

Integrating omic data to detect association between sHSP transcripts and phenotypic variability in tomato fruits

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INTRODUCTION

Fruit ripening is a complex developmental process highly coordinated by different gene families such as small Heat Shock Proteins (sHSP), which maintain cell homeostasis and are a superfamily of chaperones that have been characterized in other organisms. sHSP promotes protein folding and disaggregation during stress or developmental changes (Arce *et al.*, 2014 and 2016). Previously, we obtained the transcriptome of cv. Caimanta (*C. S. lycopersicum*), exotic LA0722 (*P. S. pimpinellifolium*), and their interspecific hybrid (CxP) in 3 main stages of ripening (Pratta *et al.*, 2011). Also, agronomic characterization of fruit attributes (Figure 2) was achieved in the three genotypes.

MATERIALS AND METHODS

A Generalized Procrustean Analysis (GPA) was performed on the gene expression levels of two clusters of sHSP located on chromosomes 6 and 9, using transcriptomic data, along with 11 quantitative fruit traits as phenomic data. Traits in this experiment were: Soluble solids (SS), pH, titratable acidity (TA), colour coefficient A/B, reflectance percentage (L), firmness, diameter, height, shape, weight, and shelf-life (Figure 2). An estimation of the degrees of dominance (d/a) was carried out for values of gene expression in sHSP in chr06 and chr09. Thus, the objective of this communication was to evaluate the association between transcriptome and phenotypic datasets.

RESULTS

Principal Components 1 (PC1) and 2 (PC2) from the GPA explained 77.4% and 22.6% of the total variability, respectively. In the biplot, the consensus positions of P and CxP were close at positive values of PC1, while C was located at negative values. Contrarily, P and CxP were discriminated against by PC2 because the exotic parent was on its negative values and the hybrid on the positive ones. C was located at 0 value (Figure 1). Nevertheless, for each genotype positions according to transcriptomic and phenomic characterizations were similar, indicating a high association among both datasets. A gene action analysis was carried out and d/a coefficient for all traits evidenced a high dominance of the wild genome, which agreed to the proximity of P and CxP in the biplot. In all cases, the F_1 value was towards the wild parent. Solyc06g076520 on chromosome 6 and Solyc09g015000 on chromosome 9 showed positive overdominance and the rest of the genes showed partial dominance towards higher values (table 1).

