Report of Progress (AD-421)

Project Number: 6202-21000-027-00D **Accession:** 0412234 **FY:** 2009

ModeCode: 6202-40-20 SOUTHERN PLAINS AREA
COLLEGE STATION, TEXAS
SOUTHERN PLAINS AGRICULTURAL RESEARCH CENTER
CROP GERMPLASM RESEARCH

NPL Leader: MARY W SIMMONS **Prin Invs:** ROBERT R KLEIN

Start Date: 03/01/2008 **Term Date:** 02/28/2013

National Programs: 301 N Plant Genetic Resources, Genomics and Genetic Improvement

Title: GENETIC ANALYSES AND TRAIT MAPPING TO EXPLOIT UNTAPPED GENETIC DIVERSITY IN SORGHUM

Period Covered From: 10 / 2008 **To:** 9 / 2009 **Final Report?** No
Terminate in Two Months? No

Progress and Outcomes:

1a. Objectives (from AD-416)

~~Objective 1: Refine the sorghum genome map to accelerate map-based gene discovery and comparative analyses of genes and gene networks in the Poaceae family. Completion of a genome map of sorghum will permit direct cross-referencing of the genomes of sorghum, rice, and maize, thereby permitting a unified Poaceae genome map to be assembled. This map and associated technology platforms will enhance gene discovery and expedite germplasm development via marker-assisted selection of key agronomic traits.~~
~~Objective 2: Utilize the sorghum genome map and genetic resources to clone key genes, including those controlling pollen fertility and drought tolerance. As the products of Objective 1 are developed and released, positional cloning of genes will be simplified when complemented with high-quality linkage analyses.~~
~~Sub-objective 2.A: Elucidate the genetic basis of drought tolerance by positional cloning of a major stay-green QTL in sorghum. Utilizing genetic stocks that are isogenic for a given stay-green QTL, high resolution maps have been constructed and continued refinement of each QTL will be achieved. The further refinement of the QTL, coupled with detailed genetic, physiological, and molecular analyses of gene candidates will ultimately permit the gene(s) conditioning the stay-green phenotype to be cloned.~~
~~Sub-objective 2.B: Elucidate the genetic basis of pollen fertility restoration in sorghum by positional cloning of the Rf2 fertility gene. Armed with fine mapping populations, genomic technology platforms for sorghum, and having cloned the first major sorghum fertility gene, positional cloning of Rf2 fertility restoration gene is achievable.~~
~~Objective 3: Map genome regions controlling photoperiodism and plant height in sorghum and identify robust molecular markers linked to these traits. Completion of the genome map flanking these trait loci will expedite high-resolution mapping by revealing sequences representing potential markers for additional fine mapping, while also revealing candidate genes conditioning photoperiodic-insensitivity and reduced plant height.~~
Objective 4: Conduct proof-of-concept study, utilizing molecular markers, to expedite the conversion of tropical sorghum to temperate adaptation. We will utilize the genome map and molecular markers discovered under Objective 3 to evaluate the introgression of recessive alleles conditioning photoperiod insensitivity, plus reduced plant height, into tropical germplasm. This molecular evaluation will supplant the additional selfing generations and associated phenotypic evaluation normally required to track the introgression of recessive

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alleles into exotic germplasm during their conversion to photoperiod-insensitive, short-stature cultivars suitable for production in the U.S.

1b. Approach (from AD-416)

The long-term goal of this project is to develop and utilize appropriate approaches and techniques in genomics and biotechnology to discover genes that control key agronomic traits, and to utilize these to augment breeding strategies that will facilitate the development of improved sorghum cultivars. At present, positional cloning in sorghum is a daunting task, but the further refinement of a sequenced-based sorghum genome map will greatly simplify gene discovery. We have targeted several agronomically critical genes for positional cloning, including the stay-green gene(s) conditioning sorghum's exceptional tolerance to post-anthesis drought. In ongoing collaboration with scientists at Texas A&M University and the Department of Primary Industries and Fisheries, Queensland, Australia, an integrated approach that includes the plant disciplines of physiology, breeding, molecular genetics, and genomics is being employed to clone stay-green genes. This information, and markers linked to these genes, will be exploited to introgress post-anthesis drought tolerance into elite sorghum cultivars. Additionally, the molecular tools developed under Objective 1 and Sub-objective 2.A will facilitate our ongoing efforts to clone pollen fertility restoration genes. Work with our Queensland collaborator will target cloning of Rf2 because of its importance in hybrid seed production, and the need for informative markers tightly linked to Rf2 for germplasm evaluation. We also seek to map, at high resolution, the height and photoperiod-insensitive genes required to convert tropical sorghums to photoperiod-insensitive, short-stature cultivars suitable for production in the U.S. Objectives 1-3 are complementary, and the knowledge gained under one objective will facilitate success in all. Continued map resolution of photoperiodic and height trait loci obtained under Objective 3 will provide the foundation for identification of additional robust molecular markers and potential candidate genes, which will positively impact achievement of Objective 4.

