V(A). Planned Program (Summary)

Program # 3

1. Name of the Planned Program

Global Food Security and Hunger--Fundamental Plant and Animal Systems

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			25%	
206	Basic Plant Biology			15%	
301	Reproductive Performance of Animals			25%	
302	Nutrient Utilization in Animals			15%	
304	Animal Genome			10%	
305	Animal Physiological Processes			10%	
	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	4.0	0.0
Actual	0.0	0.0	5.4	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**
0	0	735928	0
1862 Matching	**1890 Matching**	**1862 Matching**	**1890 Matching**
0	0	983102	0
1862 All Other	**1890 All Other**	**1862 All Other**	**1890 All Other**
0	0	305802	0

V(D). Planned Program (Activity)

1. Brief description of the Activity

Research involving fundamental plant and animal systems is designed to increase our basic science understanding of reproductive, nutritional and general physiological systems and processes. On the animal side, practical problems addressed include embryonic mortality in sheep and cattle, performance limiting amino acids in animal rations, and health and disease resistance in poultry. For plants, the program emphasis varies from determining functions of ubiquitin and other polypeptide tags, to understanding basic mechanisms of flower senescence and cold shock adaptation, to combating the impacts of phytophthora and Chestnut blight, to defining and eliminating negative effects on grazing animals of ergot alkaloids produced by fungi symbiotic with pasture grasses.

Considering the animal systems fundamental research first, one project continued culturing primary hepatic cells with various CYP450 and other enzyme inhibitors to begin to assess the relative contribution of different enzyme systems to the catabolism of progesterone. The investigators have clearly demonstrated that providing sufficient nutrition to maintain milk production, while simply altering the feedstuffs utilized to stimulate insulin secretion, leads to a dramatic decrease in the activity of the enzymes responsible for progesterone, an increase in progesterone half life and a decrease in the metabolic clearance rate of progesterone. At the same time this hyperinsulinemic diet does not alter feed intake, milk yield or blood flow to the liver. The data indicate that CYP2C is the primary cytochrome responsible for progesterone catabolism in the lactating dairy cow, followed by CYP3A and aldoketo reductase.

Another study examined ovarian influences on embryonic survival in ruminants. The investigators found that NOBOX (a homeobox gene that is preferentially expressed in bovine oocytes) is an essential maternal factor during bovine early embryogenesis, and that it functions in the regulation of embryonic genome activation, pluripotency gene expression and blastocyst cell allocation. Intracellular calcium homeostasis is crucial in regulating progesterone production and apoptosis. This finding therefore contributes to our understanding of the mechanisms that render the early CL resistant to luteolytic actions of PGF2&alpha. The work with the oxytocin receptor inhibitor, atosiban, may shed light on why oxytocin appears to be luteolytic in some situations, but is not a necessary component of the action of prostaglandin F2 alpha in regression of the ovine and bovine CL.

On the plant science front, work continued on identifying the triggers of flower senescence. The investigator has developed a new model of flower senescence in which CEBP, a nuclear-encoded chloroplast protein, acts as a repressor of flower senescence. This protein, because of its putative pivotal role in the trigger mechanism of flowers senescence, will in future work be targeted for genetic engineering applications. Understanding flower senescence at the molecular level will help efforts of increasing the economic value and productivity of agricultural crops through genetic engineering. Specifically, manipulating flower longevity will lead to higher crop productivity by increasing the window of opportunity for flowers to be pollinated. This in turn has the potential of increasing crop yields. In contrast inducing full or partial flower senescence may lead to more efficient breeding efforts by alleviating the need to emasculate flowers. In addition decreased flower longevity may result in a decrease of invasiveness of crop and ornamental plant species.

