

# Plant Genomics

Plant Genomics

## V(A). Planned Program (Summary)

### 1. Name of the Planned Program

Plant 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
201	Plant Genome, Genetics, and Genetic Mechanisms				50%
202	Plant Genetic Resources				35%
204	Plant Product Quality and Utility (Preharvest)				15%
	<b>Total</b>				100%

## V(C). Planned Program (Inputs)

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

Year: 2007	Extension		Research	
	1862	1890	1862	1890
<b>Plan</b>	0.0	0.0	0.0	5.2
<b>Actual</b>	0.0	0.0	0.0	2.0

### 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	0	190536
1862 Matching	1890 Matching	1862 Matching	1890 Matching
0	0	0	133844
1862 All Other	1890 All Other	1862 All Other	1890 All Other
0	0	0	240158

**V(D). Planned Program (Activity)****1. Brief description of the Activity**

There are three research projects in progress under this research program. These projects include: (1) development and characterization of molecular markers for genetic improvement of pepper and watermelon, (2) mapping biomass QTLs for Arabidopsis, and (3) greenhouse tomato breeding project. The pepper and watermelon research focuses on mapping fruit quality and yield related traits using DNA marker technology. Molecular markers like AFLP, SNP and SSR markers have been developed for marker assisted selection in pepper and watermelon. Genetic mapping of F2 populations using these markers is in progress. Sixty microsatellites and 20 AFLP primer combinations are being used to estimate the molecular diversity among cultivated pepper species namely *Capsicum annuum*, *Capsicum baccatum*, *Capsicum pubescens*, *Capsicum frutescens* and *Capsicum chinense*. We identified 1155 polymorphic markers that are used for phylogenetic analysis and principle component analysis. Results indicated that molecular markers could clearly differentiate different species specific clades in the tree diagram that is drawn from genetic distances estimated from UPGMA analysis. Two F2 crosses (*Capsicum frutescens* X *Capsicum annuum* and *Capsicum baccatum* X *Capsicum baccatum*) are selected as they are developed involving promising accessions from our previous germplasm evaluations.

As the genetic diversity in cultivated watermelon (*Citrullus lanatus* var. *lanatus*) is not very high, 31 watermelon Plant Introductions collected from diverse geographical locations and representing major groups of *Citrullus* species are selected to understand the molecular diversity using AFLP and SSR polymorphisms. AFLP markers showed high polymorphism (3098 polymorphic bands) and the SSR markers produced 294 polymorphisms among the watermelon germplasm collections. Based on the diversity data, crosses were made among the diverse accessions from two different subspecies (*Citrullus lanatus* var. *lanatus* and *Citrullus lanatus* var. *citroides*). The F1 seed has been collected from these crosses for field evaluation and to develop interspecific F2 population for genetic mapping and to select segregants for various fruit traits, more female flowers and disease resistance.

A recombinant inbred population of Arabidopsis (*Columbia* X *Landsberg erecta*) consisting 100 progenies was grown in three replications under controlled growth conditions. We recorded several traits that are related to growth and hence contributing to the total biomass accumulation. We identified several QTLs using the maps that are previously published with genome wide markers in this cross. Several QTLs that are highly significant were identified. Currently we are recording the data of all the traits in 96 different ecotypes that are collected from all over the world.

Tomato germplasm and experimental hybrids were evaluated for plant and fruit quality traits under greenhouse conditions. Promising hybrids were advanced and additional crosses were made. Seed from these fruit were extracted and inventoried. DNA from germplasm and promising hybrids were extracted and quantified for use in PCR-based marker systems and AFLP analysis. Data on fruit quality was summarized and presented at research meetings along with preliminary marker and AFLP analysis.

**2. Brief description of the target audience**

- Germplasm Collectors/Curators
- Plant Breeders
- Plant Pathologist/Entomologists
- Horticulturalists/Agronomists
- Seed Companies
- Growers/Farmers
- Extension Agents

Plant Geneticists

**V(E). Planned Program (Outputs)****1. Standard output measures****Target for the number of persons (contacts) reached through direct and indirect contact methods**

	<b>Direct Contacts Adults</b>	<b>Indirect Contacts Adults</b>	<b>Direct Contacts Youth</b>	<b>Indirect Contacts Youth</b>
<b>Year</b>	<b>Target</b>	<b>Target</b>	<b>Target</b>	<b>Target</b>
<b>Plan</b>	0	0	0	0
2007	20	15	50	0

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

**Patent Applications Submitted**

<b>Year</b>	<b>Target</b>
<b>Plan:</b>	0
2007:	0

**Patents listed**

**3. Publications (Standard General Output Measure)**

**Number of Peer Reviewed Publications**

	<b>Extension</b>	<b>Research</b>	<b>Total</b>
<b>Plan</b>			
2007	0	2	0

**V(F). State Defined Outputs**

**Output Target**

**Output #1**

**Output Measure**

Scientific publications and/or presentations

<b>Year</b>	<b>Target</b>	<b>Actual</b>
2007	2	7

**V(G). State Defined Outcomes**

<b>O No.</b>	<b>Outcome Name</b>
1	Increase profitability of hydroponic tomatoes (%)
2	Gene map for vegetable crops (#)

**Outcome #1**

**1. Outcome Measures**

*Not reporting on this Outcome for this Annual Report*

**2. Associated Institution Types**

**3a. Outcome Type:**

**3b. Quantitative Outcome**

Year	Quantitative Target	Actual
------	---------------------	--------

**3c. Qualitative Outcome or Impact Statement**

**Issue (Who cares and Why)**

**What has been done**

**Results**

**4. Associated Knowledge Areas**

KA Code	Knowledge Area
---------	----------------

**V(H). Planned Program (External Factors)**

**External factors which affected outcomes**

Natural Disasters (drought, weather extremes, etc.)

Economy

**Brief Explanation**

Physical facilities not adequate (laboratory, greenhouse and fields).

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

**1. Evaluation Studies Planned**

Retrospective (post program)

**Evaluation Results**

**Key Items of Evaluation**