
NCBI	National Center For Biotechnology Information Dana-Farber Cancer Institute		
DFCI			
BLAST WU-BLAST	Basic Local Alignment Search Tool Washington University-Basic Local Alignment Search Tool		
3D	3 Dimensional		
Phyer MES	Protein Homology/AnalogY Recognition Engine 2-(N-morpholino)ethanesulfonic acid		
EMSA	Electrophoretic Mobility Shift Assay		
LiAc	Lithium Acetate		
PEG	Polyethylene Glycol		
110	i oryemytene oryeor		

 \bigcirc

PVP	Polyvinylpyrrolidone
ABA	Abscisic Acid
pI	Isoelectric point
KDa	Kilodalton
ACS	1-aminocyclopropane-1-carboxylic acid synthase
ACO	1-aminocyclopropane-1-carboxylic acid oxydase
PG	polygalacturonase
PDS	phytoene desaturase
PSY	phytoene ussatutuse phytoene synthetase
NCED	9-cis-epoxycarotenoid dioxygenase
w/v	Weight/volume
	6
v/v	Volume/volume
ANOVA	Analysis of variance
mRNA	Messenger RNA
TDZ	Thidiazuron
BAP	Benzyl amino purine
Kin	Kinetin
2iP	6-(gamma,gamma-Dimethylallylamino)purine
IAA	Indole Acetic Acid
NAA	Naphthalene Acetic Acid
CaMV	Cauliflower Mosaic Virus
WT	Wild Type
	71

 (\mathbf{C})

CHAPTER 1

INTRODUCTION

Oil palm (*Elaeis guineensis* Jacq.) is a perennial monocot crop originated from West and Central Africa (Soh et al., 2009). Oil palm trees produce oil rich fruits and it is the highest yielder among oil producing crops. This tree is cultivated in 16.4 million hectares of agricultural lands worldwide (FAO, 2013), and Malaysia is undoubtedly one of the biggest producers and exporters of the oil palm products, by having about 17.6 million tons (24.1%) of the total global palm oil trade (Oil World, 2013). It is reported that 77% of the arable land (15% of the total land) in Malaysia is devoted to oil palm (MPOB 2012). The most economic part of this crop is the fruit, in which two types of vegetable oil are produced. Almost 95% of total oil of the fruit is crude palm oil (CPO) produced from the mesocarp tissue, and about 5% of oil is the non-edible palm kernel oil (PKO).

The oil palm fruit, like tomato and many other fruits where there is a burst in ethylene production during the ripening stage (Tranbarger et al., 2011), is categorized as a climacteric fruit. This gaseous hormone plays a key regulatory role in the ripening process in these fruits. This is clearly indicated through comparative transcriptome analysis where 37% of the differentially expressed genes during fruit development and ripening stages in tomato are influenced by ethylene (Alba et al., 2005). Expression of proteins involved in fruit development and ripening is modulated by regulatory proteins and transcription factors (TF) especially play a major role in transcriptional regulation of these genes. Extensive studies have been made on characterization of different classes of TFs regulating the fruit ripening process, upstream as well as downstream of the ethylene signaling pathway, however function of the APETALA2/Ethylene Response Factors (AP2/ERF) proteins have received very little attention. This AP2/ERF superfamily is one of the largest plant specific TFs. The AP2/ERF is classified into three subfamilies: the APETALA2 (AP2) family with two AP2/ERF domains; the RAV (Related to ABI3/VP1) family with a B3 domain and an AP2/ERF domain; and Ethylene Response Factor (ERF) family with one AP2/ERF domain. There are two major subfamilies of the ERF; the Ethylene Responsive Factors (ERF) and the C-repeat-binding factor/dehydration responsive element-binding factor (CBF/DREB). It has been well documented that members of AP2/ERF act as key regulators in plant developmental processes, plant architecture (Chung et al., 2010), and biotic and abiotic stress tolerance in plants (Mei et al., 2007). These proteins are major regulators of fruit ripening via regulation of ethylene biosynthesis and the signaling pathway (Karlova et al., 2011; Tiznado-hernández and Mattoo 2012). Despite the economic importance of oil palm fruits, functions of the regulatory proteins involved in different aspects of fruit ripening process are not thoroughly understood.

Fruit ripening transcriptome analysis for lipid and carotenoid metabolism in oil palm was reported by Tranbarger et al. (2011). Although, their study provided a better understanding of the molecular mechanisms regulating fruit ripening in oil palm, but the mechanism is not fully discovered. Tranbarger et al. (2011) reported that a member of type VII and a type IX transcription factor of AP2/ERF superfamily showed up-regulation at the transition stage from system I of ethylene production to system II (Tranbarger et al., 2011) in the mesocarp tissue of oil palm fruits. Data mining of

transcriptomic datasets provided by Xu et al. (2011), Bourgis et al. (2011) and Tranbarger et al. (2011) showed no evidence of expression of *CBF/DREB* in oil palm ripening fruit.

Although, it has been shown that the CBFs play an important role in plant resistance to abiotic stresses, especially freezing tolerance, their function in biotic stress tolerance, as well as fruit ripening process is still under investigation (Yamaguchi-Shinozaki and Shinozaki, 1994; Stockinger et al., 1997; Thomashow, 1999; Medina et al., 2011; Zhang et al., 2009b; Li et al., 2011). Alongside the *in vitro* DNA-protein binding assay demonstrating preference of the CBFs for the DRE/CRT element, there are some recent finding verifying possible affinity of this protein with both DRE/CRT and GCC-box elements in *in vivo* condition (Gutha and Reddy, 2008; Li et al., 2011).

Among the different biotic and abiotic stresses, freezing condition is a key factor with adverse effects on plant yield and geographical distribution. However, several reports showed contradictory role of ethylene in plant cold acclimation. While cold acclimation in tomato and tobacco was reported to be enhanced by ethylene (Ciardi et al. 1997; Zhang and Huang 2010), new recent findings indicate negative effects of ethylene in plant freezing tolerance (Shi et al., 2012; Zhao et al., 2014). In addition, more recent report indicated that the freezing tolerance in *Arabidopsis* was negatively affected by suppression of CBF through ethylene production (Shi et al., 2012).

Ethylene biosynthesis related enzymes contain different *cis* elements like GCC-box and DRE/CRT on their promoter sequences (Zhang et al., 2009b). So, it is hypothesized that a mechanism for the CBFs, to regulate chilling tolerance in plants is mediated partly through ethylene biosynthesis pathway and as a result, it can regulate plant growth, development and disease resistance, either directly by binding to the related *cis*-elements on different target genes or indirectly by ethylene biosynthesis pathway. So, the main objectives of this study were:

- 1. To isolate and clone the oil palm *EgCBF3* expressed in ripening oil palm fruit
- 2. To determine the *EgCBF3* responsiveness to different hormonal and stress treatments in oil palm mesocarp tissue
- 3. To characterize the DNA-protein binding and trans-activation abilities of *EgCBF3* using *in vitro* and *in vivo* assays.
- 4. To characterize the possible function of *EgCBF3* in regulating ethylene biosynthesis-related genes, pathogenesis-related genes and abiotic stress tolerance in tomato cv. MT1 using transgenic approaches.

