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Advances and current challenges in understanding postharvest abiotic stresses in perishables

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ABSTRACT

Postharvest abiotic stresses impact not only quality, eating and nutritional attributes of perishables but shelf life and susceptibility to physiological and pathological disorders and thus postharvest losses. Classical postharvest technologies involve applying stress conditions (cold, controlled atmosphere conditions, addition of chemicals) to extend storage and shelf-life. However, recent research has concerned itself with understanding the mechanisms by which abiotic stresses affect postharvest commodity quality. Thus, holistic approaches that incorporate the use of transcriptomic, proteomic, and metabolomic platforms, complemented with biochemical analysis as well as phenotyping are being used to understand stress physiology and its complex regulation at the different levels of cellular control (e.g., epigenetic control, post-transcriptional, post-translational) in order to develop and improve current technological processes. This review aims to highlight key methodological points that need to be addressed for further understanding of key postharvest abiotic stresses (cold/heat, low oxygen/high carbon dioxide and dehydration) and to review research over the last ten years dedicated to understanding postharvest abiotic stresses.

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1. Introduction

Fruits and vegetables are still alive and respiring after being harvested. However, they are cut off from their nutrient and water resources, and thus susceptible to fast deterioration if the right measures are not taken. Reduction of postharvest losses, which are significant and might represent up to 40% of the harvested crop, is one of the leading strategies to assure food safety (quantity and quality of food) given the constantly growing population (FAO, 2011). Different postharvest strategies (e.g., low temperature, air atmosphere modification, chemical treatments) are commercially used to reduce the respiratory rate, retard ripening and senescence, deter pathogen development and extend shelf life while

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Table 1
Selected studies at different levels of cellular control related to cold and heat postharvest (PHT) treatments.

