V(A). Planned Program (Summary)

Program # 4

1. Name of the Planned Program

Biotechnology and Genomics

V(B). Program Knowledge Area(s)

1. Program Knowledge Areas and Percentage

KA Code	Knowledge Area	%1862 Extension	%1890 Extension	%1862 Research	%1890 Research
131	Alternative Uses of Land	0%	0%	10%	0%
201	Plant Genome, Genetics, and Genetic Mechanisms	20%	0%	20%	50%
206	Basic Plant Biology	0%	0%	15%	0%
212	Pathogens and Nematodes Affecting Plants	20%	0%	20%	0%
302	Nutrient Utilization in Animals	20%	0%	5%	0%
303	Genetic Improvement of Animals	20%	0%	5%	0%
304	Animal Genome	0%	0%	15%	50%
311	Animal Diseases	20%	0%	10%	0%
	Total	100%	0%	100%	100%

V(C). Planned Program (Inputs)

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

Year: 2009	Extension		Research	
	1862	1890	1862	1890
Plan	1.0	0.0	0.8	1.0
Actual	1.3	0.0	1.1	1.0

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

Extension		Research	
Smith-Lever 3b & 3c	**1890 Extension**	**Hatch**	**Evans-Allen**
32898	0	20802	52000
1862 Matching	**1890 Matching**	**1862 Matching**	**1890 Matching**
42649	0	69736	100000
1862 All Other	**1890 All Other**	**1862 All Other**	**1890 All Other**
83509	0	204342	0

V(D). Planned Program (Activity)

1. Brief description of the Activity

Processes of research studies, dissemination of research results, papers and citations, commercialization of techniques and products, conduct research experiments, conduct workshops, meetings, develop products, resources, work with media and establish and sustain partnerships.

2. Brief description of the target audience

Research scientists, high school teachers

V(E). Planned Program (Outputs)

1. Standard output measures

2009	Direct Contacts Adults	Indirect Contacts Adults	Direct Contacts Youth	Indirect Contacts Youth
Plan	130	10	0	0
Actual	99	252	21	132

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

Year: 2009
Plan: 0
Actual: 0

Patents listed

3. Publications (Standard General Output Measure)

Number of Peer Reviewed Publications

2009	Extension	Research	Total
Plan	0	50	
Actual	0	73	73

V(F). State Defined Outputs

Output Target

Output #1

Output Measure

- Number of research projects in program areas
  Not reporting on this Output for this Annual Report

Output #2

Output Measure

- Number of peer reviewed research papers published

Year	Target	Actual
2009	40	73

Output #3

Output Measure

- Number of presentations

Year	Target	Actual
2009	45	63

V(G). State Defined Outcomes

V. State Defined Outcomes Table of Content

O. No.	OUTCOME NAME
1	Research articles published in peer-reviewed journals
2	Partnerships with high schools
3	Number of presentations, publications and non-peer-reviewed journals disseminating biotechnology research results.
4	Number of projects estimating parameters useful for risk assessment of growth hormone-transgenic Atlantic salmon
5	Number of projects addressing genetic improvement of aquaculture stocks
6	Number of projects assembling transcriptomes for vertebrates and invertebrates from the Southern Appalachian Mountains
7	Projects to aid in identification of bacterial plant pathogens
8	Projects to improve disease resistance and profitability of peanut production through biotechnology
9	Manipulating genomes of insects vectoring diseases

Outcome #1

1. Outcome Measures

Research articles published in peer-reviewed journals

2. Associated Institution Types

- 1862 Research
- 1890 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	50	73

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
Biotechnology, molecular and classical genetics, and genomics are powerful state-of-the-art approaches to the generation of knowledge in most knowledge areas applicable to agriculture. It is important that results of research be peer-reviewed and made available publicly.

What has been done
Research leaders submit completed articles to scholarly journals for peer review and publication.

Results
Knowledge gained from faculty and graduate student research using biotechnology, genetics and genomes has been published in peer-reviewed journals, and several other articles are in press or under review. Additional articles are reported under other planned program areas

4. Associated Knowledge Areas

KA Code	Knowledge Area
131	Alternative Uses of Land
201	Plant Genome, Genetics, and Genetic Mechanisms
206	Basic Plant Biology
212	Pathogens and Nematodes Affecting Plants
302	Nutrient Utilization in Animals
303	Genetic Improvement of Animals
304	Animal Genome
311	Animal Diseases

Outcome #2

1. Outcome Measures

Partnerships with high schools

Not Reporting on this Outcome Measure

Outcome #3

1. Outcome Measures

Number of presentations, publications and non-peer-reviewed journals disseminating biotechnology research results.