REFERENCES

- Abu-Qamar, S., Luo, H., Laluk, K., Mickelbart, M. V. and Mengiste, T. (2009). Crosstalk between biotic and abiotic stress responses in tomato is mediated by the AIM1 transcription factor. *The Plant Journal*, 58:347–60.
- Achard, P, Gong, F., Cheminant, S., Alioua, M., Hedden, P. and Genschik, P. (2008). The cold-inducible CBF1 factor-dependent signaling pathway modulates the accumulation of the growth-repressing DELLA proteins via its effect on gibberellin metabolism. *The Plant Cell Online*, 20:2117–2129.
- Adams-Phillips, L., Barry, C. and Giovannoni, J. J. (2004a). Signal transduction systems regulating fruit ripening. *Trends in plant science*, 9:331-8.
- Adams-Phillips, L., Barry, C., Kannanz, P., Leclercq, J., Bouzayen, M. and Giovannoni, J. J. (2004b). Evidence that CTR1-mediated ethylene signal transduction in tomato is encoded by a multigene family whose members display distinct regulatory features. *Plant Molecular Biology*. 54:387-404.
- Agarwal, P. K., Agarwal, P., Reddy, M. K. and Sopory, S. K. (2006). Role of DREB transcription factors in abiotic and biotic stress tolerance in plants. *Plant Cell Reports*, 25:1263-1274.
- Ajenifujah-Solebo, S. O. A., Isu, N. A., Olorode, O. and Ingelbrecht, I. (2013). Effect of cultivar and explants type on tissue culture regeneration of three Nigerian cultivars of tomatoes. *Sustainable Agriculture Research*. 2:58-64.
- Akhtar, M., Jaiswal, A., Taj, G., Jaiswal, J. P., Qureshi, M. I. and Singh, N. K. (2012). DREB1/CBF transcription factors: their structure, function and role in abiotic stress tolerance in plants. *Journal of Genetics*. 91:385-395.
- Alba, R., Payton, P., Fei, Z., McQuinn, R., Debbie, P., Martin, G. B., Tanksley, S. D. and Giovannoni, J. J. (2005). Transcriptome and selected metabolite analyses reveal multiple points of ethylene control during tomato fruit development. *The Plant Cell Online*. 17:2954-2965.
- Allen, T. C., Cagle, P.T. and Popper, H. H. (2009). Basic Concepts of Molecular Pathology. *Archives of pathology and laboratory medicine*, *132*: 1551.
- Argueso, C. T., Hansen, M. and Kieber, J. J. (2007). Regulation of ethylene biosynthesis. *Journal of Plant Growth Regulation*. 26:92-105.

- Ashakiran, K., Sivankalyani, V., Jayanthi, M., Govindasamy, V. and Girija, S. (2011). Genotype specific shoots regeneration from different explants of tomato (Solanum lycopersicum L.) using TDZ. Asian Journal of Plant Science and Research. 1(2):107-113.
- Bapat, V. A., Trivedi, P. K., Ghosh, A., Sane, V. A, Ganapathi, T. R., and Nath, P. (2010). Ripening of fleshy fruit: molecular insight and the role of ethylene. *Biotechnology Advances*, 28:94-107.
- Barry, C. S. and Giovannoni, J. J. (2007). Ethylene and fruit ripening. *Journal of Plant Growth Regulation*, 26:143-159.
- Barry, C. S., Immaculada, Ilop-Tous, M. and Grierson, D. (2000). The regulation of 1-aminocyclopropane-1-carboxylic acid synthase gene expression during the transition from system-1 to system-2 ethylene synthesis in tomato. *Plant Physiology*, 123:979-986.
- Bastías, A., López-Climent, M., Valcarcel, M., Rosello, S., Gómez-Cadenas, A., Casaretto, J.A. (2011). Modulation of organic acids and sugar content in tomato fruits by an abscisic acid-regulated transcription factor. *Physiologia Plantarum*, 141:215-226.
- Baud, S., Mendoza, M. S., Harscoë, t A., Lepiniec, E. L. and Dubreucq, B. (2007). WRINKLED1 specifies the regulatory action of LEAFY COTYLEDON 2 towards fatty acid metabolism during seed maturation in *Arabidopsis. The Plant Journal*, 50:825-838.
- Bhatia, P., Ashwath, N. and Midmore, D. (2005). Effects of genotype, explant orientation, and wounding on shoot regeneration in tomato. In Vitro Cellular and Developmental Biology Plant. 41:457-464.
- Bhatia, P., Ashwath, N., Senaratna, T. and Midmore, D. (2004). Tissue culture studies of tomato (*Lycopersicon esculentum*). *Plant Cell, Tissue and Organ Culture*, 78:1-21.
- Bleeker, A. and Kende, H. (2000). Ethylene: a gaseous signal molecule in plants. *Annual Review of Cell and Developmental Biology*, 16:1-18.
- Bogs, J., Jaffé, F. W., Takos, A. M., Walker, A. R. and Robinson, S. P. (2007). The grapevine transcription factor VvMYBPA1 regulates proanthocyanidin synthesis during fruit development. *Plant Physiology*, 143:1347-1361.

- Bourgis, F., Kilaru, A., Cao, X., Ngando-Ebongue, G. F., Drira, N., Ohlrogge, J. B., Arondel, V. (2011). Comparative transcriptome and metabolite analysis of oil palm and date palm mesocarp that differ dramatically in carbon partitioning. *Proceedings of the National Academy of Sciences*, 108: 12527-12532.
- Bovy, A., de Vos, R., Kemper, M., Schijlen, E., Pertejo, M.A., Muir, S., Collins, G., Robinson, S., Verhoeyen, M., Hughes, S., Santos-Buelga, C., and van Tunen, A. (2002). High-flavonol tomatoes resulting from the heterologous expression of the maize transcription factor genes LC and C1. *The Plant Cell Online*, 14: 2509-2526.
- Brivanlou, A. H. and Darnell, J. E. (2002). Signal transduction and the control of gene expression. *Science*, 295: 813–8.
- Butelli, E., Titta, L., Giorgio, M., Mock, H.P., Matros, A., Peterek, S., Schijlen, E.G.W.M., Hall, R.D., Bovy, A.G., Luo, J. and Martin, C. (2008). Enrichment of tomato fruit with health-promoting anthocyanins by expression of select transcription factors. *Nature Biotechnology*, 26:1301-1308.
- Cao, X. and Hammerschlag, F. A. (2002). A two-step pretreatment significantly enhances shoot organogenesis from leaf explants of highbush blueberry cv. bluecrop. *HortScience*. 37:819-821.
- Cara, B. and Giovannoni, J. J. (2008). Molecular biology of ethylene during tomato fruit development and maturation. *Plant Science*, 175:106-113.
- Cernac, A. and Benning, C. (2004). WRINKLED1 encodes an AP2/EREB domain protein involved in the control of storage compound biosynthesis in Arabidopsis. The Plant Journal, 40:575-585.
- Chandel, G. and Katiyar, S.K. (2000). Organogenesis and somatic embryogenesis in tomato (*Lycopersicon esculantum Mill.*). *Advance in Plant Sciences*, 13:11-17.
- Chao, Q., Rothenberg, M., Solano, R., Roman, G., Terzaghi, W. and Ecker, J. R. (1997). Activation of the ethylene gas response pathway in *Arabidopsis* by the nuclear protein ETHYLENE-INSENSITIVE3 and related proteins. *Cell*, 89:1133-1144.
- Chinnusamy, V., Schumaker, K. and Zhu, J. K. (2004). Molecular genetic perspectives on cross-talk and specifcity in abiotic stress signaling in plants. *Journal of Experimental Botany*, 55:225-236.

