

CIHEAM - International Centre for Advanced Mediterranean Agronomic Studies

Mediterranean Agronomic Institute of Chania

SUPPRESSION OF A TOMATO PROLYL 4 HYDROXYLASE RESULTS IN MULTIPLE ALTERATIONS ON FRUIT DEVELOPMENT, RIPENING AND HEALTH COMPONENTS

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Enzymatic Activity of Prolyl 4 Hydroxylases



[not basic]-[not T]-[AVSG]-Hyp-[AVST]-[GAVPSTC]-[APS]



The posttranslational modifications of O-glycosylated cell wall proteins are of broad importance to cell differentiation and plant development



Arabidopsis P4Hs

(Velasquez et al., Science, 2011)

Arabidopsis P4H9 is involved in root length determination by regulating cell elongation





P4h9-1 wt

	For	tilizati						Upstrear TAGL1, (MADS9	R, NR,			
Anthesis			011	Imma	ature Green	N	fature Green	Breaker	Yellow	Orange	Red Ripe	
,	*	*	•									
	Frui	Fruit set Early		y fruit growth		Maturation	Trigge	er 🛛	Ripening	5		
	-3	0	10	15	20	30	40	41	43	45	50 DPA	
	Cell	Cell division			ell expansion	on	Competence	Competence to ripen and progression of ripeni				
	DELLA, GAox 1 ARF8, ARF7, BR6ox1, PIN4, IAA9, CDKs, TIR1 Cyclins?				ARF12 SAM	IDC, Spo	ARF4 iSyn	ARF4, GH3 ACS4, ACS2, ACO1, ETR3, ETR4, ETR6, CTR1, EIN2, ERF6, AP2a (SAMS, CTR1)				
[YUC10, TAA			A1, TA	R1,	PIN7, IAA27,		[ACS1-4	, ACO2-3]	[ACO1]	
GAox1, GAox3, RG ACS2, ACO2, ACO4 EIN5c, ERF1; NCE				GL3; GL3; 4; ED3,	DWARF1, E EREBP-3, E JERF1, gene encoding enz	RF2, RF3, ss wmes			BR	60x1		
CYP707A1/3, SnRK2.10; CYP ARR2b, LOG3, 1 CKX2, CKX8; C BRL1, BZR2]			, YP73: 3, LO 3; CPE]	5A1, G7,),	zeatin O- glucosyltransferase, 12-oxophytodienoate reductase, arginine decarboxylase,		NCEDI, PYL SnRK2 (NCE PYR1)	., PP2C, D1,	DEF1, SPR Prosystemi	12, M. n M.	MAPK1-3	

Color codes of hormones/growth regulators: ABA, BR, CK, Ethylene, GA, IAA, JA, NO, PA





Control

P4H1



P4H7



Fragostefanakis et a.



Relative expression of P4H3 in RNAi – P4H3 line #7



Hydroxyproline content during fruit ripening



Fruit Diameter (cm) at BK

(A) Fruit diameter determined at the full-ripe stage (BK + 10).(B) The data represent the mean values of line #7All nine independent transformants gave similar results



Fruit diameter was recorded every two days, for the first six inflorescences of 50 plants from 9 independent transformants

TRANSVERSE SECTIONS OF TOMATO FRUITS



A) From left to right: Transverse sections of day 1 PA. Transverse section of 16 and 30 days fruits after pollination. Effect of RNAi gene silencing of SIP4H3 on cell area (**B**) and total number of pericarp cells (**C**). Error bars represent SD and asterisk significant different. Area of measurement $250\mu m^2$, Bar 400 μm



CHARACTERISTICS OF SEEDS



Seed weight of SIP4H RNAi and pBi121 (Control). The data represent the mean values obtained from 8 plants of three independent SIP4H RNAi transgenic lines and 21 pBi121 (control) plants. Statistical analyses were realized using the Student's test P<0.005;

Micro Computer Tomography Results



Images captured by Micro Computer Tomographer. A) Outer image of P4H3 RNAi and W.T. seeds. B) Cross-section of P4H3 RNAi and W.T seeds. Image shows the development of radicle, which was used to calculate the average radicle area (C) and length (D) among six seeds per line that were examined. Significant differences based on Student-t test (P < 0.05) are indicated using asterisk.

Slides from Microscope



RNAi



Day 16



Image segmentation: We created a semi-automatic algorithm for cell contour extraction using the Image



Proportional size of boxes has been selected according on each image resolution.

