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Strategic Plan for Soybean Rust Research

United States Department of Agriculture

Research, EE

Agricultural Research Service

National Program Staff

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National Strategic Plan for the Integration and Coordination of Soybean Rust Research

Asian Soybean Rust
Phakopsora pachyrhizi

CUTIVE SUMMARY

rchers with expert knowledge of the critical fields of
shop hosted by the United Soybean Board Production
sts reviewed the current status of soybean genomic
llowing strategic plan framework for outlining research
tones that represent 'quantum leaps' in the advancement

goals and five research objectives—provides both a
that the soybean genomics community attains planned
. The strategic goals span the programmatic range of the
ectives address initiatives that seek to improve core

	Research Objectives
nomics research	Develop useful gene markers for soybean
ulation in genomes	Develop useful transformation methods for functional genomic research in soybean
ture of the soybean	Identify and determine the position of genes in the soybean genome
ulation	Determine the biological basis for gene function, and mechanisms of gene expression
5. Provide bioinformatics management of genomic databases and related natural resources	Establish state-of-art interactive databases and curation mechanisms for genomic data

To achieve these strategic goals and scientific objectives, this plan emphasizes achievements that hinge on teamwork throughout the soybean genomics community. For that reason, all actions and results will be attained in a manner that is both inclusive and open to public scrutiny. As part of this plan, the ability of the research community to carry out and advance soybean genomics in the U.S. public and private sectors will be evaluated in reference to the following performance measures and expected research accomplishments in soybean genomics over the next four years.

n for Soybean Genomics 2003-2007

e 2003	Target in 2005	Target in 2007
NP markers	Position 1500 SNP markers (2500 total) on genetic maps	Position 2500 new SNP markers (5,000 total) on genetic maps
or applying STS atabases	Locate 500 STSs in G max, Medicago truncatula, Common bean	Locate 1,500 STSs in G max, Medicago truncatula, Common bean
s for inbred ns in G. max	Develop BC populations from G.max x G.soja, and North x South elite cvs	Develop RIL populations from genetically diverse backcrosses.
ion patterns with raits	Explore HAPPY map technology. Genetic trait association analysis	Collect data for 2000 SNP on 100 cvs with high phenotypic diversity
0 transgenic lines	Ability to produce 400 transgenic lines per year per person	Ability to produce 500 transgenic lines per year per person
proaches to tion	Develop short season cultivars for more rapid reproductive cycle	
romoters, terminators	Develop new gene promoters, selectable markers, terminators	Publicly available inducible promoters
s (KY, NE, IA, GA,)	Improve capacity of each Center to meet community needs	
specific single	Continue to develop site-specific single gene insertion technology	
gineer plants with	Successful example of BAC insertions	
ene functionality ns	Evaluate heterologous systems like AC/DS TNT	Reevaluate non-tissue based transformation systems
transformation	Confirm utility of VIGS, RNAi methods for targeted knockouts	
technology, by transformation	Improve efficiency of 'stacked gene' insertions for multiple genes	Reduced to practice the ability to introduce multiple gene pathway
Ts of expressed	Sequence 2000 targeted cDNAs and corresponding genomic sequences	Sequence 10,000 targeted cDNAs and corresponding sequences
Sequencing	Sequence gene rich regions in Williams 82.	Whole genome sequence project underway, with Williams 82.
complete (Forrest) oints.	10X Williams 82 physical map w/ HICF fingerprints of BAC-ends	Compare and integrate Williams82 and Forrest physical maps
g generation and	Evaluation of Forrest and Williams 82 physical maps. 1000 ESTs on BACs	Completed 5000 ESTs on BACs
xpression patterns enes	Adopt and develop standard protocol for oligoDNA micro arrays	Align plant gene expression patterns in response to signals & phenotype
00 expressed d micro arrays	3' sequences of 30,000 expressed genes for oligobased micro arrays	
ssignment to	Proteome map of developing seed (morphological, developmental)	Initiate metabolomics technology
n in transformed	Proof of principle large scale transposon tagging in soybean	Generate 200,000 independent insertions in soybean
to discover gene function	Establish TILLING facility with appropriate mutant populations	Develop TILLING libraries and populations
5.1 Development of bioinformatic systems and tools	Migrated SoyBase to LIS relational database	Improve LIS with customer input and feedback mechanisms	Establish mechanism for manual curation and annotation in LIS
	Convened expert bioinformatics panel for soybean genomic needs	Convene steering committee to coordinate management of LIS	Hold educational workshop for end users