- Chung, M., Vrebalov, J., Alba, R., Lee, J., McQuinn, R., Chung, J. D., Klein, P. and Giovannoni, J. J. (2010). A tomato (*Solanum lycopersicum*) APETALA2/ERF gene, SIAP2a, is a negative regulator of fruit ripening. *The Plant Journal*, 64:936-947.
- Ciardi, J. A., Deikman, J., Orzolek, M. D. (1997). Increased ethylene synthesis enhances chilling tolerance in tomato. *Physiologia Plantarum*, 101:333-340.
- Compton, M. E. and Veilleux, R. E. (1991). Shoot, root and flower morphogenesis on tomato inflorescence explants. *Plant cell, tissue and organ culture*, 24:223-231.
- Constabel, C. P., Bergey, D. R. and Ryan, C. A. (1995). Systemin activates synthesis of wound-inducible tomato leaf polyphenol oxidase via the octadecanoid defense signaling pathway. *Proceedings of the National Academy of Sciences*, 92:407-411.
- Costa, M. G. C., Nogueira, F. T. S., Figueira, M. L., Otoni, W. C., Brommonschenkel, S. H. and Cecon, P. R. (2000). Influence of the antibiotic timentin on plant regeneration of tomato (Lycopersicon esculentum Mill.) cultivars. *Plant Cell Reports*, 19:327-332.
- Curtis, M. D. and Grossniklaus, U. (2003). A gateway cloning vector set for highthroughput functional analysis of genes in planta. *Plant Physiology*, 133:462-469.
- D'Onofrio, C. and Morini, S. (2006). Somatic embryo, adventitious root and shoot regeneration in in vitro grown quince leaves as influenced by treatments of different length with growth regulators. *Scientia horticulturae*, 107:194-199.
- Davis, D. G., Breiland, K. A., Frear, D. S. and Secor, G. A. (1994). Callus initiation and regeneration of tomato (*Lycopersicon esculentum*) cultivars with different sensitivities to metribuzin. *Quarterly (Plant Growth Regulator Society of America)*, 22:65-73.
- Deluc, L., Barrieu, F., Marchive, C., Lauvergeat, V., Decendit, A., Richard, T., Carde, J. P., Merillon, J. M., and Hamdi, S. (2006). Characterization of a grapevine R2R3-MYB transcription factor that regulates the phenylpropanoid pathway. *Plant Physiology*, 140: 499-511.
- Dietz, K. J., Vogel, M. O. and Viehhauser, A. (2010). AP2/EREBP transcription factors are part of gene regulatory networks and integrate metabolic,

hormonal and environmental signals in stress acclimation and retrograde signaling. *Protoplasma*, 245:3-14.

- Diez, M. J. and Nuez, F. (2008). Tomato. In Vegetables II, 249-323.
- Dong, T., Chen, G., Tian, S., Xie, Q., Yin, W., Zhang, Y. and Hu, Z. (2014). A non-climacteric fruit gene CaMADS-RIN regulates fruit ripening and ethylene biosynthesis in climacteric fruit. *PloS one*, 9: e95559.
- Dong, T., Hu, Z., Deng, L., Wang, Y., Zhu, M., Zhang, J. and Chen, G. (2013). A tomato MADS-box transcription factor, SLMADS1, acts as a negative regulator of fruit ripening. *Plant Physiology*, 163:1026-1036.
- Doyle, J. J. and Doyle, J. L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissues. *Phytochemical Bulletin*, 19:11-15.
- Drews, G. N., Bowman, J. L. and Meyerowitz, E. M. (1991). Negative regulation of the Arabidopsis homeotic gene AGAMOUS by the APETALA2 product. *Cell*, 65:991-1002.
- Druege, U. (2006). Ethylene and Plant Responses to Abiotic Stress. In: *Ethylene Action in Plants*, 81-118. Springer Berlin Heidelberg.
- Du, L., Ali, G. S., Simons, K. A., Hou, J., Yang, T., Reddy, A. S. N. and Poovaiah, B. W. (2009). Ca²+/calmodulin regulates salicylic-acid-mediated plant immunity. *Nature*, 457: 1154-1158.
- Dutta, A., Sen, J. and Deswal, R. (2007). Down regulation of terpenoid indole alkaloid biosynthetic pathway by low temperature and cloning of a AP2 type C-repeat binding factor (CBF) from *Catharanthus roseus* (L). G. Don. *Plant Cell Reports*, 26: 1869-1878.
- Espley, R. V., Hellens, R. P., Putterill, J., Stevenson, D. E., Kutty-Amma, S. and Allan, A. C. (2007). Red colouration in apple fruit is due to the activity of the MYB transcription factor, MdMYB10. *The Plant Journal*, 49: 414-427.
- Fang, J. and Chu, C. (2008). Abscisic acid and the pre-harvest sprouting in cereals. Plant *Signaling and Behavior*, 3:1046-1048.
- Farrell, R. E. (2007). The Regulation of Gene Expression in Plants and Animals. In *Regulation of Gene Expression in Plants*. Springer US.

- Fei, Z. J., Tang, X., Alba, R. M., White, J. A., Ronning, C. M., Martin, G. B., Tanksley, S. D. and Giovannoni, J. J. (2004). Comprehensive EST analysis of tomato and comparative genomics of fruit ripening. *The Plant Journal*, 40:47-59.
- Food and Agriculture Organization of the United Nations (FAO) (2013). FAOSTAT. Rome, Italy. Online at <u>http://faostat.fao.org</u>, accessed on October 17.
- Fowler, S. and Thomashow, M. F. (2002). Arabidopsis transcriptome profiling indicates that multiple regulatory pathways are activated during cold acclimation in addition to the CBF cold response pathway. *The Plant Cell Online*, 14:1675-1690.
- Fujimoto, S. Y., Ohta, M., Usui, A., Shinshi, H. and Ohme-Takagi, M. (2000). Arabidopsis ethylene-responsive element binding factors act as transcriptional activators or repressors of GCC box-mediated gene expression. *The Plant Cell Online*, 12:393-404.
- Gamborg, O. L., Miller, R. A. and Ojima, O. (1968). Nutrient requirements of suspension cultures of soybean root cell. *Experimental cell research*, 50:151-158.
- Gapper, N. E., McQuinn, R. P. and Giovannoni, J. J. (2013). Molecular and genetic regulation of fruit ripening. *Plant Molecular Biology*, 82:575-591.
- George, E. F. (1993). Factors affecting growth and morphogenesis. In *Plant* propagation by tissue culture. London: Exegetics Limited. 231-271.
- Gilmour, S. J., Fowler, S. G. and Thomashow, M. F. (2004). Arabidopsis transcriptional activators *CBF1*, *CBF2*, and *CBF3* have matching functional activities. *Plant Molecular Biology*, 54:767-781.
- Gilmour, S. J., Sebolt, A. M., Salazar, M. P., Everard, J. D. and Thomashow, M. F. (2000). Overexpression of the *Arabidopsis CBF3* transcriptional activator mimics multiple biochemical changes associated with cold acclimation. *Plant Physiology*, 124:1854-1865.
- Gilmour, S. J., Zarka, D. G., Stockinger, E. J., Salazar, M. P., Houghton, J. M. and Thomashow, M. F. (1998). Low temperature regulation of the *Arabidopsis* CBF family of AP2 transcriptional activators as an early step in cold-induced COR gene expression. *The Plant Journal*, 16:433-442.