2. Milestones for FY2009

1. Align sequence across trait loci targeted for gene cloning.
   Milestone Fully Met

2. Refine ma1, dw2 trait loci.
   Milestone Fully Met

3. Produce F1 hybrids.
   Milestone Fully Met

3. Progress Report

During FY 2009, genome sorghum sequences were integrated into the refined sorghum genome map that spanned trait loci targeted for gene cloning. Work was continued on fine mapping genes that condition pollen fertility restoration, photoperiodism, and plant height; significant progress was made during the reporting period. Work was initiated to produce first-generation hybrids by crossing photoperiod-sensitive sorghum germplasm and elite sorghum inbreds; this is the first step towards converting tropical sorghum accessions to temperate-adapted inbreds. The information obtained and methodologies developed by this work will be critical for the successful exploitation of a wealth of previously unusable tropical sorghum germplasm in development of higher-producing sorghum hybrids for U.S. farmers.

NP / Component Coding

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301 2 B 2006
301 2 C 2006

4. Accomplishments

01 Conversion of Photoperiod-Sensitive Sorghum to Temperate Zone-Adapted Germplasm: Sorghum is an important grain crop in many areas of the world including the U.S., and efforts are needed to utilize molecular tools to genetically improve the crop. Much potentially valuable sorghum germplasm is of tropical origin and, because these accessions evolved under conditions where day-length is relatively constant, they do not successfully flower and produce seed in temperate environments (including U.S. growing areas) where day-length in much longer during the growing season. Tropical accessions with value-added traits were identified for conversion to temperate adaptation, in cooperation with scientists at MMR Genetics, LLC, and the process of converting these valuable tropical accessions to photoperiod insensitivity was initiated. Valuable tools known as molecular markers were developed to permit marker-assisted selection of photoperiod-response genes and to monitor the progress of genome conversion at each stage of the breeding process. This accomplishment is important because it provides the foundational molecular and breeding methodology for rapid exploitation of the wealth of previously unusable sorghum germplasm in development of higher-producing sorghum varieties for U.S. farmers.

301 2 B 2006

5. Significant Activities that Support Special Target Populations

7. International Cooperation / Collaboration

01 AUSTRALIA 58-6202-7-038FN

Collaborative work is ongoing with scientists at the Department of Primary Industries and Fisheries, Queensland, which focuses on fine mapping and cloning of genes controlling pollen fertility restoration (rf2, rf5). Work during FY 2009 resulted in one refereed journal scientific paper accepted for publication. The discoveries made by this collaborative team will facilitate ongoing efforts focused on exploiting newly developed molecular technologies in developing improved sorghum varieties.

Scientific Publications: **Log 115:**

1. Ramasamy, P., Menz, M.A., Metha, P.J., Katile, S., Gutierrez, R.L., Klein, R.R., Klein, P.E., Prom, L.K., Schlueter, J.A., Rooney, W.L., Magill, C.W. 2009. Molecular mapping of cgl, a gene for resistance to anthracnose (Collectotrichum sublineolum) in sorghum. Euphytica. 165:597-606. **0000240071**

2. Mace, E.S., Rami, J., Bouchet, S., Klein, P.E., Klein, R.R., Kilian, A., Wenzl, P., Zia, L., Halloran, K., Jordan, D. 2009. A consensus genetic map of sorghum that integrates multiple component maps and high-throughput diversity array technology (DArT) markers. BMC Plant Biology. 9:13. **0000242052**

Approved: COPPEDGE JAMES R **Date:** 09/30/2009