ANUT GENOME INITIATIVE
SEARCH TO MITIGATE PEANUT
ERGY
ot listed in a prioritized order)

ase for DNA- markers, genetic maps, and
genomic regions associated with peanut
TORS: Kelly Chenault, Stillwater OK; Mark Burow,

at encode allergenic proteins will ensure success
peanut. A database of expressed sequence tags
me, will facilitate gene discovery via microarray
eanut genome (ca 2800 Mb) is nearly the size of
kely that the peanut genome will be assembled
wever, EST libraries may provide comprehensive
ontain genes of interest. Selected EST may be
(BAC), created with segments of peanut DNA
genes. 'Data-Mining' these EST and genomic
kers that locate all members of the allergen gene
important traits as well. Analysis of how these
ble the design of more effective breeding
chips to select progeny with desired gene
l enhance the efficiency of developing varieties
ker and phenotypic data in peanut bioinformatic
e Legume Information System, will provide the
structure, chromosomal location. Comparative
the construction of genetic-roadmaps to
the peanut genome that influence peanut allergy,

otocols for higher efficiency in the recovery
Weissinger, Raleigh NC
provement and enabled production of cultivars
d for research to enhance transformation
in functional genomics. Transformation
function, but at present it is unlikely that all U.S.
orking in concert, could analyze more than about
elop greater transformation capacity in order to
regulatory elements) that will be generated from
sting transformation approaches is needed to
ater efficiency and capacity. Advances also could
s for transforming peanut with large DNA
velopment of tagging strategies that could
ltaneously interrupting normal function and by
ences. Therefore, to meet pending demand for this
hat help ensure greater efficiency and

Functional Genomics/Proteomics: Genetic regulation of allergen synthesis, structure, and composition. ***COORDINATORS: Eliot Herman, St. Louis MO, Niels Nielsen, W. Lafayette IN***
The diversity of allergen genes may be determined from ESTs representing all major peanut seed proteins. With clinically relevant serum, IgE-binding proteins may be identified for individual

www.apsnet.org/online/sbr

Why Do We Need a Plan?

Reassure the Public, competitors, Congress & the Executive Branch that an effective process is in place for oversight of research on a National and community-wide scale

Define actions that will be taken to solve the problem & show how progress will be measured

Create an interactive, highly coordinated research/communication network

Gain credibility, enhance position for funding opportunities

Framework for Soybean Rust Plan

	Strategic Goals	Research Objectives
1	Determine the efficacy of fungicides for controlling soybean rust	Develop useful technologies and disease management strategies for soybean rust
2	Improve understanding of pathogen genomics, biology and epidemiology	Identify and characterize genes that mediate virulence among isolates of P. pachyrhizi
3	Improve understanding of host plant functional genomics and interaction with soybean rust	Determine the biological mechanisms in host plants that are impeded by soybean rust
4	Determine the biological basis for genetic regulation of plant resistance to soybean rust	Develop genomic tools to discover and utilize genes that impart resistance to soybean rust
5	Provide decision models and biological tools to monitor soybean rust	Develop diagnostic systems to detect, identify or distinguish isolates of soybean rust

Performance Plan for Soybean Rust

Strategic Goal / Research Objective Topic for Breakout Groups

Disease Management

Pathogen Biology

Host Resistance

Host Biology

Predictive Models

Performance Plan

Performance Measures: A series of Actions that need to be taken to achieve the overarching Objective for each Breakout group

Targets or Milestones: Current status & time-line for delivery of measurable results for each Action

PM	Performance Measure	Baseline-2005	Target in 2007
1.1.0	Establish an Ad Hoc Coordinating Committee	Publish strategic, performance and action plans. Develop governance including election of the full committee, and policy for IP issues. Identify funding opportunities. Establish communication network including annual meetings and progress reports of the research community.	Full committee established.
1.2.0	Develop and maintain a soybean rust information network	Existing SBR information is accessible to producers, extension agents and researchers through a number of separate ARS, NGO and University websites. Internet links are provided to access existing libraries such as the SoyBase, LIS, phytophthora database, APHIS' Integrated Atmospheric Model System, and the Penn State pathogen database. No central web-based decision support system exists for dissemination of relevant information.	Establish and effectively maintain network that integrates model inputs with decision criteria, and establish customer base. Protocols for updating information, adding or removing links, adapting the web site, increasing network of collaborators, obtaining and using funds, defining and overseeing responsibilities, evaluating quality, and other work.
1.3.0	Develop an interactive database to integrate soybean and pathogen genomic resources with transcriptomic, proteomic, and metabolomic information.	The Legume Information System (LIS) is under continuing development and has been selected by the soybean community as the central bioinformatic resource. A variety of other specialized sites deal with various aspects of soybean biology.	LIS will be improved to allow incorporation of, or seamless linkages to, functional genomic information from transcriptomic, proteomic, and metabolomic studies. Coordination and networking will begin to integrate computer databases and programs developed by individual public labs into LIS.
2.1.0	Develop field friendly diagnostic tools for identification of Phakopsora pachyrhizi and selected soybean foliar diseases	Antibodies raised against Phakopsora pachyrhizi and other selected soybean foliar pathogens	Evaluations of hand-held diagnostics as a decision making tool for fungicide decisions, Antibody screening in place for selected soybean foliar diseases
2.2.0	Develop, compare and evaluate sampling protocols and early detection tools for efficacy of application	Test existing rapid diagnostic methodologies and sampling protocols, including rainwater and air sampling and collection systems; use ground truth measurements to evaluate remotely sensed spectral reflectance data; expand outreach and training network	Develop new and refined rain and air sampling and diagnostic methodologies with increased sensitivity and ease of use, including tissue and spore assays; assess accuracy of remote sensing for disease diagnosis; improve training and outreach network
2.3.0	Improve and validate climatic, atmospheric transport, biological/epidemiological, and socio-economic impact components of integrated disease predictive systems	Integrate monitoring and survey data with predictive climatic and atmospheric transport models; test existing components of climatic model for seasonal predictive capability; produce daily risk assessment of transport and deposition in U.S. soybean growing regions and conduct preliminary validation studies; Initiate studies on disease progress in SB fields to develop epidemiological models; link atmospheric	Link and validate climatic and disease forecast systems