- Giovannoni, J. J. (2001). Molecular biology of fruit maturation and ripening. Annual Review of Plant Physiology and Plant Molecular Biology, 52:725-749.
- Giovannoni, J. J. (2004). Genetic regulation of fruit development and ripening. *The Plant Cell Online*, 16:S170-S180.
- Godt, D. E. and Roitsch, T. (1997). Regulation and tissue-specific distribution of mRNAs for three extracellular invertase isoenzymes of tomato suggests an important function in establishing and maintaining sink metabolism. *Plant Physiology*, 115:273-282.
- Guo, H. and Ecker, J. R. (2004). The ethylene signaling pathway: new insights. *Current opinion in plant biology*, 7:40-49.
- Gutha, L. R. and Reddy, A. R. (2008). Rice *DREB1B* promoter shows distinct stress-specific responses, and the overexpression of cDNA in tobacco confers improved abiotic and biotic stress tolerance. *Plant molecular biology*, 68:533-55.
- Hao, D., Ohme-Takagi, M. and Sarai, A. (1998). Unique mode of GCC box recognition by the DNA-binding domain of ethylene-responsive elementbinding factor (ERF domain) in plant. *Journal of Biological Chemistry*, 273:26857-26861.
- He, L. G., Wang, H. L., Liu, D. C., Zhao, Y. J., Xu, M., Zhu, M., Wei, G. Q. and Sun, Z. H. (2012). Isolation and expression of a cold-responsive gene *PtCBF* in *Poncirus trifoliata* and isolation of citrus CBF promoters. *Biologia plantarum*. 56:484-492.
- Heidarvand, L. and Amiri, R. M. (2010). What happens in plant molecular responses to cold stress. Acta Physiologiae Plantarum, 32:419-431.
- Hsieh, T., Lee, J., Charng, Y. and Chan, M. (2002). Tomato Plants Ectopically Expressing *Arabidopsis CBF1* Show Enhanced Resistance to Water Deficit Stress. *Plant Physiology*, 1:618-626.
- Hua, J. (2009). From freezing to scorching, transcriptional responses to temperature variations in plants. *Current opinion in plant biology*, 12:568-573.

- Huang, Y., Li, H., Hutchison, C. E., Laskey, J. and Kieber, J. J. (2003). Biochemical and functional analysis of *CTR1*, a protein kinase that negatively regulates ethylene signaling in *Arabidopsis*. *The Plant Journal*, 33:221-233.
- Ithnin, M., Singh, R. and Din, A. K. (2011). *Elaeis*. In *Wild Crop Relatives: Genomic and Breeding Resources, Plantation and Ornamental Crops*. Springer Berlin Heidelberg.
- Jaglo-Ottosen, K. R., Gilmour, S. J., Zarka, D.G., Schabenberger, O. and Thomashow, M. F. (1998). *Arabidopsis CBF1* overexpression induces COR genes and enhances freezing tolerance. *Science*, 280:104-106.
- Jan, N., Mahboob-ul-Hussain, and Andrab, K. I. (2009). Cold resistance in plants: A mystery unresolved. *Electronic Journal of Biotechnology*, 12:0717-3458.
- Jiang, F., Wang, F., Wu, Z., Li, Y., Shi, G., Hu, J. and Hou, X. (2011). Components of the *Arabidopsis* CBF cold-response pathway are conserved in non-heading Chinese cabbage. *Plant Molecular Biology Report*, 29:525-532.
- Jofuku, K.D., Denboer, B.G.W., van Montagu, M. and Okamuro, J.K. (1994). Control of *Arabidopsis* flower and seed development by the homeotic gene APETALA2. *The Plant Cell Online*, 6:1211-1225.
- Jofuku, K.D., Omidyar, P.K., Gee, Z. and Okamuro, J.K. (2005). Control of seed mass and seed yield by the floral homeotic gene APETALA2. Proceedings of the National Academy of Sciences of America, 102:3117-3122.
- Joo, S., Kim, W.T. and Louis, S. (2007). A Gaseous Plant Hormone Ethylene : The Signalling Pathway. *Journal of Plant Biology*, 50:109-116.
- Kagaya, Y., Ohmiya, K. and Hattori, T. (1999). *RAV1*, a novel DNA-binding protein, binds to bipartite recognition sequence through two distinct DNA-binding domains uniquely found in higher plants. *Nucleic Acids Research*, 27:470-478.
- Kantor, M., Sestras, R. and Chowdhury, K. (2010). Identification of the most organogenic-responsive variety of tomato using the variety x medium interaction. *Romanian Biotechnological Letters*, 15:5640-5645.
- Karim, M.R., Hirota, A., Kwiatkowska, D., Tasaka, M. and Aida, M. (2009). A role for *Arabidopsis PUCHI* in floral meristem identity and bract suppression. *The Plant Cell Online*, 21:1360-1372.

- Karlova, R., Rosin, F.M., Busscher-Lange, J., Parapunova, V., Do P.T., Fernie, A.R., Fraser, P.D., Baxter, C., Angenent, G.C. and de Maagd, R.A. (2011). Transcriptome and metabolite profiling show that *APETALA2a* is a major regulator of tomato fruit ripening. *The Plant Cell Online*, 23:923-941.
- Kasuga, M., Liu, Q., Miura, S., Yamaguchi-Shinozaki, K. and Shinozaki, K. (1999). Improving plant drought, salt, and freezing tolerance by gene transfer of a single stress-inducible transcription factor. *Nature Biotechnology*, 17:287-291.
- Kaur, P. and Bansal, K. C. (2010). Efficient production of transgenic tomatoes via Agrobacterium- mediated transformation. Biologia plantarum, 54:344-348.
- Kelley, L. A. and Sternberg, M. J. E. (2009). Protein structure prediction on the Web: a case study using the Phyre server. *Nature Protocols*, 4:363-371.
- Kendrick, M.D. and Chang, C. (2008). Ethylene signaling: new levels of complexity and regulation. *Current opinion in plant biology*, 11:479-485.
- Kieber, J. J., Rothenberg, M., Roman, G., Feldman, K. A. and Ecker, J. R. (1993). *CTR1*, a negative regulator of the ethylene response pathway in *Arabidopsis*, encodes a member of the Raf family of protein kinases. *Cell*, 72:427-441.
- Kintzios, S., Sereti, E., Bluchos, P., Drossopoulos, J.B., Kitsaki, C.K. and Liopa Tsakalidis, A. (2002). Growth regulator pretreatment improves somatic embryogenesis from leaves of squash (*Cucurbita pepo L.*) and melon (*Cucumis melo L.*). *Plant Cell Reports*, 21:1-8.
- Kirik, V., Kölle, K., Miséra, S., Bäumlein, H. (1998). Two novel MYB homologues with changed expression in late embryogenesis-defective *Arabidopsis* mutants. *Plant molecular biology*, 37:819-827.
- Klee, H. J. (2004). Ethylene signal transduction. Moving beyond *Arabidopsis*. *Plant Physiology*, 135:660-667.
- Kramer, M. G. and Redenbaugh, K. (1994). Commercialization of a tomato with an antisense polygalacturonase gene: The FLAVR SAVR[™] tomato story. *Euphytica*, 79:293-297.
- Kurtz, S. M. and Lineberger, R. D. (1983). Genotypic differences in morphogenic capacity of cultured leaf explants of tomato (*Lycopersicon esculentum*). *Journal-American Society for Horticultural Science*, 108:710-714.

- Lata, C. and Prasad, M. (2011). Role of DREBs in regulation of abiotic stress responses in plants. *Journal of experimental botany*, 62:4731-4748.
- Lewin, B. (2004). Genes VIII, Pearson Education, *Upper Saddle River, NJ*. pp.1027.
- Li, C. W., Su, R. C., Cheng, C. P., Sanjaya, Y. S. J., Hsieh, T. H., Chao, T. C. and Chan, M. T. (2011). Tomato RAV transcription factor is a pivotal modulator involved in the *AP2/EREBP*-mediated defence pathway. *Plant physiology*, 156:213-227.
- Li, H. and Guo, H. (2007). Molecular basis of the ethylene signaling and response pathway in *Arabidopsis*. *Journal of Plant Growth Regulation*, 26:106-117.
- Lin, Z., Alexander, L., Hackett, R. and Grierson, D. (2008). LeCTR2, a CTR1like protein kinase from tomato, plays a role in ethylene signaling, development and defense. The Plant Journal, 54:1083-1093.
- Lin, Z., Zhong, S. and Grierson, D. (2009). Recent advances in ethylene research. *Journal of experimental botany*, 60:3311-3336.
- Lissarre, M., Ohta, M., Sato, A. and Miura, K. (2010). Cold-Responsive gene regulation during cold acclimation in plants. *Plant signaling and behavior*, 5:948-952.
- Litt, A. and Irish, V.F. (2003). Duplication and diversification in the APETALA1/FRUITFULL floral homeotic gene lineage: Implications for the evolution of floral development. *Genetics*, 165:821-833.
- Liu, J. J., Sturrock, R. and Ekramoddoullah, A. K. M. (2010). The superfamily of thaumatin-like proteins: its origin, evolution, and expression towards biological function. *Plant cell reports*, 29:419-436.
- Liu, L., White, M. J. and Thomas, H. M. (1999). Transcription factors and their genes in higher plants Functional domains, evolution and regulation. *European Journal of Biochemistry*, 262:247-257.
- Liu, Q., Kasuga, M., Sakuma, Y., Abe, H., Miura, S., Yamaguchi-Shinozaki, K. and Shinozaki, K. (1998). Two transcription factors, *DREB1* and *DREB2*, with an EREBP/AP2 DNA binding domain separate two cellular signal transduction pathways in drought- and low-temperature-responsive gene expression, respectively, in *Arabidopsis. The Plant Cell Online*, 10:1391-1406.

