Potential Allocation of Funding Dollars to the Sub- and Main Topics of the

2008 – 2012 STRATEGIC PLAN FOR SOYBEAN GENOMICS RESEARCH

Based on the Results of a Survey of 12 Current and Past Members of the Soybean Genetics Executive Committee (SoyGEC)

"Final Draft"

BACKGROUND

A 5-Year Strategic Plan for Soybean Genomics Research for 2008 – 2012 was developed and co-authored by a representative group of 45+ scientists who attended a 30-31 May 2007 Planning Meeting held in St. Louis, Missouri. This Strategic Plan is available as a downloadable document from the SoyBase Web-site. The Main Topic and Sub-Topic titles used below here were essentially identical to those used in the Strategic Plan Document, though a few were shortened in length for use in the tables and figures presented here.

The then Chair of the SoyGEC (J. E. Specht) was asked by a USB representative to survey representative Soybean Scientists as to potential funding allocations or priorities that might be assigned to the Strategic Plan sub-topics. It was decided that, for sampling purposes, the best method of accomplishing this task was to survey the six current members of the SoyGEC (Gary Stacey, Brian Diers, Scott Jackson, Tommy Carter, David Grant, & Grover Shannon), plus the six past members of SoyGEC (Jim Specht, Randy Nelson, Randy Shoemaker, Jim Orf, Wayne Parrot, & Roger Boerma). Of these 12, six have a molecular (i.e., genomics) disciplinary orientation and six have a whole-plant (i.e., breeder-geneticist) disciplinary orientation. This group is effectively representative of the 45+ scientists who authored the Strategic Plan, and (in rendering SoyGEC service) is also representative of the broader soybean research community.

INTRODUCTION

Each of the 12 SoyGEC members was e-mailed an Excel worksheet to complete (see the sample copy in Table 1). Each person was given a hypothetical *10 million dollars* in grant funding for the 2-year period 2008-09. Each was asked to allocate these funds to the Strategic Plan sub-topics listed in the worksheet using their expertise and vision and to be as objective as possible in devising an funding allocation pattern that would generate the "biggest bang for the funding buck" (i.e., lead to scientific discoveries that could be implemented into genetic technologies that would lead to improvements in soybean productivity). The allocation process was to be repeated for two successive 2-year periods of 2010-11 and 2012-2013, to allow each person to make funding allocation judgments over time relative to the Strategic Plan sub-topics and thus main topics. Technically, these three 2-year periods total to six years (not the 5 years of the Strategic Plan), but asking members to do only three separate allocations was considered more convenient that requesting an allocation for each year for five years. One final note - the 10 million dollar number was purely arbitrary – it had no implied or explicit meaning – it was just a convenient large number to use for allocation purposes in this survey.

COMPILATION OF THE SURVEY DATA

All 12 individuals returned a completed survey form, although one person chose not to make an allocation in the last 2-year period for the reason noted above (5- not 6-year plan) on his submission. The raw and summarized results of the survey, along with some tables and charts of that data were incorporated into an Excel.xls file (which will accompany the present document when it is distributed). The results were first summarized into a worksheet of summed data (Table 2). Examination of the data sums in the light blue cells of Table 2 reveal substantive variance amongst the sub-topic dollar amounts allocations. Such variance presumptively arises from individual and collective perceptions of the 12 members as to funding allocation priorities within each 2-year periods, and their perceptions as to changes in funding allocation priority between the first and second 2-year periods, and between the second and third 2-year periods.

The data in Table 2 were translated into a more readily interpretable form using <u>two</u> <u>different methods</u>. The <u>first method</u> resulted in the conversion of the dollar funding allocation amounts within each column into an <u>allocation percentage</u>, using as a base the total dollar amount per 2-yar period (Table 3). The <u>second method</u> resulted in the conversion of funding allocation amount within each given column into an <u>allocation</u> <u>rank</u>, using a numerical ranking scale of 10-to-1 for a high-to-low rank (Table 4). This conversion was computed (for each 2-year period) by subtracting the lowest allocation amount (i.e., the cell assigned the rank of 1) from the highest allocation amount (i.e., the cell assigned the rank of 10), and then dividing by nine (i.e., the number of intervals between the integer ranks of 1 and 10). This computation generated a dollar amount associated with a one-integer rank change. Then, for any given cell in the column, a decimal rank was computed for that cell's dollar amount by subtracting from it the lowest (rank 1) allocation amount, dividing by the interval dollar amount, and then adding the integer one. For computational details, see the formulas in the Excel file. Table 1. Sample copy of the Excel Worksheet Survey Form. Those surveyed were asked to distribute 10 million funding dollars (in no less than 0.25 million dollar increments) to the Strategic Plan sub-topic research areas (i.e., the light blue-shaded cells). They were also asked to think about the entire Strategic Plan of sub-topics (not just those of their own personal research area), and given the discretion to differentially allocate the dollar amounts based on their thoughts as to how the various sub-topics should be prioritized within any given 2-year period and also across the three 2-year periods, given that some sub-topical research areas may not be effectively started until prerequisite data or technology (either partially or wholly) is first acquired in other sub-topic areas.

	StratPlan	2008-	- 2009	2010	-2011	2012	2-2013
Below are the Main and Sub-Topics in the Soy Strategic Plan	Document	Gross	Specific	Gross	Specific	Gross	Specific
If you don't recall details, see the Strategic Plan - and access this:	PageNo	Dollars	Dollars	Dollars	Dollars	Dollars	Dollars
Main Topic A - Genome Sequence	6	0.00		0.00		0.00)
Sub-Topic A.1 - Genome Informatics	6						
Sub-Topic A.2 - Genome Finishing	7						
Sub-Topic A.3 - Transformation/Transgenics (moved to D)	8						
Sub-Topic A.4 - Genome Resequencing	8						
Sub-Topic A.5 - Phaseoloid Genomics	9						
Sub-Topic A.6 - Breeder Needs as to Soybean Sequence	10						
Main Topic B - Gene Function	11	0.00		0.00		0.00)
Sub-Topic B.1 - Gene Function Annotation/Informatics	12						
Sub-Topic B.2 - Discovery via Mutagenesis	12						
Sub-Topic B.3 - Functional Genomics Approaches	14						
Sub-Topic B.4 - Transformation/Transgenics (moved to D)	16						
Sub-Topic B.5 - Breeder Perspectives on Gene Function	16						
Sub-Topic B.6 - Soybean Producer Expectations - Genomics	16						
Main Topic C - Germplasm Genomics	17	0.00		0.00		0.00)
Sub-Topic C.1 - Association Mapping	17						
Sub-Topic C.2 - Track Breeding-Induced Genomic Change	18						
Sub-Topic C.3 - Mining Yield QTLs in Exotic Germplasm	19						
Sub-Topic C.4 - Marker-Assisted Selection Resources	20						
Sub-Topic C.5 - Germplasm Genomics Informatics	21						
Sub-Topic C.6 - Transformation/Transgenics (moved to D)	22						
Main Topic D - Transformation/Trangenics	22	0.00		0.00		0.00)
Sub-Topic D.1 - Create a Transgenic Event Repository	23						
Sub-Topic D.2 - Create a Virtual Center for Transgenics/Transformation	23						
Sub-Topic D.3 - Establish A Soybean Regulatory Promoter Set	23						
Sub-Topic D.4 - Improve Soybean Transformation Efficiency	23						
TOTAL DOLLARS (must equal 10.00 million dollars):		0.00		0.00		0.00)

Table 2. This Excel worksheet summarizes the <u>dollar data</u> obtained from the 12 worksheets submitted by the surveyed SoyGEC members. The numbers in the light blue cells are the collective <u>sums</u> of sub-topic funding dollar allocation amounts submitted by the 12 respondents. The numbers in the white cells are the corresponding main topic <u>sums</u>. Since there were 12 persons surveyed and 10 Million in funds to allocate, e the bottom line sums to 120 million in each 2-year period, except in the final 2-year period because one SoyGEC member elected not allocate dollars for that column for the reasons indicated in his worksheet.

