

NITROGEN DYNAMICS AND BUD DORMANCY: A TRANSCRIPTOMIC STUDY IN PEACH

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Climate change is a growing threat to all life on earth and especially the florae that are used to seasonal weather patterns. Over recent years agriculture dependent upon these trees have been challenging due to not meeting the required climatic conditions necessary to produce a good yield. Proper tree-growth does not only determine fruit yield, but it also affects the uptake of nutrients and hence the efficiency of fertilization measures. Carbon and nitrogen are the two basic nutrients that are monitored in this regard. Nitrogen regulation is an integral part of transporting nitrogen in the form of nitrates, nitrites and amino acids as well as different nutrients along with this across the plant network. In fruit trees, the movement and localization of nitrogen before, during and after bud dormancy is considered fundamental for the proper growth of flowers and subsequently fruit development. Therefore, it is important to study nitrogen dynamics during bud dormancy to understand nitrogen utilization efficiency and its role in the growth cycle of the tree. Peach, due to its economic significance, and abundance in the temperate region is an ideal candidate for research on temperate trees and has several studies on bud dormancy and related phenomena. In this study we are making use of our repository of RNAseq data on peach floral and vegetative buds during dormancy, to draw some meaningful conclusions. To this end existing differential gene expression data from peach flower buds has enabled us to identify some interesting targets involved in nitrogen transport and regulation that are significantly expressed in the flower buds. There is a considerable number of studies being done on dormancy as a whole in different varieties of peach and other *Rosaceae* plants which would aid in co-relating the role of nitrogen in this process. The two main pathways for the movement of nitrogen before and after dormancy are the initial absorption of nitrogen from leaves into the bark before the onset of dormancy and subsequent reallocation of the stored nitrogen to the growing parts of the tree. Nitrate transporters belonging to the NTR family as well as a PII nitrogen regulatory gene were some of the genes identified, which follow a hypothetical mode of activity observed in poplar, and would help in detecting the movement of nitrogen from different parts of the tree. Preliminary evidence indicates co-relation between the regulation of Trehalose phosphate genes, involved in the carbon metabolism, and the regulation of nitrogen. This is significant with respect to flowering and the development of fruit post-dormancy as well as the accumulation of carbon and nitrogen in the fruit. As an end goal, we aim to identify genetic markers that would help detect the levels of nitrogen accumulation in flower buds and their resultant effects on flowering and fruit development further down the line.