

# **Expression patterns of cell wall modifying genes from banana during fruit ripening and in relationship with finger drop**

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**Supplementary Data**

**Table S1:** Sequences of primers used in this study

Target	Name	Oligonucleotide sequence 5'→ 3'	Product size (bp)	Reference
	dT <sub>17</sub> -adapter	GACTCGAGTCGACATCGA-T <sub>17</sub>		Frohman (1990)
	Adapter	GACTCGAGTCGACATCGA		
	Xth-F1	CAYGAYGARATIGAYTTYGARTT		This study
<i>αMaEXP1</i>	EXP1-SPF	GGTGGAGGCATTCGGTCTGGTT	221	
	EXP1-SPR	GGGAGGTGACACGATGAGAAGATGG		
<i>αMaEXP2</i>	EXP2-SPF	GCAGAGCAACGCGTACCTCACT	165	
	EXP2-SPR	GAGAAGAGGTTCGAACAGCGCGA		
<i>αMaEXP3</i>	EXP3-SPF	GGAAGTGGGGTCAGAAGTGGCA	187	Trivedi <i>et al.</i> , 2004, Sane <i>et al.</i> , 2007
	EXP3-SPR	GGCGGAAGGAGTTTGAGCTTG		
<i>αMaEXP4</i>	EXP4-SPF	TCGGCCAATCCCTCTCCTTCCG	150	
	EXP4-SPR	AGAGTGGAGCAGCATTTCGAGTTGCAGT		
<i>αMaEXP5</i>	EXP5-SPF	GCGGTGCGACAATGGCAGTAGA	208	
	EXP5-SPR	GCAGCCACTTCAGCCTCTGCTA		
<i>MaPG1</i>	PG1-SPF	TCTTCATTCTTTCTTTTTCTGC	150	
	PG1-SPR	TTAGTATGCAGCCAAATTAGATCC		
<i>MaPG1/2</i>	PG1/2SPF	TCATTACAGCATTGAAGGGAAA	131	
	PG1/2SPR	GTCAAGTTATTTGGGGTGCATT		Asif <i>et al.</i> , 2005
<i>MaPG3</i>	PG3-SPF	GAGCCTGGGTATGCACAACT	132	
	PG3-SPR	GTACACCGTGTCTGAAGCTGAT		
<i>MaPG4</i>	PG4-SPF	GTATTGGAAGCTTAGGAAAGCAG	150	
	PG4-SPR	ACGGTGTCCATGCGTATGTT		
<i>MaPEL1</i>	PEL1-SPF	TGCTCATTTCTTTCTTTTCACG	153	
	PEL1-SPR	TCCCAAGTCAAGTAGTATCAACACA		Pua <i>et al.</i> , 2001
<i>MaPEL2</i>	PEL2-SPF	GGAAGCGTTGTCAAGTTTCTTTT	177	
	PEL2-SPR	GGATAACGGGCAAAAGACTAAA		
<i>MaXET1</i>	XET1-SPF	CGGAGTGCTCCATTGCCTGAGAGAA	153	
	XET1-SPR	AGCCGATGTGTGCTTTTCAATTGGTTGT		Lu <i>et al.</i> , 2004
<i>MaXET2</i>	XET2-SPF	GGAATGCTTCGCCGCATCTAAG	188	
	XET2-SPR	TCACATCCAATACAATTCTTCTTATCGCA		
<i>MaXTH3</i>	XTH3-SPF	GACAGGATGAGGTGGGTGCAGAAGA	222	
	XTH3-SPR	TGCTAATCCGGTAGACGCAGAACAGA		
<i>MaXTH4</i>	XTH4-SPF	CGACTGATGGCTGCTGGAT	101	
	XTH4-SPR	TCCATCTTTTACATACAAAACGGAACT		
<i>MaXTH5</i>	XTH5-SPF	CACATTCGGGACTGCGATTACGTC	247	
	XTH5-SPR	CTTCGAACACCAATCCCCGATGCTC		
<i>MaXTH6</i>	XTH6-SPF	TGCTACGACCAGCATCGATATGGCA	167	This study
	XTH6-SPR	GATGGTTGATCGTCGACGGCACTTG		
<i>MaXTH7</i>	XTH7-SPF	ACAGAGGATGAAGTGGGTGCAGAGG	114	
	XTH7-SPR	CTCTGTCTCTCAGGCGATGGAGC		
<i>MaXTH8</i>	XTH8-SPF	TACAACACTGCAACGACGCCAAGC	204	
	XTH8-SPR	CCTGAGAACA TGGTTTGCAGGTT		
<i>MaXTH9</i>	XTH9-SPF	CGCAGAAGA ACTACATGATCTACAAC	196	
	XTH9-SPR	CAGAGAGACTAGTATATTGCTTGTTCG		
<i>MaPME1</i>	PME1-SPF	CTTTTACCGCAGGGTTGAACTAAG	125	This study
	PME1-SPR	GAAGAAACGTTTTATTCCACACATC		
<i>MaPME2</i>	PME2-SPF	CGTGGAGCATTTTCATCCAGGGCAAC	185	

