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David Goad

Valparaiso University, david.goad@valpo.edu

Ann Carlson

Valparaiso University

Hui Gong

Valparaiso University

Robert Swanson

Valparaiso University

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Defining the Genetic Basis for Seed Yield in *Arabidopsis thaliana*

David Goad, Ann Carlson, Hui Gong, Robert Swanson

Departmental Affiliation: Biology
College of Arts and Sciences

Seed number per fruit is a vitally important trait because it determines total agricultural yield. Despite its importance, the genes that direct seed yield remain relatively unknown. We are using Recombinant Inbred Lines (RILs) in the weedy plant *Arabidopsis thaliana* to explore the heritability of seed yield and genetically map the genes responsible. Up to eight fruits were collected per plant from each RIL. Seeds were scanned using a flatbed scanner and counted using Adobe Photoshop CS6. With this data, we performed an ANOVA to calculate heritability, the amount of variance in the seed yield trait due to genetics. The heritability of seed yield was found to be 23.24 percent. Using the same data set, we are currently performing composite interval mapping to identify the genomic regions that contain the genes that direct seed yield, an analysis we will report on. Locating the genomic regions that contain seed yield is the first vital step in defining the gene network that directs seed number in fruit.

Information about the Authors:

David Goad is a senior biology major who has been working with Dr. Swanson for three years. For two of those years, the team worked to identify the genes responsible for non-random mating in *Arabidopsis*. Last fall, David switched to the current project to try his hand at genetic mapping. Next year, David will be attending Washington University in St. Louis to pursue a Ph.D. in Evolution, Ecology, and Population Biology.

Faculty Sponsor: Dr. Rob Swanson

Student Contact: david.goad@valpo.edu