- Liu, Y., Zhao, T. J., Liu, J.M., Liu, W.Q., Liu, Q., Yan, Y. B. and Zhou, H. M. (2006). The conserved Ala37 in the ERF/AP2 domain is essential for binding with the DRE element and the GCC box. *FEBS letters*, 580:1303-1308.
- Ludwig, A. A., Saitoh, H., Felix, G., Freymark, G., Miersch, O., Wasternack, C., Boller, T., Jones, J. D. and Romeis, T. (2005). Ethylene-mediated cross-talk between calcium-dependent protein kinase and MAPK signaling controls stress responses in plants. *Proceedings of the National academy of Sciences of the United States of America*, 102:10736-10741.
- Luo, J., Butelli, E., Hill, L., Parr, A., Niggeweg, R., Bailey, P., Weisshaar, B. and Martin, C. (2008). AtMYB12 regulates caffeoyl quinic acid and flavonol synthesis in tomato: expression in fruit results in very high levels of both types of polyphenol. *The Plant Journal*, 56:316-326.
- Malaysian Palm Oil Board. (2012). Oil palm and the environment. Kuala Lumpur, Malaysia. Online at http://www.mpob.gov.my/en/palm-info/environment/520-achievements, accessed on October 3, 2013.
- Manning, K., Tor, M., Poole, M., Hong, Y., Thompson, A. J., King, G. J., Giovannoni, J. J. and Seymour, G. B. (2006). A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. *Nature genetics*, 38:948-952.
- Mathews, H., Clendennen, S. K., Caldwell, C. G., Liu, X. L., Connors, K., Matheis, N., Schuster, D. K., Menasco, D. J., Wagoner, W., Lightner, J. and Wagner, D. R. (2003). Activation tagging in tomato identifies a transcriptional regulator of anthocyanin biosynthesis, modification, and transport. *The Plant Cell Online*, 15:1689-1703.
- Matsui, A., Ishida, J., Morosawa, T., Mochizuki, Y., Kaminuma, E., Endo, T. A., Okamoto, M., Nambara, E., Nakajima, M., Kawashima, M., Satou, M., Kim, J. M., Kobayashi, N., Toyoda, T., Shinozaki, K. and Seki, M. (2008). *Arabidopsis* transcriptome analysis under drought, cold, high-salinity and ABA treatment conditions using a tiling array. *Plant and Cell Physiology*, 49:1135-1149.
- Medina, J., Bargues, M., Terol, J., Perez-Alonso, M. and Salinas, J. (1999). The *Arabidopsis* CBF gene family is composed of three genes encoding AP2 domain-containing proteins whose expression is regulated by low temperature but not by abscisic acid or dehydration. *Plant Physiology*, 119:463-470.

- Medina, J., Catalá, R. and Salinas, J. (2011). The CBFs: Three Arabidopsis transcription factors to cold acclimate. *Plant Science*, 180:3-11.
- Mehrtens, F., Kranz, H., Bednarek, P. and Weisshaar, B. (2005). The Arabidopsis transcription factor MYB12 is a flavonol-specific regulator of phenylpropanoid biosynthesis. *Plant Physiology*, 138:1083-1096.
- Mei WQ, Lei J, Xu Y, Wei G, Zhu YX (2007). Characterization of three *Arabidopsis* AP2/EREBP family transcription factors involved in ABA sensitivity, freeze and salt tolerance. *Chinese Science Bulletin*, 52: 1746-1753.
- Melzer, R. and Theißen, G. (2011). MADS and more: transcription factors that shape the plant. In *Plant Transcription Factors, Methods in Molecular Biology*, 754.
- Miura, K. and Furumoto, T. (2013). Cold signaling and cold response in plants. *International Journal of Molecular Sciences*, 14:5312-5337.
- Mizoi, J., Shinozaki, K. and Yamaguchi-Shinozaki, K. (2012). AP2/ERF family transcription factors in plant abiotic stress responses. Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms, 1819:86-96.
- Mukkun, L. and Singh, Z. (2009). Methyl jasmonate plays a role in fruit ripening of 'Pajaro' strawberry through stimulation of ethylene biosynthesis. *Scientia horticulturae*, 123:5-10.
- Murashige, T. and Skoog, F. (1962). A revised medium for rapid growth and bioassays with tobacco tissue cultures. *Physiologia Plantarum*, 15:472-493.
- Murphy, D.J. (2009). Oil palm: future prospects for yield and quality improvements. *Lipid Technology*, 21:257-260.
- Nakano, T., Suzuki, K., Fujimura, T. and Shinshi, H. (2006). Genome-wide analysis of the ERF gene family in *Arabidopsis* and rice. *Plant Physiology*, 140:411-432.
- Nakashima, K. and Yamaguchi-Shinozaki, K. (2010). Promoters and transcription factors in abiotic-stress responsive gene expression. In *Abiotic stress* adaptation in plants. pp. 199–216. Springer Netherlands.
- Nambara, E. and Marion-Poll, A. (2005). Abscisic acid biosynthesis and catabolism. *Annual review of plant biology*, 56:165-185.

- Namitha, K. K. and Negi, P. S. (2013). Morphogenetic Potential of Tomato (*Lycopersicon esculentum*) cv. 'Arka Ahuti' to Plant Growth Regulators. *Notulae Scientia Biologicae*, 5:220-225.
- Narváez-Vásquez, J., Tu, C. J., Park, S. Y. and Walling, L. L. (2008). Targeting and localization of wound-inducible leucine aminopeptidase A in tomato leaves. *Planta*, 227:341-351.
- Ngando-Ebongue, G. F., Ajambang, W. N., Koona, P., Lalu Firman, B. and Arondel, V. (2012). Oil Palm. In *Technological Innovations in Major World Oil Crops, Volume 1* (pp. 165-200). Springer New York.
- Nitsch, L. M., Oplaat, C., Feron, R., Ma, Q., Wolters-Arts, M., Hedden, P., Mariani, C. and Vriezen, W. H. (2009). Abscisic acid levels in tomato ovaries are regulated by *SINCED1* and *SICYP707A1*. *Planta*, 229:1335-1346.
- Nole-Wilson, S. and Krizek, B. A. (2000). DNA binding properties of the *Arabidopsis* floral development protein AINTEGUMENTA. *Nucleic Acids Research*, 21:4076-4082.
- Novillo, F., Alonso, J. M., Ecker, J.R. and Salinas, J. (2004). CBF2/DREB1C is a negative regulator of CBF1/DREB1B and CBF3/DREB1A expression and plays a central role in stress tolerance in *Arabidopsis*. *Proceedings of the National Academy of Sciences of the United States of America*, 101:3985-3990.
- Novillo, F., Medina, J. and Salinas, J. (2007). *Arabidopsis* CBF1 and CBF3 have a different function than CBF2 in cold acclimation and define different gene classes in the CBF regulon. *Proceedings of the National Academy of Sciences of the United States of America*, 104:21002-21007.
- Nualwijit, N., and Lerslerwong, L. (2014). Post harvest ripening of oil palm fruit is accelerated by application of exogenous ethylene. *Songklanakarin Journal of Science and Technology*, 36:255-259.
- Ogas, J., Kaufmann, S., Henderson, J. and Somerville, C. (1999). *PICKLE* is a CHD3 chromatin-remodeling factor that regulates the transition from embryonic to vegetative development in *Arabidopsis*. *Proceedings of the National Academy of Sciences of the United States of America*, 96:13839-13844.

