



# Integrating Genetics & Molecular Biology for Soybean Researchers

George Graef, Katy Rainey, David Grant & Rich Wilson



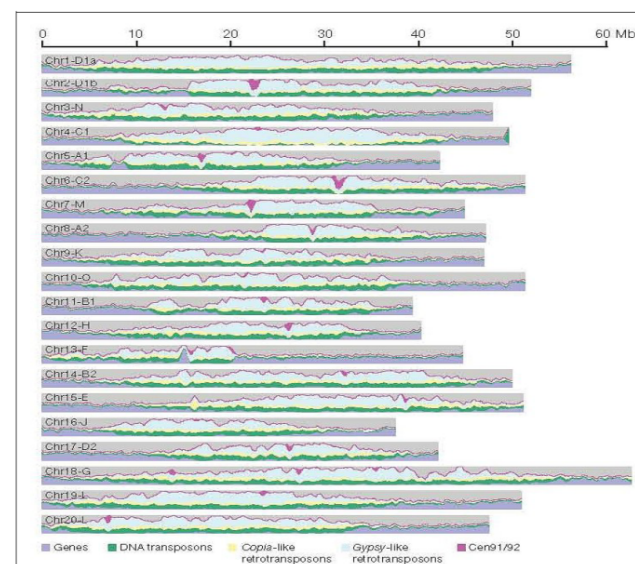
# Research Accountability

## Soybean Genomics Research Accomplishment Report

### National Soybean Genomics Research Initiative Accomplishments

Meeting Strategic Milestones for  
2008 to 2012 in a Timely Manner

v 1.0 March 2010



**Figure 1 | Genomic landscape of the 20 assembled soybean chromosomes.**

Schmutz, J., et al. 2010. Genome sequence of the palaeopolyploid soybean. *Nature* 463:178-183.

<http://soybase.org/resources/soygec.php>

## Soybean Genomics Research Program Strategic Plan Implementing Research to Meet 2012–2016 Strategic Milestones

Edited by Roger Boerma (University of Georgia, Athens GA),  
Richard Wilson (Oilseeds & Bioscience Consulting, Raleigh NC),  
and Ed Ready (United Soybean Board, St. Louis MO)

### Executive Summary

This strategic plan builds on the soybean communities' previous efforts (October, 1999; July, 2001; May, 2003; July, 2005; and May, 2007) to review progress on the development and deployment of soybean genomic resources. The results are impressive [see *Soybean Genomics Research Program Accomplishments Report, 2010*, available at <http://soybase.org/SoyGenStrat2007/SoyGenStratPlan2008-2012-Accomplishments%20v1.6.pdf> (verified 17 Mar. 2011)]. For example, in the last 5 yr the soybean research community has produced a genetic linkage map with over 5,500 mapped markers spanning the entire 2,296 cM soybean genome. A set of 1,536 SNP markers that are evenly distributed across the 20 linkage groups was developed for whole genome analysis of polymorphisms in both elite North American cultivars and breeding lines. In addition, an expanded array of 50,000 SNPs is under development which will be used to create haplotype maps of over 18,000 accessions of the USDA soybean germplasm collection. This research is scheduled for completion in late 2010 and the SNP haplotype map of each accession will be placed on the HapMap Browser on SoyBase. Large-scale shotgun sequencing of the soybean cultivar Williams 82 was completed late in 2008 by the U.S. Department of Energy Joint Genome Institute (DOE|JGI) and recently reported in the scientific journal *Nature* (Schmutz et al., 2010). The present soybean assembly (Glyma.1.01) captured approximately 975 Mbp of its 1,100 Mbp genome. The gene set integrates ~1.6 million ESTs with homology and predicts 66,153 protein-coding loci available at <http://www.phytozome.net/soybean> (verified 17 Mar. 2011).

Published in *The Plant Genome* 4:1–11. Published 17 Mar. 2011.  
doi: 10.3835/plantgenome2011.12.0001  
© Crop Science Society of America  
5585 Guilford Rd., Madison, WI 53711 USA  
An open-access publication

All rights reserved. No part of this periodical may be reproduced or transmitted in any form or by any means, electronic or mechanical, including photocopying, recording, or any information storage and retrieval system, without permission in writing from the publisher. Permission for printing and for reprinting the material contained herein has been obtained by the publisher.