Commodity	PHT Treatment	Phenotyping	Platform(s)	Main findings	Reference
Citrus					
Citrus paradisi Macf cv. Marsh	5 °C × 3 weeks (non-conditioned) 16 °C × 7d + 5 °C × 3 weeks (conditioned)	CI index	Targeted RT-PCR	Decreased lipid transfer protein, LEA, stress response zinc finger protein, catalase and metallothionein & induced galactinol synthase, ACO, pathogen inducible oxygenase and temperature induced lipocalin.	Maul et al. (2011)
Citrus sinensis cv. Valencia	HT (37 °C × 2 d and 90% RH + 2 d at 20 °C). Storage simulation (5 °C + 30 d & 5 °C + 60 d)	RR, SSC, TA EtOH & Acet EL, HP, WL	Gel-based DIGE proteomics Metabolomics GC–MS Targeted ascorbate–glutathione enzymes	HT induced pathogenesis related proteins, SOD in flavedo but decreased in sacs; increased peroxidase in flavedo only and increased alcohol dehydrogenase in flavedo but not in sacs.	Perotti et al. (2011)
Citrus grandis × *Citrus paradise*	8–10 °C, 85–90% RH up to 120 d	SS, OA, EtOH, Acet, MeOH, ABA, Asc	Digital gene expression profiling and gel based proteomics and qRT-PCR	ABA not involved in cold stress. Increased chitinase, cysteine synthase, cysteine protease inhibitor, allyl alcohol dehydrogenase, mitochondrial aldehyde dehydrogenase. Increased heat shock protein, COR15 and cold responsive genes. Down regulation of genes involved in carbon, nitrogen, lipid and secondary metabolism. Increased limonin, nomilin, methanol & acetaldehyde.	Yun et al. (2012)
Citrus unshiu cv. Marc	52 °C × 2 min	RR, WL, TSS	Gel-based proteomics and GC-MS and LC-MS metabolomics	Increased glucanases, chitinases, low MW HSPs and reduced redox metabolism (isoflavone reductase, oxidoreductase and SOD) Decreased primary metabolism (OA and aminoacids) but increased PUFAs, gluconic acid.	Yun et al. (2013)
Murcott tangor (tangerine x sweet orange)	4 °C × 15 d	Water loss	Gel-based proteomics	Increase in cysteine protenase, decrease in ascorbate peroxidase	Lliso et al. (2007)
Grape					
Vitis labruscana	2 °C × 50 d, 95% RH	F, TSS, TA, reducing sugars	Gel-based proteomics, targeted organic and phenolic acid analysis	Decreased glycolysis and TCA enzymes. Increased cell wall degrading, HSPs and antioxidant enzymes and proteasomes.	Yun et al. (2014)
Peach					
Prunus persica L. Batsch var ‘nectarina’cv. Venus	0 °C × 1 h + 5 w at 5 °C 85–90% RH + 20 °C × 1 d	F, CI index	Gel-based proteomics Targeted RT-PCR	Increased stress related PR (Pru p 1.05, Pru du 1.06A., Pru p 2.01 A and Pru p 2.01) proteins.	Giraldo et al. (2012)
Prunus persica L. Batsch cv. O'Henry	4 °C × 21 d + 21 °C × 5 d (WI)	F, TSS, RR, E, JC	Microarray qRT-PCR	Decreased SAM synthetase, 1-ACC, expansin and endo-PG. Increased of stress defensive enzymes: catalase, superoxide dismutase, glutathione reductase.	Pavez et al. (2013)
Prunus persica L. Batsch cv. Dixiland	0 °C × 5 d and 90% RH (cold) 39 ± 1 °C and 90% RH (heat) 39 ± 1 °C and 90% RH × 3 d + 5 d at 0 °C + 2 d at 20 °C (heat & cold)	F, SSC, TA	Metabolomic GC-MS Targeted RT-PCR	Increased putrescine & benzoate due only to cold. Increased saccharate, glucoheptose, malitol, fructose, trehalose, maltose, serine only due to heat. Increased galactinol & raffinose, 1-O methylglucoside, Glc, Thr, Asp, Asn, Tyr, glycerate and urea.	Lauxmann et al. (2014)
Prunus persica L. Batsch cv Dixiland	39 ± 1 °C and 90% RH × 3 d	F	Transcriptomics qRT-PCR	Increased TFs:ZAT12, WRKY40, IAA2, NF-YA4 involved in plant stress responses, auxins and PR.	Lauxmann et al. (2012)
Prunus persica L. Batsch cv Dixiland	39 ± 1 °C and 90% RH × 3 d	in situ IML proteins	Gel-based DIGE proteomics qRT-PCR	Reduced ACO1, 12 cell wall modifying enzymes and DUF642 proteins and increased glyceraldehyde 3-phosphate dehydrogenase (apoplastic)	Bustamante et al. (2012)
Pepper					
Capsicum annuum L. var. California	10 °C, 80% RH × 21 d	Cellular ultrastructure	Gel-based DIGE proteomics	Decreased glycolysis, Calvin and TCA cycle and catalase enzymes.	Sánchez-Bel et al. (2012)
		E, MDA, SS, OA	Targeted ascorbate-glutathione enzymes	Increased ethylene and MDA and changes in sugars and organic acids in chilled fruits.	
Tomato					
Solanum lycopersicum L. cv. Micro-Tom	6 °C × 48 h	none	Transcriptomics	Induction of a LEA (dehydrin type protein) Genes involved in carotenoid, cell wall, ethylene and signalling are involved in the uneven ripening	Weiss et al. (2009)
Line M82IL2-2	3 °C × 4 weeks	E, F, color	Microarray based transcriptomics, RT-PCR and targeted HPLC carotenoid analysis		Rungkong et al. (2011)
Solanum lycopersicum L. cv. Micro-Tom	20 °C × 7 min + 14 d at 2.5 °C	CI, EL, RR	Metabolomics GC-MS	Low T: increased arabinose, citric acid, dehydroascorbic acid, fructose 6-P, glucose 6-P, rhamnose and valine and reduced glutamic and shikimic acid. HT: increased alanine, allantoin,	Luengwilai et al. (2012)