<i>MaPME3</i>	PME2-SPR	ACTGCAATGCTTACAACCTGGGCACG	180	Liu <i>et al.</i> , (1997)
	PME3-SPF	ATTCTGGGGGATAACTGGCTGCCTC		
	PME3-SPR	CCCGATGCCTCCACAATTGAATCCC		
<i>MaACT</i>	Act-F	GAGAAGATACAGTGTCTGGA	231	Liu <i>et al.</i> , (1997)
	Act-R	ATTACCATCGAAATATTTAAAAG		

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**Table S2**

Name	Consensus	MA-PME2 promoter	MA-PME3 promoter	Function
TATABox	TATA	-30	-31	Basal promoter elements for transcription
CAATBOX1	CAAT	-451	-484	
CURECORECR	GTAC	-	-457, -601, -800, -879	Copper/O <sub>2</sub> -response element
MYBGAHV	TAACAAA	-429	-	Gibberellin related element
CAREOSREP1	CAACTC	-	-129, -285	
GARE2OSREP1	TAACGTA	-1155		
SURECOREATSULTR11	GAGAC	-531	-	Sulfur responsive element containing the auxin response factor (ARF) binding sequence (GAGACA)
POLLENILELAT52	AGAAA	-611, -787	-753	Pollen specific expression
WBOXATNPR1	TTGACC	-1080, -1091	-561, -942	Plant defense responsiveness
ARFAT	TGTCTC	-1347	-688	Auxin responsive factor
ACGTATERD1	ACGTA	-362	-727	Early response to dehydration
CATATGGMSAUR	CATATG	-117	-968	Auxin related element
TCA-element	CCATCTTTTT	-206	-619	Cis-acting element involved in salicylic acid responsiveness
WBOXNTERF3	TGACY	-1081, -1092, -1324	-263, -542, -563, -713, -944, -1009, -1061, -1102	Wounded related element through ethylene response factor 3

### Different cis-regulatory elements found within the promoter of MaPME2 and 3 genomic sequences.

Analysis of *MaPME2* and three promoter sequences was performed using PLACE (Prestridge 1991; Higo *et al.*, 1999) and PLANT CARE (Lescot *et al.*, 2002) programs. These numerous cis-regulatory sequences might be involved in tissue-specific or developmentally-regulated gene expression. Some of them are present in common in both *Ma-PME2* and *MaPME3* promoter sequences, including the basal TATA- and CAAT-box promoter elements for transcription, pollen-specific expression, plant-defense response element, auxin, gibberellin and salicylic-acid response elements. Other motifs like the sulphur-response element that contains the auxin–response factor (ARF) binding sequence (GAGACA) and the copper/O<sub>2</sub>-reponse element appeared to be specific to *Ma-PME2* and *MaPME3* promoter sequences, respectively.

## FIGURE S1

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MA-XET1 -----MAMRFLLVACSLVAIASAGNFYQEFDVTWGGDRAKNDNGQLLTLSLDKASGSG
MA-XET2 MGHTTILSLAFFILALVAFAGARPANFLQDFRITWAGTHIKQLQGGSAIQMLDPSSGCF
MA-XTH3 -----
MA-XTH4 -----
MA-XTH5 -----
MA-XTH6 -----
MA-XTH7 -----
MA-XTH8 -----
MA-XTH9 -----

                                DEIDFEFLG
MA-XET1 FQSKNQYLFQKIDMQIKLVPGNAGTVAAYLSSQGPTHDEIDFEFLGNPSGDPPYTLHTN
MA-XET2 ASNKQYHYGRVSMKIKLIPGDSAGTVAFYMNSDTDAVRDELDFEFLGNRSGQRTRSKTF
MA-XTH3 -----HDEMDFEFLGNLTGDPYTLHTN
MA-XTH4 -----HDEMDFEFLGNTSGEPYVLHTN
MA-XTH5 -----HDEMDFEFLGNVRGKDWRIQTN
MA-XTH6 -----HDEMDFEFLGNVRGKDWRIQTN
MA-XTH7 -----HDEMDFEFLGNLSGDPYTLHTN
MA-XTH8 -----HDEMDFEFLGNLSGDPYALHTN
MA-XTH9 -----HDEMDFEFLGNLSGDPYTLHTN