Summary - 12 SoyGEC Members (Present/Past) - 10 million allocated / yr	StratPlan	20	08-9	20	10-11	20	12-13
Below are the Main and Sub-Topics in the Soy Strategic Plan	Document	Gross	Specific	Gross	Specific	Gross	Specific
If you don't recall details, see the Strategic Plan - and access this:	PageNo	Dollars	Dollars	Dollars	Dollars	Dollars	Dollars
Main Topic A - Genome Sequence	6	47.50		36.25	5	25.50)
Sub-Topic A.1 - Genome Informatics	6		12.25		9.75		7.25
Sub-Topic A.2 - Genome Finishing	7		15.25		7.25		3.25
Sub-Topic A.3 - Transformation/Transgenics (moved to D)	8						
Sub-Topic A.4 - Genome Resequencing	8		9.75		7.75		5.25
Sub-Topic A.5 - Phaseoloid Genomics	9		2.50		3.25		3.50
Sub-Topic A.6 - Breeder Needs as to Soybean Sequence	10		7.75		8.25		6.25
Main Topic B - Gene Function	11	26.00		33.00	D	31.75	5
Sub-Topic B.1 - Gene Function Annotation/Informatics	12		8.50		8.75		7.75
Sub-Topic B.2 - Discovery via Mutagenesis	12		5.25		8.75		7.00
Sub-Topic B.3 - Functional Genomics Approaches	14		8.50		9.75		10.25
Sub-Topic B.4 - Transformation/Transgenics (moved to D)	16						
Sub-Topic B.5 - Breeder Perspectives on Gene Function	16		3.75		5.75		6.75
Sub-Topic B.6 - Soybean Producer Expectations - Genomics	16						
Main Topic C - Germplasm Genomics	17	35.25		36.50	D	38.75	5
Sub-Topic C.1 - Association Mapping	17		7.75		7.75		6.50
Sub-Topic C.2 - Track Breeding-Induced Genomic Change	18		5.50		6.75		6.50
Sub-Topic C.3 - Mining Yield QTLs in Exotic Germplasm	19		9.00		11.00		11.25
Sub-Topic C.4 - Marker-Assisted Selection Resources	20		7.00		5.25		7.75
Sub-Topic C.5 - Germplasm Genomics Informatics	21		6.00		5.75		6.75
Sub-Topic C.6 - Transformation/Transgenics (moved to D)	22						
Main Topic D - Transformation/Trangenics	22	11.25		14.25	5	14.00	
Sub-Topic D.1 - Create a Transgenic Event Repository	23		1.75		4.00		4.50
Sub-Topic D.2 - Create a Virtual Center for Transgenics/Transformation	23		3.00		2.75		3.00
Sub-Topic D.3 - Establish A Soybean Regulatory Promoter Set	23		2.50		3.75		3.50
Sub-Topic D.4 - Improve Soybean Transformation Efficiency	23		4.00		3.75		3.00
TOTAL DOLLARS (must equal 10.00 million dollars):		120.00		120.00)	110.00)

RESULTS – INTERPRETATION – DISCUSSION

Relative to the (upcoming) 1st 2-year funding period (2008-09), an examination of the percentage allocation data in Table 3 (next page) and Fig. 1 (see appendix) reveals that the 12 SovGEC members collectively assigned a substantively high percentage (i.e., double digit numbers) of their allocable funding to the sub-topics of genome finishing (13%) and genome informatics (10%). This is probably not that surprising given that the genome sequence information is going to provide a superb foundation for enhancing many of the other sub-topic genomics research activities that were envisioned in the Strategic Plan. Moreover, gene sequence information will be a critical prerequisite springboard needed to launch the functional gene approaches of proteomics and metabolomics, because with gene sequence, the discoveries made with these functional gene approaches become translatable into gene-based technologies that can be immediately used in breeding. Although the raw soybean sequence data is scheduled to be released in late 2008 by DOE-JGI (see the Strategic Plan), that raw sequence will not be readily useful on a vast scale until (a) it attains a sufficiently finished quality and (b) it is integrated into informatic databases that can be readily accessed in understandable formats by sovbean scientists with a range of disciplines. All of the above reasons likely led the SoyGEC members to allocate 40% of the total 1st period funding amount targeted at the main topic of soybean sequence.

The <u>funding allocation rank data</u> for the 1st 2-year funding period are shown in Table 4 and in Appendix Fig. 2. These data emphasize even more strongly the collective perception of the SoyGEC members that sequence finishing (rank of 10) and genome informatics (rank of 8) are critical prerequisite needs. No other sub-topic in any main topic in the 1st period had a rank in the upper quartile (i.e., a rank of 7.5 to 10.0). In fact, the next highest ranking sub-topic was genome re-sequencing (6.3).

To assess <u>disciplinary differences</u> in the 1st 2-year period, the <u>ranking data</u> attributable to the six SoyGEC members with a molecular orientation (genomicists, transformation/ transgenic specialists, molecular biologists, etc.) was compared to the ranking data attributable to the six members with a whole-plant orientation (breeders, geneticists, plant physiologists, etc.). See Appendix Table A1. The collective perception of the six molecular-oriented members was that genome finishing ranked highest (10), and though they ranked genome informatics substantively lower (6.8) than did the overall 12-member group, they still ranked this sub-topic area much higher than the next ranked sub-topic of association mapping (4.9). The collective perception of the six breeder-oriented members was that while genome finishing (10) deserved a high ranking, so did the sub-topic of mining for yield QTLs in exotic germplasm (10). Interestingly, this group expressed a collective opinion that genome re-sequencing (9.7) and genome informatics (9.3) also deserved high ranks. This group also granted an upper quartile rank to the sub-topic of breeder needs with regard to genome sequence (7.6). However, the Strategic Plan reveals that this latter sub-topic focuses on making the newly emergent multi-plex Illumina OPA assay technology for SNP genotyping more readily available for cultivar development and germplasm enhancement. This also explains their high ranking of genome re-resequencing (i.e., identify more SNPs).

 Table 3. Reformulation of the funding dollar allocation amount in each Strategic Plan sub-topic and main topic into a <u>percentage</u> amount reflecting the distribution of the funding amounts within any given 2-year period.