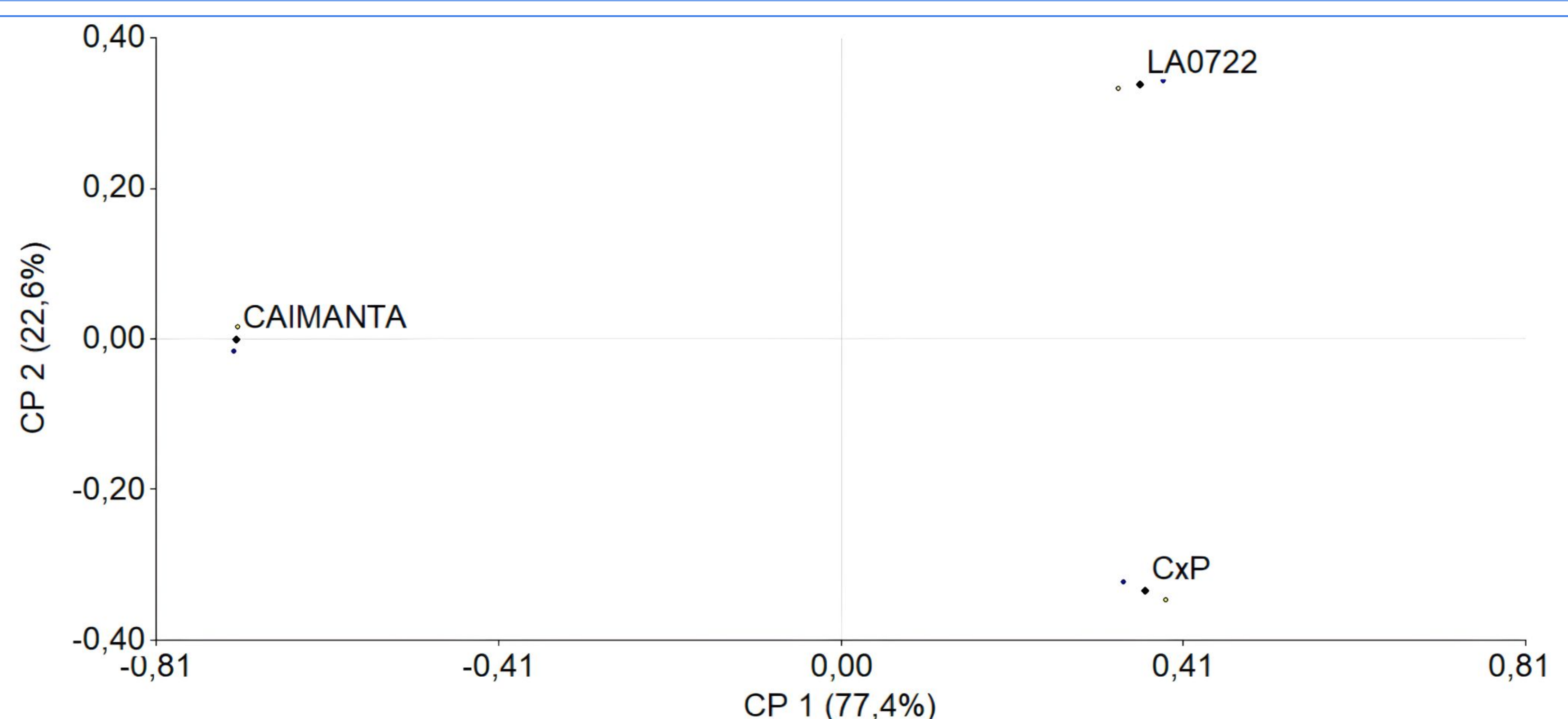


Figure 1: Generalised Procrustes Analysis in C, P and F_1 CxP. Central dot represents the genotype, with the grey dot representing the sHSPs found on chromosome 06 and the other dot corresponding to the sHSPs found on chromosome 09.

Gene ID	C	P	F_1 CxP	PO	a	-a	d	d/a	Dominance degree	Dominant
Solyc06g076520.1	10,841	12,190	12,265	11,52	0,674	-0,674	0,750	1,112	Positive overdominance	LA0722
Solyc06g076540.1	7,147	12,572	11,984	9,86	2,713	-2,713	2,124	0,783	Partial dominance to highest values	LA0722
Solyc06g076560.2	10,088	12,633	11,795	11,36	1,272	-1,272	0,435	0,342	Partial dominance to highest values	LA0722
Solyc06g076570.3	10,383	12,077	11,785	11,23	0,847	-0,847	0,554	0,655	Partial dominance to highest values	LA0722
Solyc09g015000.3	9,039	10,949	11,201	9,99	0,955	-0,955	1,207	1,264	Positive overdominance	LA0722
Solyc09g015020.1	8,640	10,292	10,130	9,47	0,826	-0,826	0,664	0,804	Partial dominance to highest values	LA0722

Table 1: Estimation of dominance in sHSPs genes on chromosomes 06 and 09.

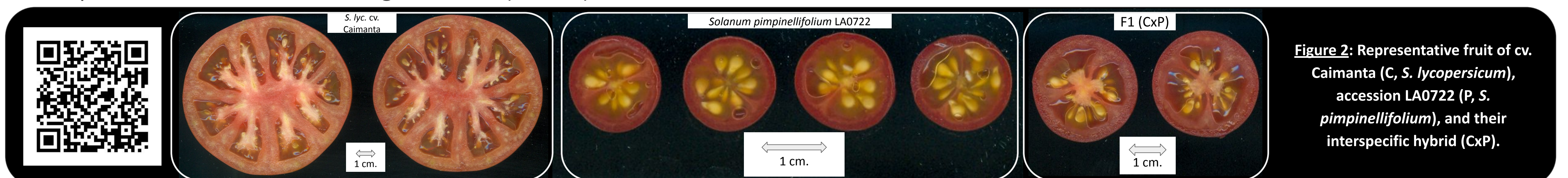


Figure 2: Representative fruit of cv. Caimanta (*C. S. lycopersicum*), accession LA0722 (*P. S. pimpinellifolium*), and their interspecific hybrid (CxP).

CONCLUSIONS

This information can be applied in breeding programs to get optimal use of exotic genes obtaining new varieties with adequate fruit quality traits.

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