Morphological analysis-Number of cells



Figure I : Number of cell per microscope slide. We observe that there is a decrease in the number of cells during the plant growth.



Relation between cell size and the number of cells.



Figure 2: Average cell size *per microscope slide.* We observe that the average cell size on the WD it is bigger than those of RNAi, especially on the 30th day.



General Comment:

It is obvious that there is an inverse relation between the cell size and the number of cells, during the plants growth.

Morphological analysis-Perimeter of the cells

400



- We observe that the average perimeter of each cell increases significantly, while the cell size increases.
- The average perimeter of the cells from RNAi seems to remain stable between the 1st and the 16th day; whereas the perimeter of the cells from WT is doubled.



Our numerical findings show that there is 50% increase in the perimeter of the average cell between the RNAi and WT, during the 16th and the 30th day respectively.

Morphological analysis-Circularity of the cells



Circularity is a dimensionless parameter that reflects the ratio of cell size to the cell boundary perimeter. For circularity, a value of one represents a perfect circle, while values approaching zero have a more linear or complex structure.



Figure: Circularity of an average cell. We observe that the cells from the RNAi preserve their shape while the WT cells tend to become more circular after the 16th day.

Morphological analysis-Solidity of the cells



Solidity describes the extent to which the shape is convex or concave. When its values approaching one correspond to rounder, more solid cells.

1 0.8 ▲ 0.6 0.4 0.2 0 Day1 Day16 Day30 Figure: Solidity of an average cell. We observe that both the cells from the RNAi and WT have similar solidity values, during the fruit development. However, WT cells appear to be slightly more solid than the RNAi.

Morphological analysis-Rectangularity of the



Rectangularity has been designed to evaluate numerically how much the shape considered differs from a perfect rectangle. The range of its values is the interval [0,1] and attain the value 1 only for perfect rectangle with a desired edge ratio.



Figure: Rectangularity of an average cell. We observe that both the cells from the RNAi and WT have similar rectangularity.

Abscission related traits of the P4H-RNAi lines



Variance of proximal/distal pedicel ratios during flower development



To summarize:

 \diamond There is a decrease in the number of cells both in the WT and RNAi, during the plant growth.

 \diamond The average cell size on the WD is bigger than this of RNAi.

There is an inverse relation between the average cell size and the number of cells, throughout the plant development.

♦ Both the cells from RNAi and WT seems to maintain their morphology features. Whereas the WT cells seems to be more circular, especially on the 30th day.

 Thus, inferring these cell shape parameters is an important and challenging task throughout the effort of unraveling the mechanism which is related in the tomato fruit development.

Immunolocalization of JIM8 epitopes



Immunihistochemistry (IHC) pericarp tissue of 30 days old fruit. JIM 8 antibody was used for the detection of specific Arabinogalactan epitopes.

Flower AZ Immunolocalization



AGPs specific antibodies were used in Flower Abscission zones. The immunolocalization analysis revealed significant differences of the RNAi-P4H3 lines when compared to the WT.

WT

Fruit AZ Immunolocalization



 AGPs specific antibodies were used in Fruit Abscission zones. The immunolocalization analysis revealed no significant differences of the RNAi-P4H3 lines when compared to the WT.











🗖 WT 📕 RNAi

 GC-FID analysis revealed a significant decrease in Arabinose (Ara) and increase in Galacturonic (GalA) acid in the transgenic lines.

Gene Expression of cell wall hydrolases and abscission zone regulators



Ethylene production rate in P4H3 RNAi line



Conclusions

- Silencing of a tomato P4H resulted in smaller fruits, decreased pericarp cell size and increased cell number, lower number of seeds and altered embryo development altered seed morphology and delayed fruit abscission.
- Immunolocalization analysis indicated a significant decrease of epitope-bound AGP proteins content in flower abscission zones of P4H3 RNAi lines compared to the wild type. However, no changes in AGP proteins content were observed in fruit abscission zones at the red ripe stage.
- These results indicate that alterations in the expression of P4Hs alter the content of substrate proteins such as AGPs which might be linked to flower abscission initiation and progression

WORK IN PROGRESS

•Screening of Tomato fruit ripening Yeast 2 Hybrids libraries with P4H3 as bait

•Stable tomato transformation of P4H3 cDNA with epitope tags (HA, FLAG) for pull down assays

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