See the Strategic Plan document for details (this PageNo) PageNo Dollars total Doll	SUMMARY DAT	A in terms of perentage of total allocation	StratPlan		2008-09	%	2010-11	%	2012-13	%
Sub-Topic A.1 Genome Informatics 6 12.25 00 9.75 7.25 Sub-Topic A.2 Genome Finishing 7 15.25 00 9.75 7.25 3.25 Sub-Topic A.4 Genome Resequencing 8 9.75 7.75 6 5.25 Sub-Topic A.5 Phaseoloid Genomics 9 2.50 2 3.25 3.50 Sub-Topic A.6 Breeders & Sequence 10 7.75 6 8.75 7.75 6 2.52 3.50 Sub-Topic B.1 Functional Annotation/Informatics 12 8.50 7 8.75 7 7.75 Sub-Topic B.2 Discovery via Mutagenesis 12 5.25 4 8.75 7 7.00 Sub-Topic B.3 Functional Genomics Approaches 14 8.50 7 7.75 6 6.50 Sub-Topic C.1 Association Mapping 17 7.75 7 6 6.50 Sub-Topic C.3 Breeding-Induced Genomic Change 18 5.50 6.75 <td>List of Sub- and</td> <td colspan="3">tt of Sub- and Main Topics in the Soy Strategic PlanDocume the Strategic Plan document for details (this PageNo):PageNPageNPageNb-Topic A.1Genome Informaticsb-Topic A.2Genome Finishingb-Topic A.4Genome Resequencingb-Topic A.5Phaseoloid Genomicsb-Topic A.6Breeders & Sequenceb-Topic B.1Functional Annotation/Informaticsb-Topic B.3Functional Genomics Approachesb-Topic B.5Breeders & Gene Functionb-Topic C.1Association Mappingb-Topic C.2Breeding-Induced Genomic Changeb-Topic C.3Mining Yield QTLs - Exotic Germplasm</td> <td>Specific</td> <td>of</td> <td>Specific</td> <td>of</td> <td>Specific</td> <td>of</td>	List of Sub- and	tt of Sub- and Main Topics in the Soy Strategic PlanDocume the Strategic Plan document for details (this PageNo):PageNPageNPageNb-Topic A.1Genome Informaticsb-Topic A.2Genome Finishingb-Topic A.4Genome Resequencingb-Topic A.5Phaseoloid Genomicsb-Topic A.6Breeders & Sequenceb-Topic B.1Functional Annotation/Informaticsb-Topic B.3Functional Genomics Approachesb-Topic B.5Breeders & Gene Functionb-Topic C.1Association Mappingb-Topic C.2Breeding-Induced Genomic Changeb-Topic C.3Mining Yield QTLs - Exotic Germplasm			Specific	of	Specific	of	Specific	of
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Sub-Topic A.2 Genome Finishing 7 15.25 15.25 3.25 Sub-Topic A.4 Genome Resequencing 8 9 7.75 7.75 5.25 Sub-Topic A.5 Phaseoloid Genomics 9 2.50 3.25 3.50 Sub-Topic A.6 Breeders & Sequence 10 7.75 8.25 7.62 6.25 Sub-Topic A.6 Breeders & Sequence 10 7.75 8.25 7.75 6.25 Sub-Topic A.5 Phaseoloid Genomics 12 8.50 7 8.75 7.75 Sub-Topic B.2 Discovery via Mutagenesis 12 8.50 7 8.75 7.00 Sub-Topic B.3 Functional Genomics Approaches 14 8.50 7 7.5 8.675 6.75 Sub-Topic C.1 Association Mapping 17 7.75 7.75 8.50 6.75 6.50 Sub-Topic C.2 Breeders & Gene Function 16 3.75 7.75 6.50 5.55 6.75 6.50 5.55 6.75 <t< td=""><td></td><td></td><td></td><td></td><td></td><td>100%</td><td></td><td>100%</td><td></td><td>100%</td></t<>						100%		100%		100%
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Sub-Topic A.5 Phaseoloid Genomics 9 2.50 2* 3.25 3* 3.50 Sub-Topic A.6 Breeders & Sequence 10 7.75 7* 8.25 7* 6.25 Sub-Topic B.1 Functional Annotation/Informatics 12 8.50 7* 8.75 7* 7.75 Sub-Topic B.2 Discovery via Mutagenesis 12 5.25 4* 8.75 7* 7.00 Sub-Topic B.3 Functional Genomics Approaches 14 8.50 7* 7.75 10.25 Sub-Topic B.5 Breeders & Gene Function 16 3.75 7* 7.75 6* 6.75 Sub-Topic C.1 Association Mapping 17 7.75 7* 6* 6.50 Sub-Topic C.3 Breeding-Induced Genomic Change 18 5.50 6* 6* 6* 7 6* 6* 6* 5 5* 7* 7* 5* 6* 75 5* 5* 7* 5* 5* 5* 5* <t< td=""><td>Sub-Topic A.2</td><td>Genome Finishing</td><td>7</td><td></td><td>15.25</td><td>13%</td><td>7.25</td><td>6%</td><td>3.25</td><td>3%</td></t<>	Sub-Topic A.2	Genome Finishing	7		15.25	13%	7.25	6%	3.25	3%
Sub-Topic A.6 Breeders & Sequence 10 7.75 8.25 7 6.25 Sub-Topic B.1 Functional Annotation/Informatics 12 8.50 7 8.75 7.75 Sub-Topic B.2 Discovery via Mutagenesis 12 5.25 8.75 7.700 Sub-Topic B.3 Functional Genomics Approaches 14 8.50 9.75 8 10.25 Sub-Topic B.3 Breeders & Gene Function 16 3.75 8 5.75 5 6.75 Sub-Topic C.1 Association Mapping 17 7.75 7.75 6 6.50 Sub-Topic C.2 Breeders & Lexotic Germplasm 19 9.00 11.00 11.25 Sub-Topic C.4 Marker-Assisted Selection Resources 20 7.00 6.25 7.75 Sub-Topic C.5 Germplasm Genomics Informatics 21 6.00 5.75 6.75 Sub-Topic D.1 Transgenics/Transformation Virtual Ctr 23 3.00 3.75 3.00 Sub-Topic D.2 Transformation Efficiency 23	Sub-Topic A.4	Genome Resequencing	8		9.75	8%	7.75	6%	5.25	4%
Sub-Topic B.1 Functional Annotation/Informatics 12 8.50 7% 8.75 7% 7.75 Sub-Topic B.2 Discovery via Mutagenesis 12 5.25 4% 8.75 7% 7.00 Sub-Topic B.3 Functional Genomics Approaches 14 8.50 7% 9.75 7% 10.25 Sub-Topic B.5 Breeders & Gene Function 16 3.75 7% 5.75 6.75 Sub-Topic C.1 Association Mapping 17 7.75 7.75 6.50 Sub-Topic C.2 Breeding-Induced Genomic Change 18 5.50 6.75 6.50 Sub-Topic C.3 Mining Yield QTLs - Exotic Germplasm 19 9.00 11.00 11.25 Sub-Topic C.4 Marker-Assisted Selection Resources 20 7.00 5.25 4% 7.75 Sub-Topic D.5 Germplasm Genomics Informatics 21 6.00 5% 5.75 6.75 5 Sub-Topic D.1 Transgenic Event Repository 23 1.75 4.00 4.50 5 Sub-Topic D.2 Transformation Efficiency 23 2.50 <t< td=""><td>Sub-Topic A.5</td><td>Phaseoloid Genomics</td><td>9</td><td></td><td>2.50</td><td>2%</td><td>3.25</td><td>3%</td><td>3.50</td><td>3%</td></t<>	Sub-Topic A.5	Phaseoloid Genomics	9		2.50	2%	3.25	3%	3.50	3%
