GLOBAL GENE EXPRESSION CHANGES IN TOMATO FRUITS EXPOSED TO HOT WATER AND COLD STORAGE CONDITIONS

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Introduction. Tomato fruit is susceptible to develop chilling injury (CI), a physiological disorder caused by low, non-freezing temperatures that impair its postharvest quality. Hot water (HW) treatments in tomato fruits have shown to induce CI tolerance [1], although the molecular mechanisms involved in that process remain unclear.
The aim of the present work was to evaluate the effects of HW and cold storage over transcriptional changes in tomato fruits.

Methods. Tomato (cv. Micro-Tom) fruits were harvested at mature green stage and immersed for 7 min in water at 40 °C (HW) or at 20 °C (C), followed by storage at 5 °C for 14 d to induce chilling stress, and then at 20 °C for 14 d to allow ripening and symptoms development [1]. Total RNA was isolated from pericarp tissue using Trizol, and purified using RNeasy MinElute Cleanup Kit. Sequencing was performed on 5500 SOLiD System with the Exact Call Chemistry module. SOLiD raw reads were analyzed with the software CLC Genomic Workbench Version 5.5. Trimmed reads (quality >20, length >25 bp) were mapped in color-space against the tomato "ITAG2.3_cdna" reference using default parameters. Unique gene reads were normalized by the quantile method, and then were statistically analyzed (Kal's test) for differential expression. Genes with FDR <0.01, and fold change ±2 were considered as differentially expressed (DE).

Results. A total of 23,375,457 reads (75 bp) were obtained from the six samples sequenced. After trimming by quality and length, 15,507,024 reads (66.3%) were retained. Of the trimmed sequences, 10,297,848 reads (66.4%) were uniquely mapped to the reference. Unique gene reads were subjected to quantile normalization to remove the bias of sequencing depth across all samples. Hierarchical clustering (Fig.1) showed that the expression profiles of tomato fruits are more affected by the storage time than by the treatment (C or HW). Interestingly, expression profiles at time zero (0h) are similar to those at ripening (14+14d), while the samples of chilling response (14d) are in a more distant group. Pair-wise comparisons against C-0h (Table 1) showed 1,753 DE genes immediately after heat shock (HW-0h), 3,245 and 3,312 DE genes were detected in the chilling response group (C-14d and HW-14d), meanwhile 2,099 and 1,985 DE genes were observed in the ripening group (C-14+14d and HW-14+14d).

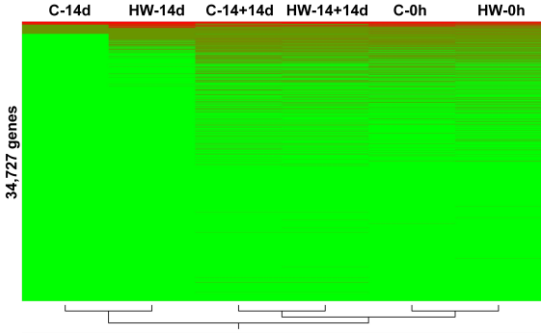

Fig.1 Hierarchical clustering of samples using normalized values of unique gene reads.

Table 1. Effects of hot water and cold storage on the transcriptome of tomato fruits

	Differentially expressed genes		
Pair-wise comparison	Up-regulated	Down-regulated	Total
C-14d/C-0h	1,935	1,310	3,245
C-14+14d/C-0h	1,134	965	2,099
HW-0h/C-0h	798	955	1,753
HW-14d/C-0h	1,707	1,605	3,312
HW-14+14d/C-0h	1,163	822	1,985

Conclusions. The transcriptional changes described here will be very useful in the identification of key genes associated with CI tolerance and susceptibility in tomato fruit.

References.

1. Luengwilai K, Beckles DM, Saltveit ME (2012). *Postharv Biol Tech* 63:123-128.