SPATIAL MAPPING OF DEFENSE INDUCIBLE GENE EXPRESSION IN
ARABIDOPSIS THALIANA TO DETERMINE ITS EFFECT ON
PHOTOSYNTHESIS

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Our research seeks to determine the indirect effect of insect herbivory on photosynthesis activity. This project will elucidate the relationship between genes expressing proteins involved in the phenyl propanoid core pathway (PAP), a herbivory-induced defense mechanism in Arabidopsis thaliana, and genes responsible for the synthesis of RUBISCO, an essential protein involved in CO2 fixation during photosynthesis. We hypothesize that up regulation of the defense mechanism would come at a cost of reduced photosynthetic activity, which would be demonstrated by the repression of RUBISCO synthesis in leaf areas where proteins essential for PAP (i.e. phenylalanine ammonia lyase, PAL-1, cinnamate 4-hydroxylase, C4H, and coumaroyl-CoA ligase, 4CL1) is up regulated. Essentially, pair-wise combinations of defensive gene promoter-GFP fusions will be constructed and their expressions will be imaged simultaneously with RbcS1a (RUBISCO) :: red fluorescent protein (RFP) gene fusions to determine whether there is a spatially coincident, reciprocal down regulation of a photosynthetic gene during defensive gene activation. Currently, the PAL-1 promoter region has been successfully amplified, and fused to RFP. Efforts are being made to incorporate this gene fusion into a Ti plasmid for Agrobacterium-mediated transformation into plants. Therefore, data is currently unavailable. Hopefully, this project will serve to further our understanding of the regulation of RUBISCO gene expression.