Sub-Topic B.2 Discovery via Mutagenesis 12 5.25 4% 8.75 7% 7.00 Sub-Topic B.3 Functional Genomics Approaches 14 8.50 7% 9.75 8% 10.25 Sub-Topic B.5 Breeders & Gene Function 16 3.75 3% 5.75 5% 6.75 Sub-Topic C.1 Association Mapping 17 7.75 6% 7.75 6% 6.50 Sub-Topic C.2 Breeding-Induced Genomic Change 18 5.50 5% 6.75 6% 6.50 Sub-Topic C.3 Mining Yield QTLs - Exotic Germplasm 19 9.00 4% 11.00 9% 11.25 3% Sub-Topic C.4 Marker-Assisted Selection Resources 20 7.00 6% 5.25 4% 7.75 6% 6.75 6% 6.75 6% 6.75 6% 6.75 6% 6.75 6% 6.50 3% 5.75 5% 6.75 6% 6.50 3% 5.75 5% 6.75 6% 6.75 6% 6.75 6% 6.75 6% 5.75 <	Sub-Topic A.6	Breeders & Sequence	10		7.75	6%	8.25	7%	6.25	5%
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Sub-Topic C.3 Mining Yield QTLs - Exotic Germplasm 19 9.00 3% 11.00 9% 11.25 3 Sub-Topic C.4 Marker-Assisted Selection Resources 20 7.00 5% 5.25 4% 7.75 6 Sub-Topic C.5 Germplasm Genomics Informatics 21 6.00 5% 5.75 5% 6.75 6 Sub-Topic D.1 Transgenic Event Repository 23 1.75 1% 4.00 3% 4.50 4 Sub-Topic D.2 Transgenics/Transformation Virtual Ctr 23 3.00 3% 2.75 2% 3.00 3% 4.50 5 5 5% 3.00 5% <td>Sub-Topic C.1</td> <td>Association Mapping</td> <td>17</td> <td></td> <td>7.75</td> <td><mark>6%</mark></td> <td>7.75</td> <td><mark>6%</mark></td> <td>6.50</td> <td>5%</td>	Sub-Topic C.1	Association Mapping	17		7.75	<mark>6%</mark>	7.75	<mark>6%</mark>	6.50	5%
Sub-Topic C.4 Marker-Assisted Selection Resources 20 7.00 6% 5.25 4% 7.75 6 Sub-Topic C.5 Germplasm Genomics Informatics 21 6.00 5% 5.75 5% 6.75 6 Sub-Topic D.1 Transgenic Event Repository 23 1.75 1% 4.00 3% 4.50 4 Sub-Topic D.2 Transgenics/Transformation Virtual Ctr 23 3.00 3% 2.75 2% 3.00 3 Sub-Topic D.3 Regulatory Promoter Set 23 2.50 2% 3.75 3% 3.50 3	Sub-Topic C.2	Breeding-Induced Genomic Change	18		5.50	5%	6.75	<mark>6%</mark>	6.50	5%
Sub-Topic C.5 Germplasm Genomics Informatics 21 6.00 5% 5.75 5% 6.75 6 Sub-Topic D.1 Transgenic Event Repository 23 1.75 1% 4.00 3% 4.50 4 Sub-Topic D.2 Transgenics/Transformation Virtual Ctr 23 3.00 3% 2.75 2% 3.00 3% 2.75 3% 3.00 3% 2.75 3% 3.00 3% 2.75 3% 3.00 3% 3.00 3% 2.75 3% 3.00<	Sub-Topic C.3	Mining Yield QTLs - Exotic Germplasm	19		9.00	8%	11.00	9%	11.25	9%
Sub-Topic D.1 Transgenic Event Repository 23 1.75 1% 4.00 3% 4.50 5.55 2.55 2.55 2.55 2.55 2.55 2.55 3.55	Sub-Topic C.4	Marker-Assisted Selection Resources	20		7.00	6%	5.25	4%	7.75	6%
Sub-Topic D.2 Transgenics/Transformation Virtual Ctr 23 3.00 3% 2.75 2% 3.00 3 Sub-Topic D.3 Regulatory Promoter Set 23 23 2.50 2% 3.75 3% 3.50 3 Sub-Topic D.4 Transformation Efficiency 23 4.00 3% 3.75 3% 3.00 3 Main Topic A Genome Sequence 6 47.50 40% 36.25 30% 25.50 24 Main Topic B Gene Function 11 26.00 22% 33.00 30% 31.75 36 Main Topic C Germplasm Genomics 17 35.25 29% 36.50 30% 38.75 36	Sub-Topic C.5	Germplasm Genomics Informatics	21		6.00	5%	5.75	5%	6.75	<mark>6%</mark>
Sub-Topic D.3 Regulatory Promoter Set 23 2.50 2% 3.75 3% 3.50 3 Sub-Topic D.4 Transformation Efficiency 23 4.00 3% 3.75 3% 3.00 3 Main Topic A Genome Sequence 6 47.50 40% 36.25 30% 25.50 24 Main Topic B Gene Function 11 26.00 22% 33.00 20% 31.75 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 30% 38.75 36.50 <td>Sub-Topic D.1</td> <td>Transgenic Event Repository</td> <td>23</td> <td></td> <td>1.75</td> <td>1%</td> <td>4.00</td> <td>3%</td> <td>4.50</td> <td>4%</td>	Sub-Topic D.1	Transgenic Event Repository	23		1.75	1%	4.00	3%	4.50	4%
Sub-Topic D.4 Transformation Efficiency 23 4.00 3% 3.75 3% 3.00 3 Main Topic A Genome Sequence 6 47.50 40% 36.25 30% 25.50 21 Main Topic B Gene Function 11 26.00 22% 33.00 28% 31.75 26 Main Topic C Germplasm Genomics 17 35.25 29% 36.50 30% 38.75 34	Sub-Topic D.2	Transgenics/Transformation Virtual Ctr	23		3.00	3%	2.75	2%	3.00	3%
Main Topic A Genome Sequence 6 47.50 40% 36.25 30% 25.50 21 Main Topic B Gene Function 11 26.00 22% 33.00 26% 31.75 26 Main Topic C Germplasm Genomics 17 35.25 29% 36.50 30% 38.75 32	Sub-Topic D.3	Regulatory Promoter Set	23		2.50	2%	3.75	3%	3.50	3%
Main Topic B Gene Function 11 26.00 22% 33.00 20% 31.75 20 Main Topic C Germplasm Genomics 17 35.25 29% 36.50 30% 38.75 37	Sub-Topic D.4	Transformation Efficiency	23		4.00	3%	3.75	3%	3.00	3%
Main Topic B Gene Function 11 26.00 22% 33.00 20% 31.75 20 Main Topic C Germplasm Genomics 17 35.25 29% 36.50 30% 38.75 37										
Main Topic C Germplasm Genomics 17 35.25 29% 36.50 30% 38.75 32	Main Topic A	Genome Sequence	6		47.50	40%	36.25	30%	25.50	21%
	Main Topic B	Gene Function	11		26.00	22%	33.00	28%	31.75	26%
	Main Topic C	Germplasm Genomics	17		35.25	29%	36.50	30%	38.75	32%
Main Topic D Transformation/Trangenics 22 11.25 5% 14.25 12% 14.00 1	Main Topic D	Transformation/Trangenics	22		11.25	9%	14.25	12%	14.00	12%
100% 100% 100% 100%						100%		100%		100%
TOTAL DOLLARS (12 raters were each given 10 million to allocate): 120.00 120.00 110.00	TOTAL DOLLA	RS (12 raters were each given 10 million to all	ocate):		120.00		120.00		110.00	

