

# **Discovery and Modification of Photomorphogenic Regulation in Maize**

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IMBA Project 2007-3

## **Project Description**

### **Objectives**

The goal of this project is to utilize functional genomics and bioinformatics tools to develop molecular transcriptional markers of the shade avoidance syndrome in maize. These markers will be utilized both to assist breeding programs and to develop biotechnology product candidates. Manipulation of the shade avoidance response using conventional breeding or transgenic approaches has the potential to increase yields and alter resource partitioning, making it potentially valuable for the development of maize as a bioenergy crop.

Three primary objectives of this project are to: (1) Conduct expression profiling of maize seedlings given EODFR treatments to identify Shade Avoidance Marker Genes [SAMGS]; (2) Identify and characterize candidate SAMGs using genome bioinformatics and comparative genomics with Arabidopsis and rice; and (3) Perform detailed transcriptional, transgenic and genetic analysis of prioritized SAMGs.

### **Procedure**

The researchers will use functional genomics tools (including a microarray available through a collaboration with Syngenta) and existing knowledge of photomorphogenesis in Arabidopsis. Through a multi-tiered approach utilizing transcriptional profiling, database mining and bioinformatics, they will develop a short list of genes to initiate an extensive functional genomics analysis.

### **Impact**

This study will be a comprehensive molecular and genetic analysis of photomorphogenesis in maize and will serve as a platform for the understanding and eventual manipulation of light signaling pathways in the world's most agronomically important cereal crops. More immediately, the study will provide SAMGs biomarkers that will allow breeders and agronomists to evaluate the importance and extent of shade avoidance responses in different environments and genotypes. In the medium term, these biomarkers will provide candidates for commercial biotechnology followup.