



# FRUIT, A LOW-TEMPERATURE STRESS-INDUCED PHYSIOLOGICAL DISORDER AFFECTING FRUIT QUALITY



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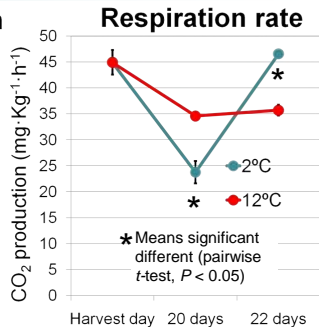
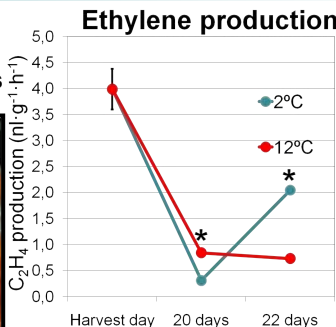
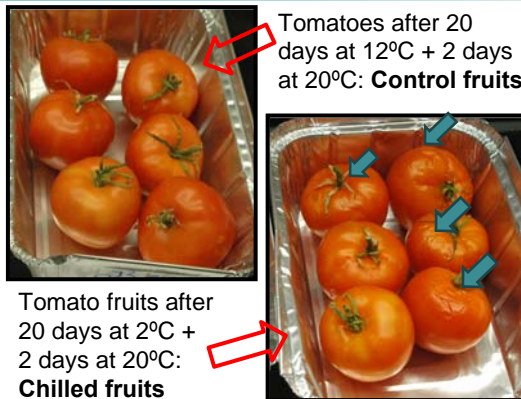
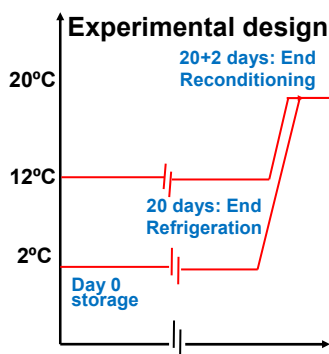
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## Introduction and objective of the research work

A proteomic approach has been undertaken to investigate chilling injury (CI) in tomato fruit (*Solanum lycopersicum* L. cv p73). This physiopathy is caused by low temperatures stress in sensitive fruits like tomato during refrigeration and it negatively affects fruit quality. The objective of the research work is the analysis of the proteome of chilled fruits vs non-chilled ones and the identification of differentially expressed proteins in fruits subjected to low temperature stress when compared with unstressed ones. The proteome of fruits conserved at a temperature that does not induce CI and of fruits conserved at a temperature of CI induction have been compared using the proteomic profile of fruits at harvest date as reference. The proteomic analysis has been performed after a reconditioning step at room temperature, when CI symptoms become evident. The physiological impact of CI on fruits has been verified by means of lipid peroxidation, respiration rate and ethylene production determinations.

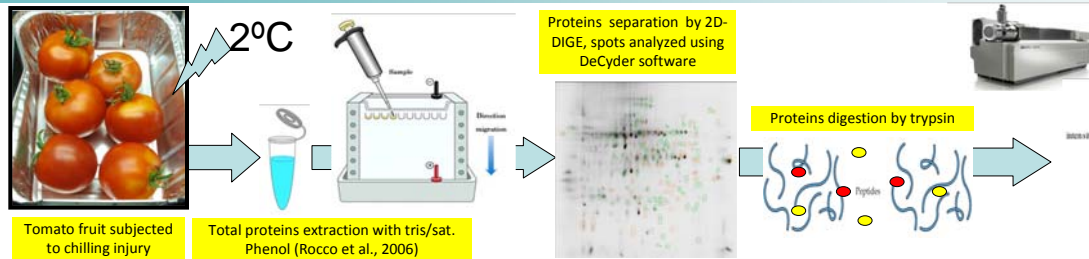
## Physiological characterization of chilled tomato samples



Lipid peroxidation (nmol MDA g <sup>-1</sup> h <sup>-1</sup> )	Fruits at harvest Control Fruits	Chilled Fruits
13.25 ± 0.27a	13.81 ± 0.22a	16.70 ± 0.49b

Different letters mean significantly different by Tukey test (P < 0.05)

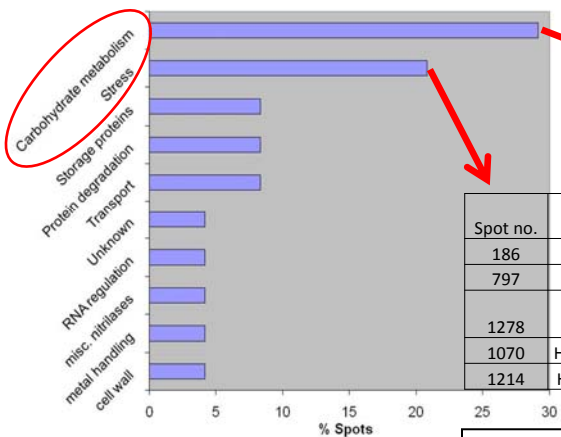
## Experimental procedure for the proteomics analysis



The MASCOT software (matrix sciences) was used to search the raw data against the databases. An homology-based comparison with the TAIR10 protein database was performed by blast. The homologous Arabidopsis proteins were clustered in the cell metabolism chart (MAPMAN 3.5.0)

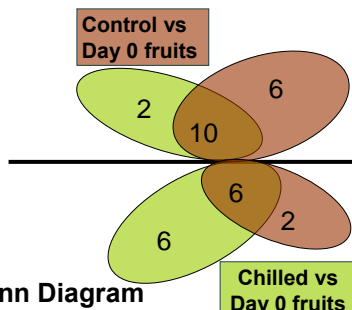
## Comparison of proteomes chilled fruits vs non-chilled ones

### Functional classification of differentially expressed proteins



Spot no.	Assignment	UniProt accession no.	Fold Change (Ch/C)
186	Hsp60	P08926	-2,11
797	IN2-1	Q8H8U5	1,51
1278	ASR1 (LEA protein)	Q08655	-1,87
1070	Hsp22.7 class IV	P19244	2,05
1214	Hsp17.4 class II	O82545	1,8

61 proteins were confirmed as differentially expressed proteins in response to low-temperature stress; 31 out of them could be identified by MS methodologies (PMF and TMS). 24 have got an expression level higher than threshold (Fold\_Change FC >1.2)



Proteins (+)

Proteins (-)

### Acknowledgments:

This work was supported by the Spanish Ministry of Science and Innovation (MICINN) through grant and PIE2009-40I080, and by the Council of Science and Technology from the Spanish Region of Murcia (Fundación SENECA) through grant no. 04553/GERM/06.

### Literature:

Rocco et al. (2006) Proteomics, 6, 3781-3791, TAIR10 database: <http://www.arabidopsis.org/> MAPMAN application: [www.mapman.gabipd.org/](http://www.mapman.gabipd.org/)