                                NxS
                                T
MA-XET1 VFTQKGKGNR--EMQFKLWFDPTEDFHTYSILWNPRHVI-----
MA-XET2 TFT-GRATR--EQRVNLWFDPAADYHTYTILWDHYHV-----
MA-XTH3 VYTQKGKGNR--EMQFKLWFDPTKDFHAYSVLWNPRHVMVFLSNPHQRCRRCSPSV--RHR
MA-XTH4 VFAQGKGR--EQQFYLWFDPTLAFHTYSVLWNPRRIV-----
MA-XTH5 VYGNGSTARGREERYLVPFDPTAAHRYSILWTPDYII-----
MA-XTH6 VYGNGSTTRGREERYLVPFDPTTEPHRYSILWTPDYII-----
MA-XTH7 VFTQKGKGNR--EMQFKLWFDPTKDFHTYSILWNPRHVMCVFHSICCLLSFHYSYAHHESV
MA-XTH8 VFTQKGKGNR--EMQFKLWFDPTEDFHTYSILWNPRHVMLDDELVTRCRNSP-----WVL
MA-XTH9 VFTQKGKGNR--EMQFKLWFDPTKDFHTYSILWNPRHI-----

MA-XET1 --FMVDG--TPIRDFKNLESRGIAFPNSQPMRIYSSLWNADDWATRGGLVKTDWSKAPFT
MA-XET2 --FSVDD--VPIRVYKNNEGRGIPYP-VQPMGVYSTLWEGDDWATRGGLVKTDWSKAPFY
MA-XTH3 CSFMVDG--TPIRDFKNLESRGIPFPKNQPMRIYSSLWNADDWATRGGLVKTWNNNAPFT
MA-XTH4 --FYVDG--TPVRFVFNSEGAGVAYPKSQAMRVYASLWDADDWATRGGLVKTDWSQAPFV
MA-XTH5 --FYVDD--VAIREVVRSDSMGGDFP-SKPMSVYATIWDGSSWATSYGKIKINYKYAPYV
MA-XTH6 --FYIDD--VPIREVVRSDAMGGDFP-SKPMSVYATIWDGSSWATSYGRIKINYKYAPYV
MA-XTH7 STFQLHGGRHANRLQEPGVEGHRVQEPPAHEDLLQPLECRRLGDQRRAGEDRLVQGAHV
MA-XTH8 RWFQLHGRRHSHQRLQEPGIEGHRLQEPTHEDLLQPLERQLGDQRRAGEDGLEQGTLR
MA-XTH9 --FMVDG--TPIRDFKNLESRGIAFPKNQPMRIYSSLWNAEDWATRGGLIKTDWTKAPFV

MA-XET1 ASYRNFKADTCVPSSATTECASNSVPSN----GWWNQELDSMGQQRMKWVQKNYMIYN
MA-XET2 AYYKDFDIEGCAVPGPANCASNPNN-----WEGSAYRQLSPEQARKYRWVRANHMIYD
MA-XTH3 ASYRNFNADACVWSSGISSSCAPRNSSAVPAAARGWWSQELDTPSQDRMRWVQKNYMIYH
MA-XTH4 ASYRGFVADACVAASVRPSCSASKA-----GWWQGLDSSGARKLKWVRDNMYVDY
MA-XTH5 SEFSDLVLRGCRVD-PIQQVDTAERCAETVEELMSADFALLTPMKRAAMRRFRERYMIYS
MA-XTH6 SEFSDLVLRGCRVG-PIQQVDSADRCAEAVEELMSADYALLTPRKRAAMRRFRERYTIYS
MA-XTH7 GVVQRLQG-----
MA-XTH8 RLLQELQRRRLRPGKLQVRRLHQERVVEPGARLDQPEDEMGEELHDLQLLQRRQAVSS
MA-XTH9 ASYRNFNANACIKASGRSSCTPAKS-----GWWNQELDSASHARMRWAQKNYMIYN

MA-XET1 YCSDLKRFSQGLPPECSIA-----
MA-XET2 YCTDKPRYPVPPPECFAGI-----
MA-XTH3 YCTDLKRFPQGFPECSMT-----
MA-XTH4 YCRDAKRFPGGFPPECSQPLD-----
MA-XTH5 FCYDQHRYGNFTFPDCDYVSPEHTRFGEWGNNRFPPKEVRRSRRRVRKPSPISVQSSE
MA-XTH6 FCYDQHRYGNVTFPDCDYVSSEHSRFGEWGNKFPPKEVRRARRRSRKPSAVDDQPSK
MA-XTH7 -----
MA-XTH8 GPAAGVRHCLNGRSRLK-----
MA-XTH9 YCNDVNRFPQGLPPECSIA-----

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### Multiple sequence alignment of polypeptide sequences of banana *XTH* genes

The predicted polypeptide of banana *MaXET1* (accession n° EF103137) and *MaXET2* (accession n° EF103136) genes, and those corresponding to *MaXTH* cDNAs isolated in this study were aligned (2A) using the CLUSTAL X program (Thompson *et al.*, 1997). The putative active site conserved among glycosyl hydrolase family 16 (GH16) enzymes with the adjacent *N*-linked glycosylation site are indicated in bold.

