PROJECT SUMMARY
Scott A. Jackson, P.I., Purdue University; Phillip SanMiguel, Co-P.I., Purdue University

The large, complex genomes of many cereal crops such as corn, oat, wheat and sugarcane have been an impediment to genetic mapping and molecular studies. Due to its small genome size, rice has emerged as a model for genetic research in the cereals. Comparative genetic studies using rice as a model from which genetic and DNA sequence data can be used to study other cereal crops are emerging as important tools for all cereal geneticists. The functional characterization of the rice genome is a crucial first step to understanding the genomic organization and evolution of the more complex cereal genomes.

The proposed research will address these needs by building sequence-ready comparative physical maps in the tribe Oryzeae in order to functionally characterize rice genomic sequence. DNA sequence from rice chromosome 1, which is the largest rice chromosome and contains ~7,000 predicted genes, will be used to assemble physical maps in six members of the Oryzeae, including rice, as well as Sorghum, a more distantly-related and more complex cereal species. The specific objectives are to (1) construct bacterial artificial chromosome (BAC) libraries for four Oryzeae species; (2) design short oligonucleotide probes for 4,000 rice chromosome 1 genes based on sequence data; (3) use the oligonucleotide probes to isolate BACs that contain gene homologues from the related species; (4) fingerprint and assemble the BACs into contigs for a sequence-ready physical map; (4) use fluorescence in situ hybridization (FISH) to evaluate gross chromosomal changes among these species; and (5) integrate all of this data into an overall picture of micro- and macro-chromosomal changes within the tribe Oryzeae. Because nearly 4,000 rice genes will be used in the construction of the high-density physical maps of the Oryzeae species and Sorghum, it will be possible to determine gene order and spacing, transpositions, and larger chromosomal rearrangements among these related species resulting in a clearer picture of the evolution of rice chromosome 1 within the Oryzeae and in the more complex genome of Sorghum. Furthermore, the evolutionary fate of gene and chromosomal duplications in polyploid Oryzeae species will be determined.

The end result of this research will be the development of an invaluable resource for rice geneticists to use for functional annotation of the rice genome, for applied and evolutionary geneticists to use to for the investigation of allelic diversity, and for cereal geneticists to use to translate rice genome sequence into a tool for the improvement of corn, wheat, oat and other cereal crops.