A long-term regional research project that had its inception at WVU, "Biological Improvement of Chestnut through Technologies that Address Management of the Species, its Pathogens, and Pests," achieved an important milestone in 2010--it was awarded both the Northeast regional award for multi-state research and the national award of excellence from the Association of Land Grant Universities. "The APLU award is indeed a significant one as it recognizes the collaborative accomplishments of researchers from 14 land-grant institutions, the federal government and a non-profit organization," said William MacDonald, professor of plant and soil sciences in the Davis College. "The scientific challenges inherent in restoring the America chestnut can only be accomplished when scientists collectively combine their knowledge and

talents."

Outcomes of this project have focused on four field-oriented studies. The first is a long-term experiment designed to initiate biological control of chestnut blight at an American chestnut stand near West Salem, Wisconsin. The study has been in place for 20 years and involves the release of hypoviruses (viruses that reduce the virulence of the chestnut blight fungus) by introducing them into the resident population of Cryphonectria parasitica. Hypovirus spread has been assessed annually by analyzing C. parasitica isolates that arise from cankers. Hypoviruses are recovered most readily from cankers on trees that receive hypovirulent inoculum and less effectively to trees that did not receive treatment inoculum. In June 2010, a study examined the spread of hypoviruses to American chestnut trees outside the permanent study plots. Samples were removed from 345 cankers on 225 trees. To date, hypovirulent isolates have been recovered from 79% of the trees in the area with the longest treatment history, and from 5-11% of the trees distant from the original treatment area. Although some trees in the stand have died, others now are in remission from the disease and should survive. As biological control is achieved, seed production should be restored so that the American chestnut component of the stand can be perpetuated.

A second research topic has involved field testing transgenic (genetically modified) strains of Cryphonectria parasitica to assess whether they can enhance the biological control potential of hypoviruses. The advantage the modified strains bring is their ability to transmit hypoviruses at high levels to asexual spores and also to sexual spores that result when fungal mating occurs. The experimentation has demonstrated that the transgenic strains can function in the forest by increasing the production of hypovirus-infected inoculum. Each year, significantly more cankers have been detected that have become hypovirus infected and greater numbers of sexual spores were detected that are hypovirus infected. Additional time will be required to confirm the effectiveness of using the transgenic strains.

A third study is designed to evaluate whether increased resistance to chestnut blight that has resulted from The American Chestnut Foundation's breeding program can be combined with biological control afforded by utilizing hypoviruses. Current efforts are to maintain optimal growth conditions for the planting that contain American, Chinese, European chestnuts and a variety of Chinese X American backcrosses. These trees eventually will be used to test whether the two approaches to disease control can be combined effectively to manage chestnut blight. A fourth study involved a survey of a population of C. parasitica isolates from American chestnut trees in the Great Smokey Mountain National Park. This study examined the diversity of the fungal population and any associated hypoviruses. Seventy-one cankers on sixty-one trees were sampled in 2010 and tests have shown that there is a great amount of diversity among the C. parasitica isolates. No hypoviruses have been detected.

The research involving ergot alkaloids produced by fungi that are symbiotic with pasture grasses continued in 2010. It is hypothesized that modification of the expression of ergot pathway genes should alter the ergot alkaloid profile of endophytic fungi in grasses and the corresponding biological properties of grasses that contain these endophytes. Since clavine alkaloids and lysergic acid derivatives have been shown to have differential effects on insects versus mammals, shifting the bulk of the pathway product towards one alkaloid class or the other should change the biological properties of the fungus-grass symbiosis. Understanding the functions of ergot alkaloid biosynthesis genes will allow for alteration of the pathway and thus the profile of ergot alkaloids that accumulate in agriculturally important fungi.

2. Brief description of the target audience

The target audience for this area is composed of animal and plant scientists, biochemists, professional practitioners, dieticians, regulators and agribusiness firms.