- Ohto, M. A., Fischer, R. L., Goldberg, R. B., Nakamura, K. and Harada, J. J. (2005). Control of seed mass by APETALA2. *Proceedings of the National Academy of Sciences of the United States of America*, 102:3123-3128.
- Oil world (2013) Statistics. Hamburg, Germany. Online at <u>http://www.oilworld.biz</u>
- Page, D., Gouble, B., Valot, B., Bouchet, J. P., Callot, C., Kretzschmar, A., Causse, M., Renard, C.M.C.G. and Faurobert, M. (2010). Protective proteins are differentially expressed in tomato genotypes differing for their tolerance to low-temperature storage. *Planta*, 232:483-500.
- Park, J. M., Park, C. J., Lee, S. B., Ham, B. K., Shin, R. and Paek, K. H. (2001). Overexpression of the Tobacco Tsi1 gene encoding an EREBP/AP2-type transcription factor enhances resistance against pathogen attack and osmotic stress in tobacco. *The Plant Cell Online*, 13:1035-1046.
- Pech, J. C., Latché, A. and Bouzayen, M. (2010). Ethylene Biosynthesis. In Plant Hormones; Biosynthesis, Signal Transduction, Action, 115-136.
- Pfaffl, M. W., Horgan, G. and Dempfle, L. (2002). Relative expression software tool (REST) for group-wise comparison and statistical analysis of relative expression results in real-time PCR. *Nucleic Acids Research*, 30: e36.
- Ping, L., Lian, Z. G., Xin, L. X., He, W. L. and Ming, Z. Z. (2009). Cloning of 9cis-epoxycarotenoid dioxygenase (NCED) gene encoding a key enzyme during abscisic acid (ABA) biosynthesis and ABA-regulated ethylene production in detached young persimmon calyx. Chinese Science Bulletin, 54:2830-2838.
- Poku, K. (2002). Small-Scale Palm Oil Processing in Africa. FAO agricultural services bulletin. 148:1010-1365.
- Prathanturarug, S., Soonthornchareonnon, N., Chuakul, W., Phaidee, Y. and Saralamp, P. (2005). Rapid micropropagation of Curcuma longa using bud explants precultured in thiadiazuron supplemented liquid medium. *Plant cell*, *tissue and organ culture*, 80:347-351.
- Prescot, A. and Martin, C. (1987). A rapid method for the quantitative assessment of levels of specific mRNAs in plants. *Plant Molecular Biology Report*, 4:219-224.

- Raghavan, C., Ong, E. K., Dalling, M. J. and Stevenson, T. W. (2006). Regulation of genes associated with auxin, ethylene and ABA pathways by 2,4-dichlorophenoxyacetic acid in *Arabidopsis*. *Functional and Integrative Genomics*, 6:60-70.
- Ramiah, M. and Rajappan, K. (1996). Direct shoot regeneration from excised cotyledonary leaf of tomato. *South Indian Horticulture*, 44:101-102.
- Ramirez, S. R. and Basu, C. (2009). Comparative Analyses of Plant Transcription Factor Databases. *Current Genomics*, 10:10-17.
- Reeves, W. M., Lynch, T.J. and Mobin, R. (2011). Direct targets of the transcription factors ABA-Insensitive(ABI)4 and ABI5 reveal synergistic action by ABI4 and several bZIP ABA response factors. *Plant Molecular Biology*, 75:347-363.
- Riechmann, J. L. and Meyerowitz, E. M. (1998). The AP2/EREBP family of plant transcription factors. *Biological Chemistry*, 379:633-646.
- Riov, J., Dagan, E., Goren, R. and Yang, S. F. (1990). Characterization of abscisic acid-induced ethylene production in citrus leaf and tomato fruit tissues. *Plant Physiology*, 92:48-53.
- Rock, C. D. (2010). Stress signaling I: the role of abscisic acid (ABA). In *Abiotic Stress Adaptation in Plants*, pp.33-73. Springer Netherlands.
- Rodrigo, M. J., Marcos, J. F., Alferez, F., Mallent, M. and Zacarias, L. (2003). Characterization of Pinalate, a novel Citrus sinensis mutant with a fruitspecific alteration that results in yellow pigmentation and decreased ABA content. *Journal of Experimental Botany*, 54:727-738.
- Roman, G., Lubarsky, B., Kieber, J. J., Rothenberg, M. and Ecker, J. R. (1995). Genetic analysis of ethylene signal transduction in *Arabidopsis* thaliana: Five novel mutant loci integrated into a stress response pathway. *Genetics*, 139:1393-1409.
- Rugkong, A., McQuinn, R., Giovannoni, J. J., Rose, J. K. C. and Watkins, C. B. (2011). Expression of ripening-related genes in cold-stored tomato fruit. *Postharvest Biology and Technology*, 61:1-14.
- Sakuma, Y., Liu, Q., Dubouzet, J.G., Abe, H., Shinozaki, K. and Yamaguchi-Shinozaki, K. (2002). DNA-binding specificity of the ERF/AP2 domain of *Arabidopsis* DREBs, transcription factors involved in dehydration- and cold-

inducible gene expression. *Biochemical and Biophysical Research Communication*, 29:998-1009.

- Sambanthamurthi, R., Sundram, K. and Tan, Y. (2000). Chemistry and biochemistry of palm oil. *Progress in Lipid Research*, 39:507-558.
- Sambrook, J. and Russel, D. W. (2001). Molecular Cloning: A Laboratory Manual. Cold Spring Harbour, New York.
- Seidman, C. E. Struhl, K., Sheen, J. and Jessen, T. (1997). Current Protocols in Molecular Biology. John Wiley and Sons, 1.8.1-1.8.10. New York.
- Seymour, G. B., Poole, M., Giovannoni, J. J. and Tucker, G. A. (2013). The Molecular Biology and Biochemistry of Fruit Ripening. John Wiley and Sons, Inc., Publication.
- Sharabi-Schwager, M., Lers, A., Samach, A., Guy, C. L. and Porat, R. (2010a). Overexpression of the *CBF2* transcriptional activator in *Arabidopsis* delays leaf senescence and extends plant Longevity. *Journal of Experimental Botany*, 61:261-273.
- Sharabi-Schwager, M., Samach, A. and Porat, R. (2010b). Overexpression of the *CBF2* transcriptional activator in *Arabidopsis* suppresses the responsiveness of leaf tissue to the stress hormone ethylene. *Plant Biology*, 12:630-638.
- Sharabi-Schwager, M., Samach, A. and Porat, R. (2010c). Overexpression of the *CBF2* transcriptional activator in *Arabidopsis* counteracts hormone activation of leaf senescence. *Plant Signaling and Behavior*, 5:3:296-299.
- Sharp, R. E. (2002). Interaction with ethylene: changing views on the role of abscisic acid in root and shoot growth responses to water stress. *Plant, Cell* and Environment, 25:211-222.
- Sharp, R. E. and LeNoble, M. E. (2002). ABA, ethylene and the control of shoot and root growth under water stress. *Journal of Experimental Botany*, 53:33-37.
- Shi, Y., Tian, S., Hou, L., Huang, X., Zhang, X., Guo, H. and Yang, S. (2012). Ethylene Signaling Negatively Regulates Freezing Tolerance by Repressing Expression of CBF and Type-A ARR Genes in *Arabidopsis*. *The Plant Cell Online*, 24:2578-2595.