Table 4. *Reformulation of the funding dollar allocation amount in each Strategic Plan sub-topic and main topic into a <u>rank</u> reflecting the distribution of the funding amounts within any given 2-year period. The dark shading identifies those sub-topics whose funding allocation rank was in the upper quartile of the 10-to-1 ranking system (i.e., a rank of 7.5 to 10.0, inclusive).*

SUMMARY DATA (plus a10 Hi - 1 Lo Ranking of the topics) StratPlan			2008-09	Rank	2010-11	Rank	2012-13	Rank
List of Sub- and	Main Topics in the Soy Strategic Plan	Document	Specific	10-1	Specific	10-1	Specific	10-1
See the Strateg	ic Plan document for details (this PageNo):	PageNo	Dollars	Scale	Dollars	Scale	Dollars	Scale
On a 10-to-1 (Hi	i-to-Lo) scale, a scale unit = this million dollar	amount >		1.50		0.92		0.92
Sub-Topic A.1	Genome Informatics	6	12.25	8.0	9.75	8.6	7.25	5.6
Sub-Topic A.2	Genome Finishing	7	15.25	10.0	7.25	5.9	3.25	1.3
Sub-Topic A.4	Genome Resequencing	8	9.75	6.3	7.75	6.5	5.25	3.5
Sub-Topic A.5	Phaseoloid Genomics	9	2.50	1.5	3.25	1.5	3.50	1.5
Sub-Topic A.6	Breeders & Sequence	10	7.75	5.0	8.25	7.0	6.25	4.5
Sub-Topic B.1	Functional Annotation/Informatics	12	8.50	5.5	8.75	7.5	7.75	6.2
Sub-Topic B.2	Discovery via Mutagenesis	12	5.25	3.3	8.75	7.5	7.00	5.4
Sub-Topic B.3	Functional Genomics Approaches	14	8.50	5.5	9.75	8.6	10.25	8.9
Sub-Topic B.5	Breeders & Gene Function	16	3.75	2.3	5.75	4.3	6.75	5.1
Sub-Topic C.1	Association Mapping	17	7.75	5.0	7.75	6.5	6.50	4.8
Sub-Topic C.2	Breeding-Induced Genomic Change	18	5.50	3.5	6.75	5.4	6.50	4.8
Sub-Topic C.3	Mining Yield QTLs - Exotic Germplasm	19	9.00	5.8	11.00	10.0	11.25	10.0
Sub-Topic C.4	Marker-Assisted Selection Resources	20	7.00	4.5	5.25	3.7	7.75	6.2
Sub-Topic C.5	Germplasm Genomics Informatics	21	6.00	3.8	5.75	4.3	6.75	5.1
Sub-Topic D.1	Transgenic Event Repository	23	1.75	1.0	4.00	2.4	4.50	2.6
Sub-Topic D.2	Transgenics/Transformation Virtual Ctr	23	3.00	1.8	2.75	1.0	3.00	1.0
Sub-Topic D.3	Regulatory Promoter Set	23	2.50	1.5	3.75	2.1	3.50	1.5
Sub-Topic D.4	Transformation Efficiency	23	4.00	2.5	3.75	2.1	3.00	1.0
Main Topic A	Genome Sequence	6	47.50	10.0	36.25	9.9	25.50	5.2
Main Topic B	Gene Function	11	26.00	4.7	33.00	8.6	31.75	7.5
Main Topic C	Germplasm Genomics	17	35.25	7.0	36.50	10.0	38.75	10.0
Main Topic D	Transformation/Trangenics	22	11.25	1.0	14.25	1.0	14.00	1.0
On a 10-to-1 (Hi	-to-Lo) scale, a scale unit = this million dollar	amount >		4.03		2.47		2.75
TOTAL DOLLA	RS (12 raters were each given 10 million to allo	ocate):	120.00		120.00		110.00	

In the 2nd period (2010-11), the allocation percentages of the 12 SoyGEC members given to the main topic of genome sequence fell rather substantively from 40% to 30% (Table 3). This reflected the common perception that, with (a) the release of the raw sequence by DOE-JGI near the end of 2008, and (b) given the progress expected to be achieved with the 40% funding allocation assigned to finishing and informatics in 1st period (2008-09), only about 30% of the total funding would be needed for the genome sequence activities in the 2nd period. As a result, the 12 members shifted the 10% freed-up funding to the gene function, and transformation / transgenic main topics. This is understandable, because as more of the sovbean sequence information becomes available and easier to use, it will provide an exceptional foundation and superlative springboard for not only for launching genesequence-dependent gene function research but also an increased use of transformation/transgenic activities that can translation of genic discoveries into practical technologies and applications aimed at improving soybean productivity. Indeed, the 12-member SovGEC perception was that at least a quarter or more of the total available funding in the last four years of the six-year period should go to gene function research, with a half-quarter going into transformation and transgenic research in that same period. Gene function activities are expected to accelerate when genome sequence annotation and informatics can be used in the design, implementation, and analysis of gene function research, so the lower priority for gene function research in the 1st period (before sequence information becomes available) was understandable.

Relative to sub-topic <u>ranks</u> in the 2nd period (2010-11), the substantive decline in funding in the genome finishing sub-topic (in particular) and the genome sequence main topic (in general) made this released funding allocable to other sub-topics (Table 3 and Appendix Fig. 3). The collective perception of the 12 SoyGEC members that this released funding should be re-allocated to increase the funding allocation (in the 2nd period) of the following sub-topics, all of which received an upper quartile rank: (a) genome informatics (8.6), (b) functional annotation/ informatics (7.5), (c) gene discovery via mutagenesis (7.5), (d) functional genomics approaches (i.e., transcriptomics, proteomics, metabolomics) (8.6), and (e) mining for yield QTLs in exotic germplasm (10.0).

With regard to <u>disciplinary ranking differences</u> within the 2nd period (2010-11) (see Tables A1 and A2 in the appendix), the collective <u>perception of the six molecular-oriented members</u> did not differ much from the 12-member collective perception with regard to identifying sub-topics deserving of an upper quartile rank. The only exception was that they believed that the sub-topic of association mapping (7.9) was worthy of an upper quartile rank, whereas the sub-topic of mining for yield QTLs (6.5) was not. In contrast, the collective <u>perception of the six breeder-oriented</u> <u>members</u> was that the only sub-topics deserving of an upper quartile ranking were the mining for yield QTLs in exotic germplasm (10.0), functional genomics approaches (7.5), and (as also noted in the 1st period) breeder needs with regard to sequence (7.5).