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	0	0	0	0

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

Patent Applications Submitted

Year: 2010
Plan: 0
Actual: 0

Patents listed

3. Publications (Standard General Output Measure)

Number of Peer Reviewed Publications

2010	Extension	Research	Total
Plan	0	6	
Actual	0	15	15

V(F). State Defined Outputs

Output Target

Output #1

Output Measure

- Presentation on research at professional meetings

Year	Target	Actual
2010	7	8

Output #2

Output Measure

- Completed graduate degree programs

Year	Target	Actual
2010	2	3

V(G). State Defined Outcomes

V. State Defined Outcomes Table of Content

O. No.	OUTCOME NAME
1	Identify and map genes affecting flower senescence - # new genes
2	Develop ergot alkaloid deficient grasses at or near wild-type vigor - # new cultivars
3	Successfully develop and employ strategies using hypovirus as a biological control agent for Chestnut blight - # new strategies employed
4	Identify ovarian-specific gene expression affecting reproductive success - # new genes identified

Outcome #1

1. Outcome Measures

Identify and map genes affecting flower senescence - # new genes

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	1	1

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
Understanding flower senescence at the molecular level will help efforts of increasing the economic value and productivity of agricultural crops through genetic engineering.

What has been done
The investigator has developed a new model of flower senescence in which CEBP, a nuclear-encoded chloroplast protein, acts as a repressor of flower senescence.

Results
This protein, because of its putative pivotal role in the trigger mechanism of flowers senescence, will in future work be targeted for genetic engineering applications. Specifically, manipulating flower longevity will lead to higher crop productivity by increasing the window of opportunity for flowers to be pollinated. This in turn has the potential of increasing crop yields.

4. Associated Knowledge Areas

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

Outcome #2

1. **Outcome Measures**

Develop ergot alkaloid deficient grasses at or near wild-type vigor - # new cultivars

Not Reporting on this Outcome Measure

Outcome #3

1. **Outcome Measures**

Successfully develop and employ strategies using hypovirus as a biological control agent for Chestnut blight - # new strategies employed

2. **Associated Institution Types**

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	0	0

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
The American chestnut was among the most valuable trees in eastern North American forests, spanning from southern Ontario to northern Florida. Chestnut blight, a disease caused by the fungus Cryphonectria parasitica, eliminated the American chestnut as a canopy species.

What has been done
WVU researchers and leaders helped organize a long-term regional research project, "Biological Improvement of Chestnut through Technologies that Address Management of the Species, its Pathogens, and Pests," that involves researchers from 14 land-grant institutions, the federal government and a non-profit organization.

Results
To date, hypovirulent isolates have been recovered from 79% of the trees in the area with the longest treatment history, and from 5-11% of the trees distant from the original treatment area. Although some trees in the stand have died, others now are in remission from the disease and should survive. As biological control is achieved, seed production should be restored so that the

American chestnut component of the stand can be perpetuated. In 2010 the project received both the Northeast regional award for multi-state research and the national award of excellence from the Association of Land Grant Universities.

4. Associated Knowledge Areas

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

Outcome #4

1. Outcome Measures

Identify ovarian-specific gene expression affecting reproductive success - # new genes identified

2. Associated Institution Types

- 1862 Research

3a. Outcome Type:

Change in Knowledge Outcome Measure

3b. Quantitative Outcome

Year	Quantitative Target	Actual
2010	1	1

3c. Qualitative Outcome or Impact Statement

Issue (Who cares and Why)
Better understanding of ovarian specific gene expression may help to increase reproductive success in ruminants and other animals.

What has been done
The investigators found that NOBOX (a homeobox gene that is preferentially expressed in bovine oocytes) is an essential maternal factor during bovine early embryogenesis, and that it functions in the regulation of embryonic genome activation, pluripotency gene expression and blastocyst cell allocation.

Results
The results of this study represent an advance in knowledge about ovarian funciton that may lead to the development of management practices and treatments to increase reproductive success in ruminants.

4. Associated Knowledge Areas

KA Code	Knowledge Area
301	Reproductive Performance of Animals
304	Animal Genome
305	Animal Physiological Processes

V(H). Planned Program (External Factors)

External factors which affected outcomes

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

Brief Explanation

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

1. Evaluation Studies Planned

- Before-After (before and after program)
- Time series (multiple points before and after program)

Evaluation Results

{No Data Entered}

Key Items of Evaluation

{No Data Entered}