- Shinozaki, K., Yamaguchi-Shinozakiy, K. and Seki, M. (2003). Regulatory network of gene expression in the drought and cold stress responses. *Current* opinion in plant biology, 6:410-417.
- Singh, R., Tan, S. G., Panandam, J.M., Rahman, R. A., Ooi, L. C. L. and Cheah, S. C. (2009). Mapping quantitative trait loci (QTLs) for fatty acid composition in an interspecific cross of oil palm. *BMC Plant Biology*, 9:114.
- Singh, S. K. and Syamal, M. M. (2001). A short preculture in thidiazuron or forchlorfenuron improves axillary shoot proliferation in rose micropropagation. *Scientia Horticulrae*, 91:169-177.
- Smart, R. E. and Bingham, G. E. (1974). Rapid Estimates of Relative Water Content. *Plant Physiology*, 53:258-260.
- Soh, A. C., Wong, C. K., Ho, Y. W. and Choong, C. W. (2009) Oil Palm. In Oil Crops. (pp. 333-367). Springer New York.
- Solano, R., Stepanova, A., Chao, Q. and Ecker J. R. (1998). Nuclear events in ethylene signaling: A transcriptional cascade mediated by ETHYLENE-INSENSITIVE3 and ETHYLENE-RESPONSE-FACTOR1. *Genes and Development*, 12:3703-3714.
- Solomons, N. W. and Orozco, M. (2003). Alleviation of vitamin A deficiency with palm fruit and its products. *Asia Pacific journal of clinical nutrition*, 12:373-384.
- Spollen, W. G., LeNoble, M. E., Samuels, T. D., Bernstein, N. and Sharp, R. E. (2000). Abscisic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. *Plant Physiology*, 122:967-976.
- Srivastava, A. and Handa, A. K. (2005). Hormonal Regulation of Tomato Fruit Development: A Molecular Perspective. *Journal of Plant Growth Regulation*, 24:67-82.
- Stockinger, E. J., Gilmour, S. J. and ThomashowThomasho, M. F. (1997). Arabidopsis thaliana CBF1 encodes an AP2 domain-containing transcriptional activator that binds to the C-repeat/DRE, a cis-acting DNA regulatory element that stimulates transcription in response to low temperature and water deficit. Proceedings of the National Academy of Sciences of the United States of America, 94:1035-1040.

- Stracke, R., Ishihara, H., Huep, G., Barsch, A., Mehrtens, F. and Weisshaar, B. (2007). Differential regulation of closely related R2R3-MYB transcription factors controls flavonol accumulation in different parts of the *Arabidopsis* thaliana seedling. *The Plant Journal*, 50:660-677.
- Sun, H. J., Uchii, S., Watanabe, S. and Ezira, H. (2006). A highly efficient transformation protocol for Micro-Tom, a model cultivar for tomato functional genomics. *Plant and Cell Physiology*, 47:426-431.
- Sun, S., Yu, J. P., Chen, F., Zhao, T. J., Fang, X. H., Li, Y. Q. and Sui, S. F. (2008). TINY, a dehydration-responsive element (DRE)-binding protein-like transcription factor connecting the DRE- and ethylene-responsive elementmediated signaling pathways in *Arabidopsis. Journal of Biological Chemistry*, 283:6261-6271.
- Tagoe, S. M. A., Dickinson, M. J. and Apetorgbor, M. M. (2012). Factors influencing quality of palm oil produced at the cottage industry in Ghana. *International Food Research Journal*, 19:271-278.
- The Arabidopsis Genome Initiative (2000). Analysis of the genome sequence of the fowering plant Arabidopsis thaliana. Nature, 408:796-815.
- Thomas, T. D. (2007). Pretreatment in thidiazuron improves the in vitro shoot induction from leaves in *Curculigo orchioides* Gaertn, an endangered medicinal plant. *Acta Physiologiae Plantarum*, 29:455-461.
- Thomashow, M. F. (1999). Plant cold acclimation: freezing tolerance genes and regulatory mechanisms. *Annual review of plant biology*, 50:571-599.
- Thompson, A. J., Jackson, A. C., Parker, R. A., Morpeth, D. R., Burbidge, A. and Taylor, I. B. (2000a). Abscisic acid biosynthesis in tomato: regulation of zeaxanthin epoxidase and 9-cis-epoxycarotenoid dioxygenase mRNAs by light/dark cycles, water stress and abscisic acid. *Plant Molecular Biology*, 42:833-845.
- Thompson, A. J., Jackson, A. C., Symonds, R.C., Mullholland, B.J., Dadswell, A.R., Ludwig Ludwig Blake, P.S., Burbidge, A. and Taylor, I.B. (2000b). Ectopic expression of a tomato 9-cis-epoxycarotenoid dioxygenase gene causes over-production of abscisic acid. *The Plant Journal*, 23:363-374.
- Tiznado-hernández, A. K. H. M. and Mattoo, A. K. (2012). Molecular perspective. In *Plant Biotechnology and Agriculture*. (pp. 405–424). Elsevier.

- Tondelli, A., Francia, E., Barabaschi, D., Pasquariello, M. and Pecchioni, N. (2011). Inside the CBF locus in Poaceae. *Plant science*, 180(1):39-45.
- Tornero, P., Gadea, J., Conejero, V. and Vera, P. (1997). Two PR-1 genes from tomato are differentially regulated and reveal a novel mode of expression for a pathogenesis-related gene during the hypersensitive response and development. *Molecular plant-microbe interaction*, 10:624-634.
- Tranbarger, T. J., Dussert, S., Joe, T., Argout, X., Summo, M., Champion, A., Cros, D., Omore, A., Nouy, B. and Morcillo, F. (2011). Regulatory mechanisms underlying oil palm fruit mesocarp maturation, ripening, and functional specialization in lipid and carotenoid metabolism. *Plant Physiology*, 156:564-584.
- Umezawa, T., Fujita, M., Fujita, Y., Yamaguchi-Shinozaki, K. and Shinozaki, K. (2006). Engineering drought tolerance in plants: discovering and tailoring genes to unlock the future. *Current opinion in biotechnology*, 17:113-122.
- Van Eck, J., Kirk, D.D. and Walmsley, A.M. (2006). Tomato (*Lycopersicum* esculentum). Methods in molecular biology, 343:459-73.
- Van Kan, J. A. L., Cozijnsen, T., Danhash, N. and de Wit, P. J. G. M. (1995). Induction of tomato stress protein mRNAs by ethephon, 2, 6dichloroisonicotinic acid and salicylate. *Plant Molecular Biology*, 27:1205-1213.
- Van Loon, L.C., Geraats, B.P.J. and Linthorst, H.J.M. (2006). Ethylene as a modulator of disease resistance in plants. *Trends in plant science*, 11:184-191.
- Vega-Garcia, M. O., Lopez-Espinoza, G., Ontiveros, J. C., Caro-Corrales, J. J., Vargas, F. D. and Lopez-Valenzuela, J. A. (2010). Changes in protein expression associated with chilling injury in tomato fruit. *Journal of the American Society for Horticultural Science*, 135:83-89.
- Venkatachalam, P., Geetha, N., Priya, P., Rajaseger, G. and Jayabalan, N. (2000).
 High frequency plantlet regeneration from hypocotyl explants of tomato (Lycopersicon esculentum Mill.) via organogenesis. *Plant Cell Biotechnology and Molecular Biology*, 1:95-100.
- Vrebalov, J., Ruezinsky, D., Padmanabhan, V., White, R., Medrano, D., Drake, R., Schuch,W. and Giovannoni, J. J. (2002). A MADS-box gene necessary for fruit ripening at the tomato ripening-inhibitor (rin) locus. *Science*, 296:343-346.