The Strategic Plan goals and objectives span a five-year period (2008-12), so one could argue (as one SoyGEC member did) that only the first year of the 3^{rd} 2-year period (2012-13) should be allocated funding. Still, it was considered worthwhile to include this last 2-year period in this survey to assess the perception the SoyGEC (of at least 11 members) with regard to how allocation percentages might change in a 2-year period coming after four years of a five-year plan. It is clear in Table 3 that, in the 3^{rd} 2-year period, the SoyGEC members were of the opinion that, when it comes to future allocations to the four main topics some four years from now, about 1/3 of the total funding should go to germplasm genomics research (32%), about 1/4 to gene function research (26%), about 1/5 to genome sequence research (21%), and about 1/8 to transformation/ transgenic research (12%).

Table 3 and Appendix Fig. 5 indicate the <u>funding allocation percentages</u> for the subtopics in the 3rd period. The range in allocation percentages was 3% to 9%, with the sub-topics of mining for yield QTLs and functional genomic approaches receiving the highest (9%) allocations.

Table 4 and Appendix Fig. 6 indicate the implicit <u>ranks</u> computed for the sub-topics based on SoyGEC perceptions for funding allocation in this 3rd period. Upper quartile ranks were limited to the sub-topics of mining for yield QTLs (10.0) and gene function (8.9).

With respect to the two <u>disciplinary</u> groups comprising the SoyGEC, the six members with a molecular orientation felt that six sub-topics were worthy of an upper quartile rank: genome informatics (9.4), functional annotation/informatics (9.4), discovery via mutagenesis (9.4), functional genomics approaches (10.0), mining for yield QTLs (8.2), and marker-assisted selection resources (8.4). In contrast the five members with a whole-plant orientation felt that only mining for yield QTLs (10.0) was worthy of an upper quartile rank.

CONCLUSIONS

It is not known with certainty as to whether the perceptions of 12 SoyGEC members regarding funding dollar allocations to the Strategic Plan components is truly reflective of the perceptions of the broader soybean genomics research community, or even reflective of the 47+ researchers who were intimately involved in the preparation and completion of the Soybean Genomics Research Strategic Plan. However, it is known that the SoyGEC is a body whose membership is determined by the broader soybean genomics research community that each year nominates and elects two new members (one each in the aforementioned discipline categories). Therefore, it is reasonable to grant at least a "face value" status to the results of this survey. Several conclusions are apparent in the foregoing discussed survey data:

(a) During the next two years (2008-09), substantive funding should be directed towards finishing the raw soybean sequence that will be released by DOE-JGI in late 2008. The SoyGEC allocation percentages and implicit priority rankings indicated that a finished and accessible soybean sequence is a

critical prerequisite for many other sub-topics of the strategic plan. One SoyGEC members suggested that NSF and USDA funding grant submissions in this area could be substantively helped if leveraged with USB funding.

- (b) Finished sequence will not be useful unless it is readily available in the informatic databases that provide the data in interpretable and understandable formats to all soybean scientists irrespective of their disciplinary interests. The SoyGEC allocation percentages and implicit priority rankings indicate that genome informatics should be supported at a high level in the next four years.
- (c) Because soybean gene sequence data is critical prerequisite for launching many gene function sub-topic projects, the funding allocation ranks of these sub-topics did not achieve upper quartile ranking in the 1st period (2008-09). However, the collective wisdom of the SoyGEC was that these activities should be supported in the 2nd and 3rd periods. Moreover, the availability of gene sequence will be crucial in the translation of discoveries made in transcriptomics, proteomics, and metabolomics into transgenic-based technologies that can be quickly incorporated into newly developed varieties.
- (d) In terms of germplasm genomics, the sub-topic of mining for yield QTLs in exotic germplasm was highly ranked in the 2nd and 3rd year funding periods. This reflects the need to use genomics-based technologies to better evaluate the utility of "banked" germplasm vis-a'-vis introgression of useful genomics segments into the current "elite" germplasm used for conventional (non-transgenic) improvement of soybean yield potential.
- (e) There were some differences between SoyGEC members that have a molecular genomics/transgenics bent and those that have a whole-plant genomics (i.e., breeding/genetics) bent. Both groups are in favor of using the first two years to focus on converting the raw soybean sequence to a refined quality sequence that will be useful to all soybean scientists. The two groups differ in their funding allocation preferences in the subsequent years, with the molecular group focusing primarily on genet function and annotation, but with the breeding group focusing primarily on germplasm genomics. However, these are not necessarily divergent opposing views, but merely preferential viewpoints that likely will converge in the future.

RECOMMENDATIONS

- (a) The <u>funding allocation percentages</u> documented in Table 3 represent a SoyGEC vision for the funding the 5-year Strategic Plan main topics and sub-topics. These data may be useful to the USB when adding new funding dollars to its portfolio of soybean production research projects.
- (b) The <u>funding allocation ranks</u> documented in Table 4 were implicitly derived from the funding allocation preferences expressed by the surveyed SoyGEC members. These data may be useful to the USB if it needs a researcherbased prioritization as to Strategic Plan sub-topic funding decisions when there is insufficient USB funding to support all newly submitted proposals.

APPENDIX

Table A1. This table is identical to Table 4 in the main document, but uses only the survey data collected from the six current and past members of the SoyGEC whose scientific disciplines fall into the <u>molecular-orientation</u> (i.e., geneticists, transformation/ transgenic specialists, molecular biologists, etc.).

SUMMARY DA	A (6 SoyGEC Raters - Molecular-Oriented)	StratPlan		2008-09	Rank	2010-11	Rank	2012-13	Rank
List of Sub- and	d Main Topics in the Soy Strategic Plan	Document		Specific	10-1	Specific	10-1	Specific	10-1
See the Strateg	ic Plan document for details (this PageNo):	PageNo		Dollars	Scale	Dollars	Scale	Dollars	Scale
On a 10-to-1 (H	i-to-Lo) scale, a scale unit = this million dollar	amount >			0.78		0.36		0.42
Sub-Topic A.1	Genome Informatics	6		6.00	<mark>6.8</mark>	5.00	10.0	4.75	9.4
Sub-Topic A.2	Genome Finishing	7		8.50	10.0	3.50	5.8	2.25	3.4
Sub-Topic A.4	Genome Resequencing	8		3.25	3.3	3.50	5.8	3.00	5.2
Sub-Topic A.5	Phaseoloid Genomics	9		2.00	1.6	2.00	1.7	1.25	1.0
Sub-Topic A.6	Breeders & Sequence	10		2.75	2.6	2.75	3.8	3.25	
Sub-Topic B.1	Functional Annotation/Informatics	12		4.00	4.2	4.50	8.6	4.75	9.4
Sub-Topic B.2	Discovery via Mutagenesis	12		3.75	3.9	5.00	10.0	4.75	9.4
Sub-Topic B.3	Functional Genomics Approaches	14		3.75	3.9	4.25	7.9	5.00	10.
Sub-Topic B.5	Breeders & Gene Function	16		2.25	2.0	3.25	5.2	3.25	5.8
Sub-Topic C.1	Association Mapping	17		4.50	4.9	4.25	7.9	3.25	5.8
Sub-Topic C.2	Breeding-Induced Genomic Change	18		3.00	2.9	3.50	5.8	2.75	4.6
Sub-Topic C.3	Mining Yield QTLs - Exotic Germplasm	19		2.25	2.0	3.75	6.5	4.25	8.2
Sub-Topic C.4	Marker-Assisted Selection Resources	20		3.25	3.3	2.75	3.8	4.75	9.4
Sub-Topic C.5	Germplasm Genomics Informatics	21		3.75	3.9	3.25	5.2	3.50	6.4
Sub-Topic D.1	Transgenic Event Repository	23		1.50	1.0	3.00	4.5	3.50	6.4
Sub-Topic D.2	Transgenics/Transformation Virtual Ctr			2.00	1.6	1.75	1.0	2.00	
Sub-Topic D.3	Regulatory Promoter Set			1.50	1.0	2.00	1.7	1.75	2.3
Sub-Topic D.4	Transformation Efficiency	23		2.00	1.6	2.00	1.7	2.00	2.8
	b-Topic C.1Association Mapping17b-Topic C.2Breeding-Induced Genomic Change18b-Topic C.3Mining Yield QTLs - Exotic Germplasm19b-Topic C.4Marker-Assisted Selection Resources20b-Topic C.5Germplasm Genomics Informatics21b-Topic D.1Transgenic Event Repository23b-Topic D.2Transgenics/Transformation Virtual Ctr23b-Topic D.3Regulatory Promoter Set23b-Topic D.4Transformation Efficiency23								
Main Topic A	Genome Sequence	6		22.50	10.0	16.75	9.2	14.50	
Main Topic B	Gene Function	11		13.75	4.9	17.00		17.75	
Main Topic C	Germplasm Genomics	17		16.75	6.7	17.50	10.0	18.50	10.
Main Topic D	Transformation/Trangenics	22		7.00	1.0	8.75	1.0	9.25	1.
On a 10-to-1 (H	i-to-Lo) scale, a scale unit = this million dollar	amount >			1.72		0.97		1.0
TOTAL DOLLA	RS (6 raters were each given 10 million to alloo	cate):		60.00		60.00		60.00	

