Invertases as Genetic Determinants of Sink Strength

P.N. Bocock[1], L.F. Huang[1], K.E. Koch[2,3], J.M. Davis[2,4]

[1]Graduate Student, Plant Molecular and Cellular Biology Program; [2]Professor, Plant Molecular and Cellular Biology Program; [3]Professor, Department of Horticultural Sciences; [4]Professor, School of Forest Resources and Conservation;
University of Florida, Gainesville, FL, USA

Current population growth combined with increasing development and urbanization worldwide is putting strain on the terrestrial ecosystem's main carbon sink, forests. One way to combat this increasing demand of decreasing forest resources is to manipulate the carbon allocation patterns in trees to direct carbon into the most desirable organs such as stems to meet industrial demands, or roots to help increase the long term carbon storage capacity in the soil. Plants utilize carbon by partitioning the reduced carbon obtained through photosynthesis into different locations within the cell and subsequently allocating it to sink tissues throughout the plant. We are utilizing *Populus* as a model system in which to study invertase and its role in sink strength determination with the aim of applying this knowledge to tree breeding and genetic modifications. Using the newly sequenced poplar genome, we have identified eight acid invertase family members through amino acid sequence similarity searches. Three of these family members encode invertases targeted to the vacuole, while the other five invertases are targeted to the apoplast. With only two exceptions, poplar invertases share the intron/ exon structure generally conserved in plants of seven exons separated by six introns. *PtIVR1*, a vacuolar invertase apparently lacks introns and constitutes the first putative intronless invertase found to date. *PtIVR4*, another vacuolar invertase is missing the conserved mini-exon NDPN. Although the absence of this exon is unusual, it is not unprecedented in plant invertases.

As invertase is found in three subcellular locations, we are also taking a transgenic approach in order to elucidate the individual roles of these invertases in sink strength determination. Three groups of transgenic plants have been made expressing Suc2, an invertase from yeast, in the apoplast, vacuole, or cytosol. These transgenics are predicted to have altered sink strengths and/ or partitioning phenotypes, and will be used in grafting experiments. These grafts will enable us to mimic the effects of organ specific promoters and thus alter the sink strength of specific organs. We predict these altered sink strengths will lead to altered wood development, storage capacity, and secondary metabolite components.

Though the invertase family has been well characterized in Arabidopsis, it is not possible to determine their respective poplar orthologs based on tissue expression patterns or sequence identity. To address this problem, we are using a microcolinearity approach by identifying invertase gene neighbors on the poplar chromosome with identical gene neighbors on the Arabidopsis chromosome. We are developing a robust statistical procedure for determining the significance of colinearity, which should in turn help us gain insights into the function and evolution of invertase genes.