V(A). Planned Program (Summary)

Program # 3

1. Name of the Planned Program

Biotechnology & 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
203	Plant Biological Efficiency and Abiotic Stresses Affecting Plants			33%	
301	Reproductive Performance of Animals			10%	
304	Animal Genome			17%	
305	Animal Physiological Processes			20%	
307	Animal Management Systems			3%	
712	Protect Food from Contamination by Pathogenic Microorganisms, Parasites, and Naturally Occurring Toxins			17%	
	Total			100%	

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	3.0	0.0
Actual	0.0	0.0	1.2	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**
0	0	137965	0
1862 Matching	**1890 Matching**	**1862 Matching**	**1890 Matching**
0	0	181469	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

Supported faculty members along with their students and collaborators completed a diversity of activities this year. As evidence of the high quality of our supported research efforts, two papers from projects this program area were published in Proceedings of the National Academy of Sciences, one of the top-ranked scientific journals in the world. Several of the projects represent investments in more fundamental aspects than for most other program areas, and are expected to provide significant payoffs through improved technologies and management tools in 5 to 15 or 20 years. Many of these projects are strongly leveraged by extramural funding from NIH, NSF, USDA and other sources, and several include excellent international collaborators.

Expression patterns of five genes involved in signal transduction pathways in plants were determined. The disappearance of amyloplasts during salt stress of plant roots, and the gravitropic response of roots under salt stress were documented. These are important issues in irrigated agriculture using marginal quality water, in arid landscapes, and certain other situations.

The Jagged1 gene is involved in adipogenesis and therefore obesity and diabetes. The regions of the murine Jagged1 gene promoter that are responsive to adipogenic signals generated by the hormones insulin and glucocorticoid were mapped using molecular biology and biochemistry techniques. This work also used bioinformatics approaches to identify promoter elements of the Jagged1 gene that are conserved among placental mammals.

Controlling reproduction either by improving efficiency or preventing population increases in commercially important and non-indigenous species, is of critical importance to farmers and fish and wildlife biologists. To control reproduction, it is critical to understand the underlying mechanisms of neuroendocrine control. The structure and function of brain and pituitary hormones in controlling reproduction was investigated using a multidisciplinary approach and a myriad of molecular, endocrinology and biochemical techniques. In addition to its fundamental importance, one application of this work is in situations where production of sterile organisms can lead to improved food animal production and management.

The structure, character, and regulation of translational initiation complexes was investigated using the model eukaryotic organism Saccharomyces cerevisiae. This research involved the novel use of analytical ultracentrifugation with fluorescent detection system (AUD-FDS).

The Frankia actinorhizal symbiosis represents an important ecological and economic role in agriculture and the environment. An increased understanding how the actinorhizal symbiosis influences the global distribution of these plants and their wide range of habitats could be extended to other plants systems. Several novel natural products biosynthetic gene clusters in three Frankia genomes that may have potential biotechnological uses were identified, and some of these pathways were documented. Bioinformatics data mining of new Frankia genomes was initiated. A semi-high throughput assay system for filamentous bacteria to reliably test multiple variables was developed, and a genome-guided approach was used to identify plant hormone biosynthetic capacity in Frankia genomes. It was demonstrated that Frankia auxin production helps guide plant organ/structural development (nodule formation). Gene expression studies were initiated via a genome-guided approach and will help to correlate gene expression to potential function. Studies on non-Frankia actinobacteria associated with actinorhizal plants were initiated to elucidate plant-microbe aspects of the symbiosis, as were comparative bioinformatics studies on Frankia genomes from different host ranges to identify potential host recognition genes. Finally, studies on the effects of host plant root exudates on Frankia physiology were also initiated. The

overall impact of this study is a greater understanding of plant-microbe beneficial interactions. The use of these actinorhizal plants in bioremediation, soil stabilization, nurse cropping, biomass production, and land reclamation applications could potentially impact the 230 million people in the United States.

2. Brief description of the target audience

The target audience for this program area includes stakeholders interested in safe measures for production of food products from "farm to plate"; lay and professional audiences interested in adipose tissue, obesity, diabetes and stem cell differentiation; agricultural and biotechnology industries, land restoration groups, environmental restoration and protection groups, farmers, health care professionals, food industry specialists, veterinarians, molecular biologists, infectious disease professionals, biomedical researchers, federal and state agencies and managers, students at the nearby 2 year college, university graduate and undergraduate students, postdoctoral scientists, faculty, and university, government and industry scientists.

