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A TRANSCRIPTOMIC APPROACH TO IDENTIFY REGULATORY GENES INVOLVED IN FRUIT SET OF WILD TYPE AND PARTHENOCARPIC TOMATO GENOTYPES

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The tomato (*Solanum lycopersicum* L.) *parthenocarpic fruit* (*pat*) mutation associates a strong competence for parthenocarpy (seedless fruit production) with homeotic transformation of anthers and aberrancy of ovules. To dissect this complex floral phenotype and to detect genes involved in the pollination-independent fruit set of the *pat* mutant, a transcriptomic approach was used. Ovaries from two pre- and one post-anthesis stages were collected to monitor and compare the expression profile of genes in the wild type (WT) and in its near-isogenic *pat* line. A microarray platform consisting of over 41,000 probes was used in this study. Normalized expression data were subjected to one-way ANOVA and 3,627 genes showed significant expression differences ($p<0.01$). Among them, 1,706 genes displayed a greater than 3-fold change in at least one of the pair-wise comparisons analyzed. Gene sequence distribution following by Gene Ontology annotation showed "catalytic activity" (43.9%) and "binding" (38.9%) as the most represented categories at the molecular function level. A clustering analysis allowed the selection of 12 clusters containing genes developmentally regulated in the WT ovary during fruit set and de-regulated in the mutant. These genes are putatively involved in the determination or in the expression of the parthenocarpic phenotype. These clusters, that were enriched of sequences encoding transcription factors (TFs), included orthologs of Arabidopsis genes involved in the regulation of flower organs development, such as *BIG PETALp*, *APETALA3* and *CRABS CLAW*. Interestingly, de-regulation in the *pat* mutant of such genes represents the first direct evidence of the association of these TFs with parthenocarpic fruit growth. Their expression profile was confirmed by qRT-PCR, which was also extended to other genes already known to be involved in controlling tomato fruit set, such as *AUXIN RESPONSE FACTOR7* (*ARF7*), *ARF8* and *INDOLE-3-ACETIC ACID9* (*IAA9*). Finally, selected genes showing a de-regulated expression pattern in *pat* compared to the WT were also studied in other tomato parthenocarpic systems (*pat-2*, *pat3/4*, *aux/iaa9*, *RNAi-ARF7*). This comparative approach raised interesting cues for developing the present model of the molecular network regulating parthenocarpy in tomato with stamen-ovule-ovary interaction as a driving feature of this trait.