

The Genetic History of Rice Domestication: Isolation, Divergence and Gene Flow in *O. Sativa*

Dr. Susan McCouch^{1*}

mccouch@cornell.edu

Drs. Chih-Wei Tung¹, Mark Wright¹, Keyan Zhao², Adam Famoso¹, Michael Kovach¹, Megan Sweeney¹, Anna McClung³, and Georgia Eizenga³

1. *Plant Breeding and Genetics Dept., Cornell University, Ithaca, NY 14853-1901*

2. *Biological Statistics & Computational Biology Dept, Cornell University, Ithaca, NY 14853-1901*

3. *Dale Bumpers National Rice Research Center, Stuttgart, AR 72160*

Knowledge about the structure and evolutionary history of naturally occurring variation in crops and their wild relatives provides insights into the complex process of domestication and new opportunities for utilizing novel alleles in crop improvement. Domesticated Asian rice (*Oryza sativa* L.) is comprised of five, well-differentiated subpopulations that evolved from a common, out-crossing wild ancestor, *O. rufipogon*, that is distributed throughout tropical Asia. We seek to understand the evolutionary forces that acted on this ancestor to generate the phenotypic diversity and subpopulation structure of modern *O. sativa*. Using re-sequencing data and recently isolated domestication genes, we trace the evolutionary history of alleles that both define and transcend the deep population subdivisions of domesticated rice. Documented patterns of allele-sharing and dispersal suggest a complex pattern of gene flow, selection and genetic exchange in rice, coupled with an underlying tendency toward genetic isolation reinforced by inbreeding. We seek to integrate archaeological, climatological, linguistic and historical data with genetic models to explore the dynamics of these opposing processes and to provide a framework for interpreting the complex history of rice domestication in Asia.