

ABSTRACT

Fruit set is an important process in the sexual reproduction of flowering plants and also has a high economic impact from the agronomic point of view. Although in recent years, there have been advances in the understanding of this process limited information is still available. Understanding the mechanisms that regulate fruit set is essential for designing strategies to improve production systems of fleshy fruits.

The development of the ovary into a fruit (fruit set) depends on pollination and fertilization, which may be compromised by extreme environmental conditions. However, in some species, the onset of the fruit can be uncoupled from fertilization, generating seedless fruits (parthenocarpic fruits). Therefore, parthenocarpy is a valuable tool to elucidate the genetic and molecular bases that control of fruit set process. In recent years, the tomato has become a model plant for studies of fruit set and development of fleshy fruits. Therefore, we decided to use different parthenocarpic tomato genotypes to identify novel genes involved in early development of the ovary and fruit set in tomato.

In the first chapter of these work, we show the characterization of the *hydra* mutation in tomato. This mutant is completely sterile since lacks gametophytes development. However, the ovary starts growing in the absence of pollination and fertilization, generating parthenocarpic fruits. The study of the molecular basis of the mutant phenotype revealed that there is an alteration in the polar auxin transport in pre-anthesis stage during flower development. This alteration is associated with activation of signaling by auxin in the stamens and auxin delocalization into the ovary. The loss of auxin gradients during flower development, possibly is the cause of no gametophytes development and independent growing of the ovary in *hydra* mutants.

In our laboratory a series of male sterile tomato lines producing parthenocarpic fruits have been generated. Through the study of the transcriptome of these plants we have identified a group of genes induced during the autonomous development of the ovary. In the second chapter of this thesis, we present the molecular characterization of one of these genes (*SIDOF10*) and the study of its role in fruit set. This gene encodes a transcription factor that belongs to plant specific protein family DOF (DNA-binding With One Finger). The analysis of gene expression by different techniques, indicated that *SIDOF10* gene is expressed in the vascular tissue throughout the development of the plant. Particularly in the reproductive stage, the transcript of *SIDOF10* is localized in the vascular tissue of the ovary, reaching the ovule funiculus. In order to carry out the functional characterization of *SIDOF10* gene, we have generated stable transgenic lines of silencing and overexpression. The number of cells in the vascular tissue of the pedicel decreases in silenced plants, while in overexpressed plants the number of cells increases. Moreover, in plants where transcript levels were reduced, there is a decrease in both, the number of seeds and fruit size, and an increase in the development of parthenocarpic fruits is observed. Our results indicate that *SIDOF10* gene is involved in the development of plant vascular tissue by controlling cell proliferation and it is necessary during ovary development for the correct formation of fruit and seeds.