Table A2. This table is identical to Table 4 in the main document, but uses only the survey data collected from the <u>six current and</u> <u>past members of the SoyGEC</u> whose disciplines fall into the <u>whole-plant orientation</u> (i.e., breeders, geneticists, plant physiologists, etc.).

SUMMARY DA	FA (<u>6 SoyGEC Raters - WholePlant-Oriented</u>)	StratPlan		2008-09	Rank	2010-11	Rank	2012-13	Ranl
List of Sub- and	d Main Topics in the Soy Strategic Plan	Document		Specific	10-1	Specific	10-1	Specific	10-1
See the Strateg	ic Plan document for details (this PageNo):	PageNo		Dollars	Scale	Dollars	Scale	Dollars	Scal
On a 10-to-1 (H	tt of Sub- and Main Topics in the Soy Strategic PlanDocumente the Strategic Plan document for details (this PageNo):PageNoa 10-to-1 (Hi-to-Lo) scale, a scale unit = this million dollar amount >b-Topic A.1Genome Informatics6b-Topic A.2Genome Finishing7b-Topic A.4Genome Resequencing8b-Topic A.5Phaseoloid Genomics9b-Topic A.6Breeders & Sequence10b-Topic B.1Functional Annotation/Informatics12b-Topic B.2Discovery via Mutagenesis12b-Topic B.3Functional Genomics Approaches14b-Topic C.1Association Mapping17b-Topic C.2Breeding-Induced Genomic Change18b-Topic C.3Mining Yield QTLs - Exotic Germplasm19b-Topic C.4Marker-Assisted Selection Resources20b-Topic D.1Transgenic Event Repository23b-Topic D.3Regulatory Promoter Set23b-Topic D.4Transformation Efficiency23				0.72		0.69		0.6
Sub-Topic A.1	Genome Informatics	6		6.25	9.3	4.75	6.4	2.50	3
Sub-Topic A.2	Genome Finishing	7		6.75	10.0	3.75	5.0	1.00	1
Sub-Topic A.4	Genome Resequencing	8		6.50	9.7	4.25	5.7	2.25	2
Sub-Topic A.5	Phaseoloid Genomics	9		0.50	1.3	1.25	1.4	2.25	2
Sub-Topic A.6	Breeders & Sequence	10		5.00	7.6	5.50	7.5	3.00	4
Sub-Topic B.1	Functional Annotation/Informatics	12		4.50	6.9	4.25	5.7	3.00	4
Sub-Topic B.2	Discovery via Mutagenesis	12		1.50	2.7	3.75	5.0	2.25	2
Sub-Topic B.3	Functional Genomics Approaches	14		4.75	7.2	5.50	7.5	5.25	7
Sub-Topic B.5	Breeders & Gene Function	16		1.50	2.7	2.50	3.2	3.50	4
Sub-Topic C.1	Association Mapping	17		3.25	5.2	3.50	4.6	3.25	4
Sub-Topic C.2	Breeding-Induced Genomic Change	18		2.50	4.1	3.25	4.2	3.75	5
Sub-Topic C.3	Mining Yield QTLs - Exotic Germplasm	19		6.75	10.0	7.25	10.0	7.00	10
Sub-Topic C.4	Marker-Assisted Selection Resources	20		3.75	5.8	2.50	3.2	3.00	4
Sub-Topic C.5	Germplasm Genomics Informatics	21		2.25	3.8	2.50	3.2	3.25	4
Sub-Topic D.1	Transgenic Event Repository	23		0.25	1.0	1.00	1.0	1.00	1
Sub-Topic D.2	Transgenics/Transformation Virtual Ctr	23		1.00	2.0	1.00	1.0	1.00	1.
Sub-Topic D.3	Regulatory Promoter Set	23		1.00	2.0	1.75	2.1	1.75	2
Sub-Topic D.4	Transformation Efficiency	23		2.00	3.4	1.75	2.1	1.00	1
Main Topic A	Genome Sequence	6		25.00	10.0	19.50	10.0	11.00	5
Main Topic B	Gene Function	11		12.25	4.5	16.00	7.8	14.00	6
Main Topic C	Germplasm Genomics	17		18.50	7.2	19.00	9.7	20.25	11
Main Topic D	Transformation/Trangenics	22		4.25	1.0	5.50	1.0	4.75	1
On a 10-to-1 (H	i-to-Lo) scale, a scale unit = this million dollar	amount >			2.30		1.56		1.7
TOTAL DOLLA	RS (6 raters were each given 10 million to allo	cate):		60.00		60.00		50.00	

Fig. 1. See the graph title.

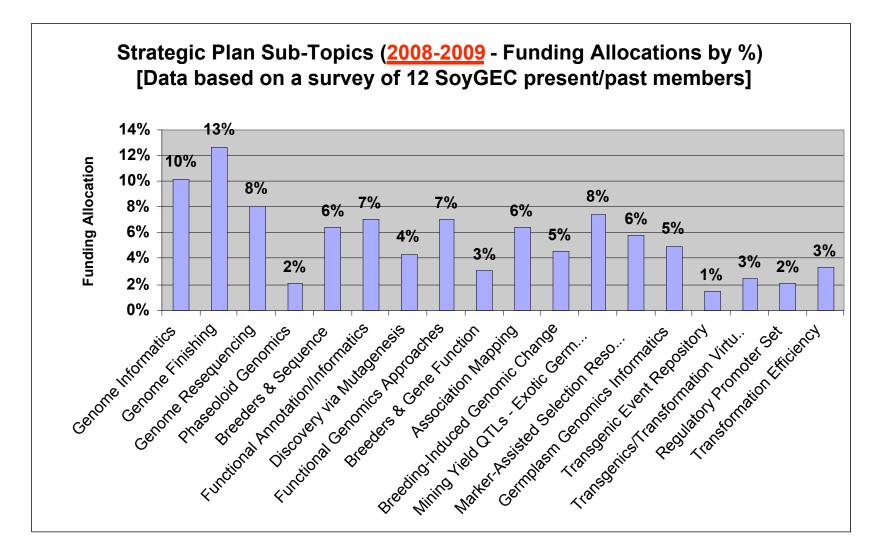


Fig. 2. See the graph title.