Soybean researchers have developed several microarray technologies for gene expression studies. The GeneChip Soybean Genome Array is commercially available for studying gene expression ([http://www.affymetrix.com/products\\_services/arrays/specific/soybean.affx#1\\_1](http://www.affymetrix.com/products_services/arrays/specific/soybean.affx#1_1) [verified 17 Mar. 2011]). This GeneChip contains 37,500 *Glycine max* transcripts, 15,800 *Phytophthora sojae* transcripts, and 7,500 *Heterodera glycines* transcripts. The achievement of milestones in previous strategic plans for soybean genomic research have advanced soybean to its current status as a crop model for translational genomics. Simply stated, soybean genomic resources in hand will accelerate the ability of plant breeders to enhance soybean productivity, pest resistance, and nutritional quality. However, many secrets of the soybean genome have yet to be revealed. To continue to make informed decisions it was critical to capture the consensus wisdom of leading soybean researchers on the next logical steps in the development and utilization of soybean's genomic resources. On 27–28 July 2010 Roger Boerma chaired a workshop sponsored by the United Soybean Board in St. Louis MO that brought together 44 eminent soybean researchers in the areas of genomic sequencing, gene function, transformation/transgenics, and translational genomics. The purpose of the Workshop was to develop a strategy for achieving the critical soybean genomic resources and information required to accelerate the rate of yield gain and addition of value to U.S. soybean cultivars. A consensus was reached on a number of high priority performance measures or research objectives. In addition the anticipated outcomes of successfully achieving these performance measures are included in the final plan.

Overall, two issues emerged as being critically important or overarching issues: (i) Provide additional support staff for continued development and population of SoyBase, and (ii) Development of a genetic repository/distribution center for soybean mutants/transgenic lines. The enhancement of SoyBase was deemed important for all four Strategic Goals. The genetic repository/distribution center was broadly supported by Workshop participants. Listed below is an outline of the four Strategic Goals and their respective Performance Measures. Within each Goal, the Performance Measures are listed in order of importance.

# Soybean Genomics Research Strategic Plan 2012–2016

[http://soybase.org/  
resources/soygec.php](http://soybase.org/resources/soygec.php)

# Strategic Goals for Soybean Genomics Research 2012-2016

- Genome sequence
- Gene function
- Transformation / Transgenics
- Translational genomics

# Strategic Plan Progress

- Develop mechanism for submission
- Simplify compilation of the annual accomplishment update
- Responsibility of Soy GEC ?

# Most Effective Content

- **What was done?**
- **When, Who, Where was it done?**
- **What were the most significant results?**
- **Citations for all relevant publications**

**We appreciate your efforts to be:**

**Clear, Concise, Correct & Complete as possible**

# Example

**Authors & Affiliation:** Su Jeoung Suh, Brian C. Bowman, Namhee Jeong, Kiwoung Yang, Christin Kastl, Sue A. Tolin, M.A. Saghai Maroof and Soon-Chun Jeong

**Title:** The *Rsv3* Locus Conferring Resistance to Soybean Mosaic Virus is Associated with a Cluster of Coiled-Coil Nucleotide-Binding Leu-Rich Repeat Genes doi:10.3835/plantgenome2010.11.0024

**Citation:** The Plant Genome 2011 4:55-64

**Abstract:** The *Soybean mosaic virus* (SMV) resistance locus, *Rsv3*, previously mapped between markers A519F/R and M3Satt in the soybean molecular linkage group B2 (chromosome 14), has been characterized by examination of the soybean genome sequence. The 154 kbp interval encompassing *Rsv3* contains a family of closely related coiled-coil nucleotide-binding leucine-rich repeat (CC-NB-LRR) genes. Tightly linked to this region are additional CC-NB-LRR genes and several leucine-rich repeat receptor-like kinase (LRR-RLK) genes, thereby indicating that members of both multigene families constitute a heterogeneous cluster at the *Rsv3* chromosomal region. To further confirm the sequence and genetic map concordance, we developed 16 markers from the genomic sequence including predicted CC-NB-LRR genes and their flanking sequences. Mapping of the resultant markers in three populations showed parallel alignment between the genetic and sequence maps in the *Rsv3*-containing region. Phylogenetic analysis of five CC-NB-LRR genes including a pseudogene showed they were highly similar to each other and formed a subclade within a CC-NB-LRR gene clade with representatives from several plant families including legume species. These results demonstrate that the *Rsv3* locus is associated with this cluster of CC-NB-LRR genes, thereby suggesting that the *Rsv3* gene most likely encodes a member of this gene family. In addition, information from this study should facilitate marker-assisted selection and pyramiding of resistance genes.

# 2102 Accomplishments

- Soy GEC nominations and elections
- Follow-up with soybean research community
  - Email, SoyBase
- Soy GEC meet at Molecular & Cellular Biology of the Soybean meeting in August



# Putting the best case forward...