Not Reporting on this Outcome Measure

Outcome #4

1. Outcome Measures

Number of projects estimating parameters useful for risk assessment of growth hormone-transgenic Atlantic salmon

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	{No Data Entered}	1

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
Production of transgenic Atlantic salmon poses benefits to aquaculture, but also poses ecological and genetic risks should such fish escape from aquaculture operations into the wild. Regulatory authorities need reliable estimates of such risks in order to reach defensible decision on whether and how to permit commercial production of transgenic Atlantic salmon expressing an introduced growth hormone gene.

What has been done
Genetic and ecological risks were assessed in the laboratory and in confined, near-natural outdoor systems. Levels of circulating growth hormone, insulin-like growth factor I, and key receptors in the growth-promoting endocrine pathway were quantified. Physiological responses of transgenic and non-transgenic fish to ecologically relevant stressors of heat and starvation were quantified.

Results
Transgenic juveniles matured as parr less frequently than non-transgenics, suggesting that transgene expression diverts energy toward growth and smoltification. Transgenic individuals had poor breeding performance in competitive breeding experiments among transgenic and wild adults. Growth hormone expression was highest at earliest life stages and declined as the fish grew in size. Plasma GH and IGF levels in salmon from approximately 50g to 6 kg did not differ significantly between transgenics and controls. Wild-type fish maintained homeostasis more effectively than transgenic fish, showing lower fluctuations in all measured hematological parameters.

4. Associated Knowledge Areas

KA Code	Knowledge Area
304	Animal Genome

Outcome #5

1. Outcome Measures

Number of projects addressing genetic improvement of aquaculture stocks

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	{No Data Entered}	1

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
The tools of quantitative and genomic genetics can be applied for improvement of cultured finfish stocks, thereby contributing to aquaculture's productivity and profitability.

What has been done
In this project, we are characterizing genetic variation for: (1) ability to effectively utilize plant-based feeds by rainbow trout, (2) resistance to cold water disease in rainbow trout, and (3) resistance to herpes virus 3 in common carp.

Results
Collaborators in Israel have spawned the families needed for mapping of disease resistance onto genetic markers. Twenty-four candidate genes for which sequence data are available have been screened for polymorphisms between the parental strains. Frequencies of DNA sequence variants at Toll-like receptor genes differed among strains of common carp that are either resistant or susceptible to herpes virus 3, suggesting an approach to marker-assisted breeding of disease resistant broodstock.

4. Associated Knowledge Areas

KA Code	Knowledge Area
302	Nutrient Utilization in Animals
303	Genetic Improvement of Animals
304	Animal Genome
311	Animal Diseases

Outcome #6

1. Outcome Measures

Number of projects assembling transcriptomes for vertebrates and invertebrates from the Southern Appalachian Mountains

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	{No Data Entered}	1

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
The southeastern United States is the global center of biodiversity for freshwater organisms. Common actors driving the imperilment of aquatic and terrestrial species in the southern Appalachians include habitat alteration, siltation, and pollution. Advances in knowledge of functional genomics will contribute to the understanding of the mechanisms through which such drivers impact declining species. We are conducting pioneering work to characterize gene expression in vertebrate and invertebrates of the southern Appalachian region.

What has been done
Using data sets provided by collaborators at the U.S. Geological Survey - Biological Resources Division, we are applying bioinformatic techniques in order to perform transcriptome assembly for vertebrate and invertebrate genomes, identifying gene models, assigning gene names, classifying gene families, aligning DNA sequences among related species, and assessing gene ontology.

Results
Raw sequencing data has been obtained for three freshwater mussel species. The quality of the raw data has been assessed and is sufficiently high to initiate assembly of the transcriptome.

4. Associated Knowledge Areas

KA Code	Knowledge Area
304	Animal Genome

Outcome #7

1. Outcome Measures

Projects to aid in identification of bacterial plant pathogens

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	{No Data Entered}	0

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)

The taxonomy and nomenclature of bacterial plant pathogens has undergone frequent changes because our knowledge with regard to the relatedness between different bacterial plant pathogens is still far from complete. Moreover, information on well-characterized reference strains that can be used for comparison with unknown strains is not easily accessible. This imposes serious limitations when diagnosing the causes of plant diseases.

