

# Genes Controlling Lateral Root Formation in Poplar

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## Goals:

1) Use the poplar genome to isolate poplar versions of all genes known to regulate root development in other model species; 2) Identify additional novel candidate genes by screening existing populations of *Populus*, which have had their gene expression altered in various ways, to identify patterns of lateral root formation; 3) Test the effects of over-expressing and silencing all candidate genes in two genotypes of poplar that exhibit contrasting rooting responses; 4) Evaluate the effects of these genetic manipulations on root formation and architecture; and 5) Conduct analyses to identify metabolic alterations that may be associated with our genetic manipulations.

## Statement of Problem:

The overall objective of this project is to utilize the poplar genome sequence to identify and functionally characterize key genes that regulate lateral root proliferation in poplar and, hence, improve carbon sequestration. There are three major ways in which carbon sequestration will benefit from this project. First, because lateral roots account for the bulk of the tree's below-ground biomass, stimulating their proliferation will promote carbon sequestration in the soil. Second, increased lateral root production will likely enhance overall plant growth via more efficient resource acquisition. Third, given that lateral root production is very similar to adventitious rooting, the many genes involved in regulating lateral root formation will also likely control adventitious root initiation. The ability to vegetatively propagate forest trees, through adventitious rooting, will allow growers to fully capture genetic gains that have already been achieved through conventional breeding. Growing elite germplasm will, in turn, lead to more efficient carbon sequestration.

## Current Activities:

Poplar orthologs of genes that have been shown to affect rooting in heterologous species have been used to assemble binary vectors. These constructs are currently being used to transform poplar. An activation tagged population of poplars has also been screened for altered rooting properties. Additional candidate genes identified through this screen are now being isolated and will ultimately be used to assemble a second generation of genetic constructs.