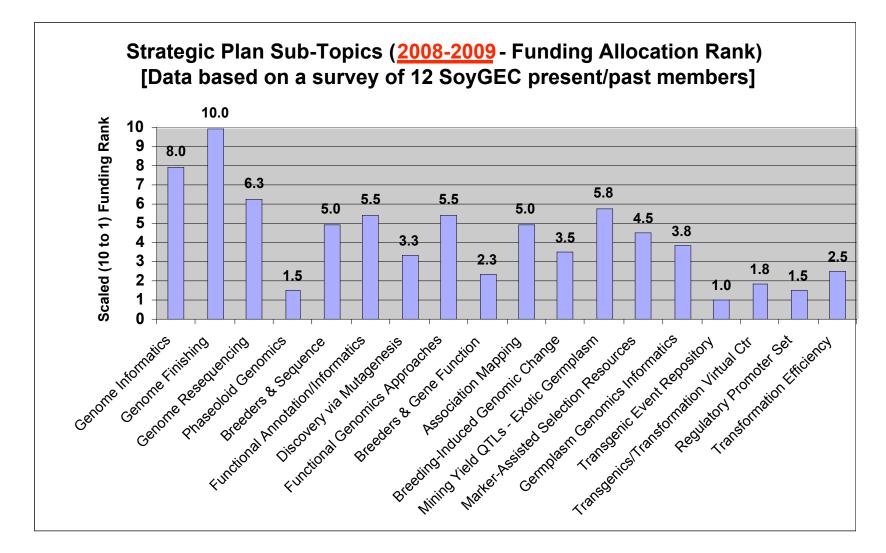


Fig. 3. See the graph title.

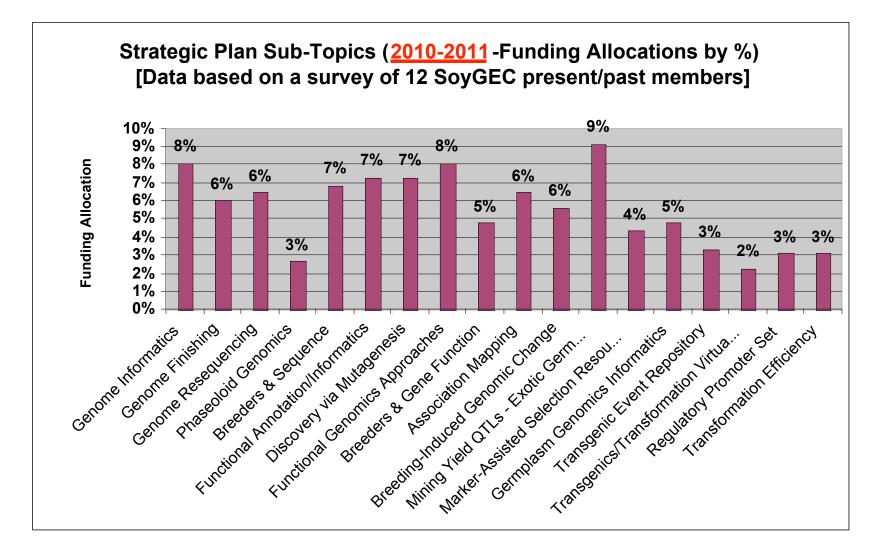


Fig. 4. See the graph title.

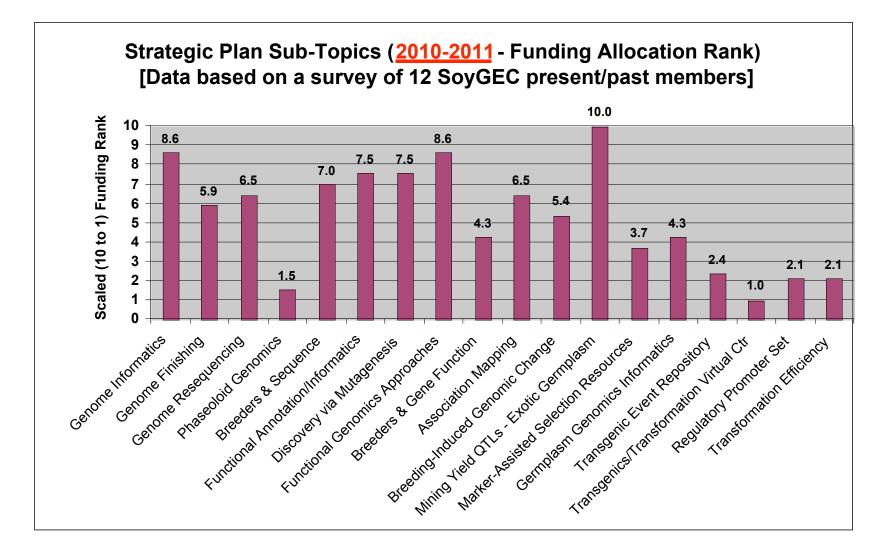


Fig. 5. See the graph title.

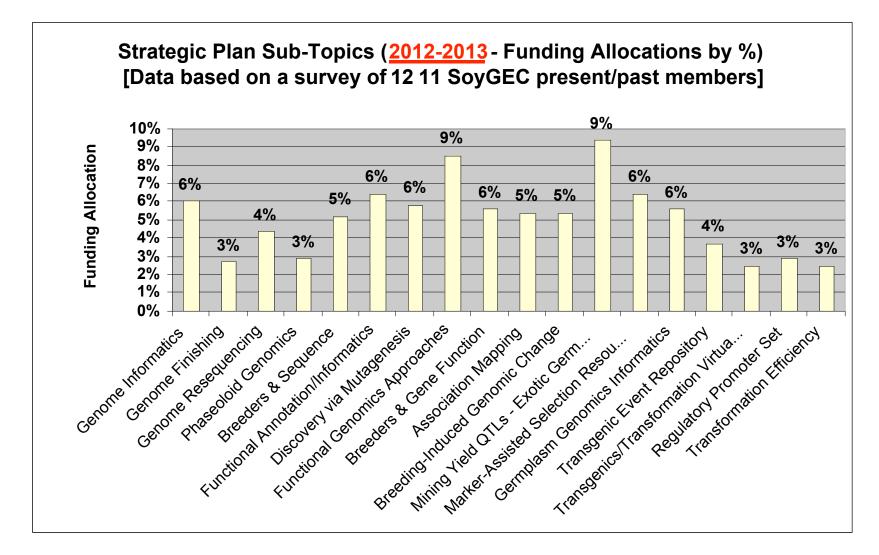


Fig. 6. See the graph title.