What has been done
To precisely identify strains belonging to species of plant pathogenic bacteria, a database with an Internet-accessible interface has been developed. The name is PAMDB (Plant Associated Microbes Database) and the web address is www.pamdb.org. The website makes it easy for users to browse and search the PAMDB database and to add new strain data and new DNA sequence data.

Results
To date, 1,299 DNA sequences from 794 strains belonging to four bacterial species that cause plant disease have been added to the PAMDB database. Availability of this information facilitates identification of plant pathogens and diagnosis of the diseases they cause. A plant pathologist can now compare the DNA sequence of an unknown pathogen and compare it with the 1,299 DNA sequences in the database. If the unknown pathogen belongs to one of the four species already added to PAMDB, the unknown pathogen can then be precisely identified by comparison with the DNA sequences of the known plant pathogenic strains in the database.

4. Associated Knowledge Areas

KA Code	Knowledge Area
212	Pathogens and Nematodes Affecting Plants

Outcome #8

1. Outcome Measures

Projects to improve disease resistance and profitability of peanut production through biotechnology

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	{No Data Entered}	0

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
Virginia peanut production has experienced a steep decline in the Virginia-North Carolina growing region as a result of decreased price supports and high disease pressure from Sclerotinia blight and other fungal diseases. The cost of fungicides for control of these fungal diseases can account for up to 50% of production costs. Peanut acreage in VA decreased from 75,000 to 23,000 acres in a six-year period, resulting in economic impact to Tidewater communities.

What has been done
Research has focused on using biotechnology and genetic engineering to improve resistance to Sclerotinia blight. Six years of field trials with transgenic peanuts have demonstrated a reduction in blight incidence and disease severity, and increased yields. Information needed to complete documents requesting deregulation and approval for commercial release is being obtained. The consultative process with USDA-APHIS, EPA, and FDA has begun.

Results
Field trials have verified expression of oxalate oxidase in transgenic peanut and its heritability through multiple

generations. Oxalate oxidase increased resistance to Sclerotinia but did not alter susceptibility to virus, early leaf spot, or other diseases. Trials show gene flow, growth habit, pod development, maturity, market traits, fatty acid profiles and minerals were identical to non-transgenic peanuts. Anticipated availability of Sclerotinia resistant cultivars will improve disease control, reduce production costs and pesticide usage, and result in higher yields. A white paper on the larger issue of transgenic traits of peanuts was prepared for various industry groups, raising awareness of the importance and value of this initiative to stakeholders.

4. Associated Knowledge Areas

KA Code	Knowledge Area
201	Plant Genome, Genetics, and Genetic Mechanisms
206	Basic Plant Biology
212	Pathogens and Nematodes Affecting Plants

Outcome #9

1. Outcome Measures

Manipulating genomes of insects vectoring diseases

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2009	{No Data Entered}	0

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
Vector-borne diseases such as dengue fever and malaria are increasing, with severe epidemics occurring worldwide. Vaccinations, chemotherapeutics, insecticides, source reduction and education have not yet been sufficient to control these severe public health crises. While additional progress in all these areas must be made, it is vital to develop any technologies that can supplement the tools we already possess. Genetic control strategies aimed at manipulating the genome of the disease vector offer the potential to support these efforts.

What has been done
A project has been established to manipulate the genome or expression of transgenes in disease vector mosquitoes. Objectives include identifying novel promoter sequences capable of driving gene expression, improving mosquito transposition rates, and improving site-specific recombination rates. We have also begun to evaluate the potential of homing endonucleases to introduce breaks in the chromosomes of mosquitoes that are vector diseases.

Results
The expression of two novel promoters derived from mosquito ubiquitin genes in transgenic Aedes aegypti (yellow fever mosquito) have been characterized. Both exhibit constitutive expression during larval development, but have unique expression patterns in adults. Several heat-inducible promoters with robust activity in early embryos have also been characterized. Four recombinant homing endonucleases have been used to generate chromosomal breaks and gene excision in mosquito DNA. This can be a novel assay to determine whether a meganuclease can induce chromosomal breaks in disease vector mosquitoes. Such tools are helpful for basic research to understand mosquito-virus interactions and for applications to generate mosquito populations unable

to transmit arboviruses such as those causing dengue or yellow fever.

4. Associated Knowledge Areas

KA Code	Knowledge Area
303	Genetic Improvement of Animals

V(H). Planned Program (External Factors)

External factors which affected outcomes

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

Brief Explanation

{No Data Entered}

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

1. Evaluation Studies Planned

- After Only (post program)
- Other (research)

Evaluation Results

{No Data Entered}

Key Items of Evaluation

{No Data Entered}