









Documenting Soybean Genomics Research

David Grant & Rich Wilson



SOYBEAN GENOMICS RESEARCH

A STRATEGIC PLAN

FOR 2008 – 2012

This Report Documents a 5-Year Strategic Plan for Soybean Genomics Research.
The Plan was Co-Authored by a Representative Group of 45+ Scientists Who
Attended a 30-31 May 2007 Planning Meeting Held in St. Louis, Missouri.
(a list of all meeting participants can be found in the appendix)

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

Soybean Genomics Research

Strategic Plan

2008-2012

Nature 463:178-183 (2010)

Genome sequence of the palaeopolyploid soybean

Jeremy Schmutz^{1,2}, Steven B. Cannon³, Jessica Schlueter^{4,5}, Jianxin Ma⁵, Therese Mitros⁶, William Nelson⁷, David L. Hyten⁸, Qijian Song^{8,9}, Jay J. Thelen¹⁰, Jianlin Cheng¹¹, Dong Xu¹¹, Uffe Hellsten², Gregory D. May¹², Yeisoo Yu¹³, Tetsuya Sakurai¹⁴, Taishi Umezawa¹⁴, Madan K. Bhattacharyya¹⁵, Devinder Sandhu¹⁶, Babu Valliyodan¹⁷, Erika Lindquist², Myron Peto³, David Grant³, Shengqiang Shu², David Goodstein², Kerrie Barry², Montona Futrell-Griggs⁵, Brian Abernathy⁵, Jianchang Du⁵, Zhixi Tian⁵, Liucun Zhu⁵, Navdeep Gill⁵, Trupti Joshi¹¹, Marc Libault¹⁷, Anand Sethuraman¹, Xue-Cheng Zhang¹⁷, Kazuo Shinozaki¹⁴, Henry T. Nguyen¹⁷, Rod A. Wing¹³, Perry Cregan⁸, James Specht¹⁸, Jane Grimwood^{1,2}, Dan Rokhsar², Gary Stacey^{10,17}, Randy C. Shoemaker³ & Scott A. Jackson⁵

Soybean (*Glycine max*) is one of the most important crop plants for seed protein and oil content, and for its capacity to fix atmospheric nitrogen through symbioses with soil-borne microorganisms. We sequenced the 1.1-gigabase genome by a whole-genome shotgun approach and integrated it with physical and high-density genetic maps to create a chromosome-scale draft sequence assembly. We predict 46,430 protein-coding genes, 70% more than *Arabidopsis* and similar to the poplar genome which, like soybean, is an ancient polyploid (palaeopolyploid). About 78% of the predicted genes occur in chromosome ends, which comprise less than one-half of the genome but account for nearly all of the genetic recombination. Genome duplications occurred at approximately 59 and 13 million years ago, resulting in a highly duplicated genome with nearly 75% of the genes present in multiple copies. The two duplication events were followed by gene diversification and loss, and numerous chromosome rearrangements. An accurate soybean genome sequence will facilitate the identification of the genetic basis of many soybean traits, and accelerate the creation of improved soybean varieties.

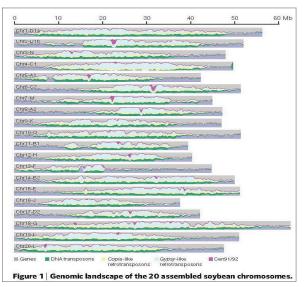
Research Accountability

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



Schmutz, J., et.al. 2010. Genome sequence of the palaeopolyploid soybean. Nature 463:178-183. http://www.soybase.org/survey/new/index.php

On-line Survey Outline Format

Research Area:

1. Glycine max Genome Structure & Analysis

Research Activity:

1.1 Annotation (A1a, A2b)
Milestones: A collage of expected products
from A1a & A2b in the Strategic Plan

Open Box: Insert relevant accomplishments

For Each Accomplishment, Report:

- · 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

National Soybean Genomics Research Initiative

Strategic Priorities & Milestones for 2013 to 2018

v 1.0



Soybean Genomics Research

Strategic
Plan
2013-2018

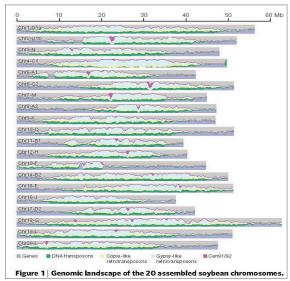
http://soybase.org/resources/soygec.php

Please submit Research Accomplishments On-line by 31 March 2010

National Soybean Genomics Research Initiative Accomplishments

Meeting Strategic Milestones for 2008 to 2012 in a Timely Manner

v 1.0 March 2010



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

Putting the best case forward...

