V(A). Planned Program (Summary)

Program # 11

1. Name of the Planned Program

New Product Development / Genomics and Cultivar Development

V(B). Program Knowledge Area(s)

1. Program Knowledge Areas and Percentage

KA Code	Knowledge Area	%1862 Extension	%1890 Extension	%1862 Research	%1890 Research
201	Plant Genome, Genetics, and Genetic Mechanisms	54%	0%	30%	0%
202	Plant Genetic Resources	40%	0%	37%	0%
203	Plant Biological Efficiency and Abiotic Stresses Affecting Plants	0%	0%	5%	0%
204	Plant Product Quality and Utility (Preharvest)	0%	0%	6%	0%
205	Plant Management Systems	0%	0%	3%	0%
206	Basic Plant Biology	6%	0%	3%	0%
212	Pathogens and Nematodes Affecting Plants	0%	0%	3%	0%
511	New and Improved Non-Food Products and Processes	0%	0%	13%	0%
	Total	100%	0%	100%	0%

V(C). Planned Program (Inputs)

1. Actual amount of professional FTE/SYs expended this Program

Year: 2010	Extension		Research	
	1862	1890	1862	1890
Plan	0.0	0.0	7.0	0.0
Actual	0.3	0.0	10.4	0.0

2. Actual dollars expended in this Program (includes Carryover Funds from previous years)

Extension		Research	
Smith-Lever 3b & 3c	**1890 Extension**	**Hatch**	**Evans-Allen**
21953	0	667513	0
1862 Matching	**1890 Matching**	**1862 Matching**	**1890 Matching**
21953	0	667513	0
1862 All Other	**1890 All Other**	**1862 All Other**	**1890 All Other**
0	0	0	0

V(D). Planned Program (Activity)

1. Brief description of the Activity

Generated more than 3000 new plant seedlings. Made more than 150 new plant selections. Evaluated more than 300 advanced blueberry selections. Released a new blueberry cultivar.

Cereal breeding/genetics/genomics- develops cultivars and germplasm adapted to the Southeast's climatic conditions, with superior yield, agronomic traits, durable pest resistance, and end-use quality.

Comparative grass genomics -- develops cross-taxon genomic tools, genetic tools , comparative functional analyses of agronomically important genes.

Crop genomics--Genomics research reveals basic principles of genetics and evolution in the genomes of model organisms, and accelerate assembly of the genomic frameworks.

Cotton breeding/genetics/genomics- develops genetically improved cotton germplasm using classical breeding techniques with a focus on new biotechnology tools such as DNA markers and gene transformation technology.

Forage breeding/genetics/genomics-- breeds grass species. Applyed genomic approaches to improve the efficiency and effectiveness of cultivar development.

Legume transgenics --develops technology to facilitate genetic engineering of crop plants, deployment of transgenes of agronomic importance, and development of improved agronomic crops.

Peanut breeding/genetics/genomics- breeds superior cultivars and genetics of important agronomic traits. Development of molecular tools and information is also undertaken to reveal intrinsic genetic potential and support more efficient cultivar development.

Soybean breeding/genetics/genomics - develops superior yielding, multiple pest resistant cultivars, utilizes molecular technologies t, identifies and characterizes useful genetic variation improvement.

Sunflower and specialty oil breeding/genetics/genomics--applies breeding and cultivar development and uses molecular techniques, translational and comparative genomics.

Turfgrass breeding/genetics/genomics - breeds superior grasses with lower water, pesticide, and management requirements and cultivars with tolerance to salinity and other stresses.

Peach was selected as a model for woody ornamental plants because it has a short juvenile period, self-fertilizing perfect flowers, and a small, sequenced, diploid genome. The level of the mutagen EMS that reduced pollen viability by 50% was determined and then used to produce mutagenized pollen. Approximately 6000 emasculated peach flowers were pollinated with mutagenized pollen. The genomic sequence of the single-copy genes was obtained. PCR primers were designed to amplify TFL1 and AG exon sequences. Genomic DNA was isolated from 36 peach varieties and TFL1 exon regions were PCR amplified. Natural polymorphisms in TFL1 coding sequence were identified using high resolution melting.

Germplasm resistant to various watermelon diseases was obtained and seed was increased. Sequence databases was screened for NBS-sequences.SNP mapping was carried out for developed populations

2. Brief description of the target audience

Scientific peers and Extension Faculty.

V(E). Planned Program (Outputs)

1. Standard output measures

2010	Direct Contacts Adults	Indirect Contacts Adults	Direct Contacts Youth	Indirect Contacts Youth
Plan	0	0	0	0
Actual	1840	3680	20	0

2. Number of Patent Applications Submitted (Standard Research Output)

Patent Applications Submitted

Year: 2010
Plan: 10
Actual: 8

Patents listed
Mixotrophic algae and their consortia for the production of algae biofuel feedstock in wastewater ponds

3. Publications (Standard General Output Measure)

Number of Peer Reviewed Publications

2010	Extension	Research	Total
Plan	0	45	
Actual	0	208	208

V(F). State Defined Outputs

Output Target

Output #1

Output Measure

- Number of significant publications including referred journals articles, bulletins and extension publications.

Year	Target	Actual
2010	45	41

Output #2

Output Measure

- Number of invited presentations by faculty directly resulting from the success of this planned program.

Year	Target	Actual
2010	65	32

V(G). State Defined Outcomes

V. State Defined Outcomes Table of Content

O. No.	OUTCOME NAME
1	Release of new cultivars or germplasms
2	Number of growers, both local and international, that are using new cultivar varities.

Outcome #1

1. Outcome Measures

Release of new cultivars or germplasms

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	15	2

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)

What has been done

Results

4. Associated Knowledge Areas

KA Code	Knowledge Area
201	Plant Genome, Genetics, and Genetic Mechanisms

Outcome #2

1. Outcome Measures

Number of growers, both local and international, that are using new cultivar varities.

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Action Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	50	100

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)

What has been done

Results
75 Georgia, 25 international

4. Associated Knowledge Areas

KA Code	Knowledge Area
201	Plant Genome, Genetics, and Genetic Mechanisms
202	Plant Genetic Resources
204	Plant Product Quality and Utility (Preharvest)

V(H). Planned Program (External Factors)

External factors which affected outcomes

- Natural Disasters (drought, weather extremes, etc.)
- Economy
- Public Policy changes
- Government Regulations
- Competing Public priorities
- Competing Programmatic Challenges

Brief Explanation

Extreme drought in 2007/2008 affected our ability to successfully grow the plant materials being evaluated.

Funding limitations limited some research activity.

Government regulations restricting water use hurt outdoor programs and badly damaged the economy of buying ornamental plants. The down swing in the economy reduced the demand for new material slowed blueberry acreage expansions.

A late spring freeze significantly reduced the number of viable peach seeds.

V(I). Planned Program (Evaluation Studies and Data Collection)

1. Evaluation Studies Planned

- After Only (post program)
- Retrospective (post program)
- Before-After (before and after program)
- During (during program)
- Other (Extramural finding & acreage occupied by new cultivars)

Evaluation Results

New promising advanced blueberry selections were identified for further testing. On-farm trials receive favorable reviews from growers of potential new varieties being evaluated. Commercial acreage of recent UGA blueberry variety releases was increased in 2010.

Reporting on funding, sales, extramural funding, released cultivars and publications was completed.

Within a group of 36 peach varieties, genetic polymorphism was found at the same locus in the fourth TFL1 exon. Two varieties were heterozygous for this nucleotide change and one was homozygous for this change. There were no other genetic changes in TFL1 sequence.

Key Items of Evaluation