- Walling, L. L. (2006). Recycling or regulation? The role of N-terminal modifying enzymes. *Current opinion in plant biology*, 9:227-233.
- Wang, H. L., Tao, J. J., He, L. G., Zhao, Y. J., Xu, M., Liu, D.C. and Sun, Z. H. (2009) cDNA cloning and expression analysis of a Poncirus trifoliata CBF gene. *Biologia Plantarum*, 53:625-630.
- Wang, K. L. C., Li, H. and Ecker, J. R. (2002). Ethylene Biosynthesis and Signaling Networks. *The Plant Cell Online*, 14:131-152.
- Wang, Q., Guan, Y., Wu, Y., Chen, H., Chen, F. and Chu, C. (2008). Overexpression of a rice OsDREB1F gene increases salt, drought, and low temperature tolerance in both Arabidopsis and rice. Plant molecular biology, 67:589-602.
- Wang, Q. J., Xu, K. Y., Tong, Z. G., Wang, S. H., Gao, Z. H., Zhang J. Y., Zong, C. W., Qiao, Y. S. and Zhang, Z. (2010). Characterization of a new dehydration responsive element binding factor in central arctic cowberry. *Plant Cell, Tissue and Organ Culture*, 101:211-219.
- Weigel, D (1995). The APETALA2 domain is related to a novel type of DNA binding domain. *The Plant Cell*, 7:388–389
- Wise, A. A., Liu, Z., and Binns, A. N. (2006). Three Methods for the Introduction of Foreign DNA into Agrobacterium. In: Agrobacterium protocols. (pp. 43-54). Humana press.
- Xie, Q., Hu, Z., Zhu, Z., Dong, T., Zhao, Z., Cui, B. and Chen, G. (2014). Overexpression of a novel MADS-box gene *SIFYFL* delays senescence, fruit ripening and abscission in tomato. Scientific reports, 4:4367.
- Xiong, L., Lee, H., Ishitani, M. and Zhu, J. K. (2002). Regulation of osmotic stress-responsive gene expression by the LOS6/ABA1 locus in Arabidopsis. Journal of Biological Chemistry, 277:8588-8596.
- Xiong, Y. and Fei, S.Z. (2006). Functional and phylogenetic analysis of a DREB/CBF-like gene in perennial ryegrass (*Lolium perenne* L.). *Planta*, 224:878-888.
- Xu, L., Yuan, Y., Zhang, L., Wan, L., Zheng, Y., Zhou, P. and Li, D. (2011). Identification and characterization of differential gene expression in the mesocarp and kernel of oil palm nuts using suppression subtractive hybridization. Tree Genetics and Genomes, 7:999-1010.

- Xu, W., Rosenow, D. T. and Nguyen, H. T. (2000). Stay green trait in grain sorghum: relationship between visual rating and leaf chlorophyll concentration. *Plant Breeding*, 119:365-367.
- Yachdav, G., Kloppmann, E., Kajan, L., Hecht, M., Goldberg, T., Hamp, T., H. and onigschmid, P. (2014). PredictProtein- an open resource for online prediction of protein structural and functional features. *Nucleic Acids Research*,gku 336.
- Yaish, M. W., El-Kereamy, A., Zhu, T., Beatty, P. H., Good, A.G., Bi, Y. M. and Rothstein, S. J. (2010). The APETALA-2-like transcription factor *OsAP2–39* controls key interactions between abscisic acid and gibberellin in rice. *PLoS Genetics*, 6: e1001098.
- Yamaguchi-Shinozaki, K. and Shinozaki, K. (1994). A novel cis-acting element in an Arabidopsis gene is involved in responsiveness to drought, lowtemperature, or high-salt stress. The Plant cell Online, 6:251-64.
- Yang, Y., Li, R. and Qi, M. (2000). In vivo analysis of promoters and transcription factors by agroinfiltration of tobacco leaves. *The Plant journal*, 22:543-551.
- Yilmaz, A. and Grotewold, E. (2010). Components and Mechanisms of Regulation of Gene Expression. In *Computational Biology of Transcription Factor Binding*. (pp. 23-32). Human Press.
- Zeller, G., Henz, S.R., Widmer, C.K., Sachsenberg, T., Rätsch, G., Weigel, D. and Laubinger, S. (2009). Stress-induced changes in the *Arabidopsis* thaliana transcriptome analyzed using whole-genome tiling arrays. *The Plant Journal*, 58:1068-1082.
- Zhang, G., Chen, M., Li, L., Xu, Z., Chen, X., Guo, J. and Ma, Y. (2009c). Overexpression of the soybean GmERF3 gene, an AP2/ERF type transcription factor for increased tolerances to salt, drought, and diseases in transgenic tobacco. *Journal of experimental botany*, 60:3781-3796.
- Zhang, H., Huang, Z., Xie, B., Chen, Q., Tian, X., Zhang, X., Zhang, H., Lu, X. and Huang, R. (2004b). The ethylene-, jasmonate-, abscisic acid- and NaCl-responsive tomato transcription factor *JERF1* modulates expression of GCC box-containing genes and salt tolerance in tobacco. *Planta*, 220:262-270.

- Zhang, H., Zhang, D., Chen, J., Yang, Y., Huang, Z., Huang, D., Wang, X.C. and Huang, R. (2004a). Tomato stress-responsive factor *TSRF1* interacts with ethylene responsive element GCC box and regulates pathogen resistance to Ralstonia solanacearum. *Plant Molecular Biology*, 55:825-834.
- Zhang, M., Yuan, B. and Ping, L. (2009b). The role of ABA in triggering ethylene biosynthesis and ripening of tomato fruit. *Journal of Experimental Botany*, 60:1579-1588.
- Zhang, S., Li, N., Gao, F., Yang, A. and Zhang, J. (2010). Overexpression of *TsCBF1* gene confers improved drought tolerance in transgenic maize. *Molecular Breeding*, 26:455-465.
- Zhang, Z. and Huang, R. (2010). Enhanced tolerance to freezing in tobacco and tomato overexpressing transcription factor *TERF2/LeERF2* is modulated by ethylene biosynthesis. *Plant molecular biology*, 73:241-249.
- Zhang, Z., Zhang, H., Quan, R., Wang, X.C. and Huang, R. (2009a). Transcriptional Regulation of the Ethylene Response Factor *LeERF2* in the Expression of Ethylene Biosynthesis Genes Controls Ethylene Production in Tomato and Tobacco. *Plant Physiology*, 150:365-377.
- Zhao, D.Y., Shen, L., Fan, B., Yu, M., Zheng, Y., Lv, S. and Sheng, J. (2009). Ethylene and cold participate in the regulation of LeCBF1 gene expression in postharvest tomato fruits. *FEBS Letters*, 583:3329-3334.
- Zhao, M., Liu, W., Xia, X., Wang, T. and Zhang, W. H. (2014). Cold acclimation-induced freezing tolerance of Medicago truncatula seedlings is negatively regulated by ethylene. *Physiologia Plantarum*, 152:115-129.
- Zhong, G. V. and Burns, J. K. (2003). Profiling ethylene-regulated gene expression in *Arabidopsis* thaliana by microarray analysis. *Plant Molecular Biology*, 53:117-131.

122