V(E). Planned Program (Outputs)

1. Standard output measures

2010	Direct Contacts Adults	Indirect Contacts Adults	Direct Contacts Youth	Indirect Contacts Youth
Plan	600	150	25	50
Actual	850	480	25	55

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

Patent Applications Submitted

Year: 2010
Plan: 1
Actual: 0

Patents listed

3. Publications (Standard General Output Measure)

Number of Peer Reviewed Publications

2010	Extension	Research	Total
Plan	0	9	
Actual	0	10	0

V(F). State Defined Outputs

Output Target

Output #1

Output Measure

- Number of participants in the project (not including audience counts)
  Not reporting on this Output for this Annual Report

Output #2

Output Measure

- Number of undergraduate students directly involved in the projects

Year	Target	Actual
2010	3	32

Output #3

Output Measure

- Number of graduate student directly involved in the projects

Year	Target	Actual
2010	4	14

Output #4

Output Measure

- Number of non-peer-reviewed publications including theses, abstracts, etc

Year	Target	Actual
2010	9	33

Output #5

Output Measure

- Number of peer-reviewed publications

Year	Target	Actual
2010	3	10

V(G). State Defined Outcomes

V. State Defined Outcomes Table of Content

O. No.	OUTCOME NAME
1	Number of graduate students involved and trained
2	Number of undergraduate students involved and trained
3	Increased knowledge through publications and other means
4	Increased knowledge of potential intervention strategies for obesity and insulin resistance.
5	Increase fundamental understanding of gene expression to support future agricultural applications.

Outcome #1

1. **Outcome Measures**

   Number of graduate students involved and trained

   Not Reporting on this Outcome Measure

Outcome #2

1. **Outcome Measures**

   Number of undergraduate students involved and trained

   Not Reporting on this Outcome Measure

Outcome #3

1. **Outcome Measures**

   Increased knowledge through publications and other means

   Not Reporting on this Outcome Measure

Outcome #4

1. **Outcome Measures**

   Increased knowledge of potential intervention strategies for obesity and insulin resistance.

2. **Associated Institution Types**

   - 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	{No Data Entered}	2010

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)

Obesity is a health care crisis in the United States and is paralleled by dramatic increase in the number of persons afflicted with some form of insulin resistance. Therapeutic agents that target pathways important for regulating adipose tissue or improve insulin sensitivity have potential to reduce the obese state, and to ameliorate or prevent development of insulin resistance and other obesity-induced conditions. One potential therapeutic intervention is Jagged1, a signaling molecule that regulates cell fate determination including the process of adipogenesis. The mechanisms that govern transcriptional regulation of the jagged1 gene in adipogenic or most other cell types are largely unknown.

What has been done
We found that Jagged1 mRNA expression levels are dramatically (over 1000 fold) downregulated by insulin in adipogenic cell lines - a finding that is, to our knowledge completely novel. Using transcriptional inhibitors, we found that insulin treatment is likely to affect Jagged1 transcription, not degradation. Furthermore, we found that insulin also causes an increase in the transport of the Jagged1 intracellular domain into the nucleus, although its role in this organelle is still unknown but may be related to regulation of cellular proliferation and survival.

Results
Results of these studies will aid in the development of treatments designed to treat obesity and its related pathologies. The training received by students performing research under this project has led to employment opportunities for undergraduates and a Thesis for one of the graduate students involved in the project.

4. Associated Knowledge Areas

KA Code	Knowledge Area
305	Animal Physiological Processes

Outcome #5

1. Outcome Measures

Increase fundamental understanding of gene expression to support future agricultural applications.

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	{No Data Entered}	2010

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
From a number of biochemical and genetic studies it has become clear that viral infection processes, aberrations in metabolic states, and the progression to diseases ultimately involve alterations in the rate and timing of gene and protein expression. It has, therefore, become of paramount importance to understand the basic mechanisms that eukaryotic organisms employ for the control of gene expression.

What has been done
We used affinity AUC-FDS to identify translational complexes from the yeast Saccharomyces cerevisiae. Our results established that affinity AUC-FDS provides a simple methodology to purify protein complexes and to identify the components within the complexes. Our studies resulted in the first identification of the novel 77S translational complex. The regulation of this complex indicates that environmental stresses act directly upon it to control mRNA translation and stress granule formation.

Results
These results indicate that the use of other Flag-tagged protein in combination with specific GFP-tagged proteins will allow the expansion of this technique to identify other biologically important complexes. This information will not only have an impact on the health and quality of life of humans but will be especially important for preserving and strengthening the vitality of agriculturally important plants and animals.

4. Associated Knowledge Areas

KA Code	Knowledge Area
304	Animal Genome

V(H). Planned Program (External Factors)

External factors which affected outcomes
- Other (None.)

Brief Explanation

A few of these external factors had minor impacts on the conduct of research, but none has materially affected the outcomes nor resulted in unmet goals.

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

1. Evaluation Studies Planned

- After Only (post program)
- Before-After (before and after program)
- During (during program)
- Time series (multiple points before and after program)

Evaluation Results

{No Data Entered}

Key Items of Evaluation

{No Data Entered}