10/3/2005

United States Department of Agriculture

Research, Education & Economics

Agricultural Research Service

National Program Staff

October, 2005

National Program Action Plan for Asian Soybean Rust Research

Mitigation of Asian Soybean Rust *Phakopspora pachyrhizi*

Version 1.2 Part A

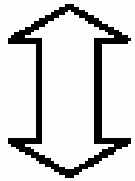
Expanded Role of SBR Action Plan

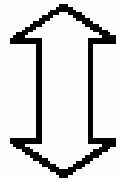
- Connects NP to USDA Strategic Plan
- Defines actions that will be taken to solve problems, rather than only statements of problems, needs and benefits
- Shows how progress will be measured ('Outputs' linked to milestones)
- Identifies who is responsible for work
- Provides information for project review and program assessment

USDA Strategic Plan FY2002-2007

Goal 1: Enhance Economic Opportunities for Agricultural Producers

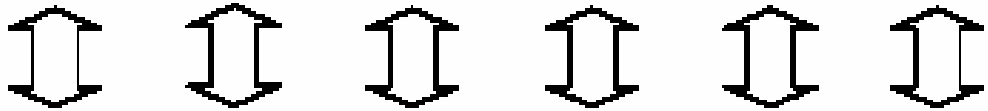
Goal 3: Enhance Protection & Safety of the Nation's Agriculture & Food Supply





ARS Strategic Plan FY2003-2007

PM 1.2.5 PM 1.2.6 PM 1.2.7 PM 3.2.4 PM 3.2.5 PM3.2.6



Strategic Plan for Soybean Rust Research

PM 1.1.0	PM 4.1.5	PM 4.1.1	PM 5.1.0	PM 6.1.0	PM 2.1.0
PM 1.2.0	PM 4.1.6	PM 4.1.2	PM 5.2.0	PM 6.2.0	PM 2.2.0
PM 1.3.0	PM 4.1.7	PM 4.1.3	PM 5.3.0		PM 2.3.0
PM 3.1.0	PM 4.1.8	PM 4.1.4	PM 5.4.0		PM 2.4.0
PM 3.2.0	PM 4.2.5	PM 4.2.1	PM 5.5.0		
PM 3.3.0	PM 4.2.6	PM 4.2.2	PM 5.6.0		
PM 3.4.0		PM 4.2.3			
PM 3.5.0		PM 4.2.4			
PM 3.6.0					

SBR Action Plan: Phase-1

Identify new sources of resistance in Glycine

Characterize and combine genes for SBR resistance

Develop DNA markers for QTL identification & MAS

Develop diagnostic tools for early detection of SBR

Evaluate fungicide efficacy & optimize cultural practices

Develop international screening nurseries for SBR

Develop interactive bioinformatic dbases to integrate host & pathogen genomic resources

SBR Strategic Plan Writing Team

Jim Bloomberg	Bayer Crop Science
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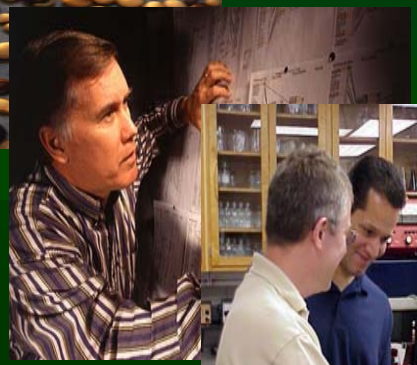
Integrated Research Approach

Exploit untapped plant genetic diversity in USDA Germplasm Collections, & collaborative resources



Plant & Pathogen genomics, gene discovery, gene markers & bioinformatics

Plant & Pathogen proteomics & molecular biology

Disease Management & Predictive Modeling

Genetic Enhancement

Partner with Universities & industry
Coordinate targeted soybean research
Facilitate nation-wide initiatives

Agricultural Research Service
Soybean Rust

Location	FY 2002	FY 2003	FY 2004	FY 2005	FY 2006 Conference Estimate
Urbana, IL	- -	$144,700	$146,000	$146,500	$296,500
Ames, IA	- -	- -	- -	394,100	544,100
Beltsville, MD	$ 80,300	81,700	457,600	863,700	863,700
Frederick, MD	852,400	871,400	871,700	1,257,300	1,257,300
Stoneville, MS	181,000	183,000	374,700	416,800	896,800
Headquarters	- -	- -	- -	803,500	803,500
Total	$1,113,700	$1,280,800	$1,850,000	$3,881,900	$4,661,900