

Dr. Doreen Ware, ARS-CSHL, Cold Spring Harbor

March 13, 2013

Dear Doreen,

We are preparing a proposal entitled "Functional resources in wild *Oryza* species for rice improvement". Our goal is to develop tools for functional genomics in wild *Oryza* species with the intent to facilitate the identification of useful genes from wild germplasm and their utilization in cultivated rice. We are building upon resources developed by the rice breeding and genomic community and by the OryzaMAP project.

1. Develop and implement protocols for optimal mutagenesis of *Oryza* species. We will evaluate methods validated on *O. sativa* on the OryzaMAP set of sequenced wild species emphasizing allotetraploids, and employ best practice for production of selected population resources that will be made available without intellectual property restrictions.

2. Implement tools for global mutation discovery and facile introgression. We will use the OryzaMAP genomic resources to develop high efficiency exome capture reagents and demonstrate their use in multiplexed capture and analysis, both for wild germplasm in the AA clade and in selected wild species. In the most promising of these species, we will construct long term in silico data base for exploiting the reference populations as a reverse genetics resource.

3. Identify useful induced variation in wild *Oryza* germplasm. We will employ forward and reverse searches to identify variants in genes determining useful phenotypes for rice improvement, such as improved agronomic performance, quality, and facility of introgression.

We have recruited an excellent group of collaborators (see Table 1 below). We are hoping that you will also be able to collaborate with us specifically in the following area: We would like your help in integrating the data generated in this project into Gramene. Specifically, we would provide SNPs and CNV with connected information (species, genomic coordinates, expected effect) in the format most suitable to your program. The proposal is due at on March 20 (we have obtained a one week delay) to the Plant Genome Research Program at the National Science Foundation. We include a template letter required by the program, which you can sign and return if you agree.

We thank you for considering our request.

Best regards,

Luca Comai



Georgia Eizenga

ARS DB National Rice Research Institute and University of Arkansas

Thomas Tai

ARS Davis and UC Davis

Table 1: List of collaborators and contributions

Collaborator	Institution	Role
Chhandak Basu	CA. State U Northridge	Contribute to program outreach via collaboration and interaction with UC Davis
Gregory Berger	U. of AR	Provide expertise in characterization of hybrid rice and assist with supervision of U of AR employees
Jorge Dubcovsky	GBM-HHMI, UC Davis	Advise on technical aspects of exome TILLING in allotetraploid grass species
Kashirod Jena	IRRI, Philippines	Advise wild species growth, genomics and introgression; rice breeding
Nori Kurata*	Natl. Inst. Genetics, Japan	Advise on incompatibility barriers, wild species genomics, gene targets, introgression, liaison with Japanese rice community
Anna McClung	DB-Natl. Rice Research Center, Stuttgart, AR	Facilitate distribution of genetic resources via GSOR; advise on rice breeding
Susan McCouch	Cornell Univ.	Advise on wild species, breeding, genomics, and introgression; provide seeds from wild species and introgression/mapping lines
Muthusamy Monoharan	UAPB (U of AR at Pine Bluff)	Contribute to program outreach via collaboration and interaction with GE at ARS and with UC Davis
Doreen Ware*	ARS, CSHL	Integrate genomic data (SNP, CNV) in Gramene database
Rod Wing	U of Arizona	Provide OMAP accession seeds, advise on growth and phenotype of wild species, provide advice and information on Oryza genomics

* Contact in progress