

## FINAL PROJECT REPORT

**Project Title:** Apple genome sequencing  
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**Total Project Request:** Year 1: 32,000

### Other funding Sources

**Agency Name:** Agriculture Research Center and Dept of Horticulture and LA  
**Amount awarded:** \$150,000  
**Notes:** Seed funding to initiate the Apple Genome Sequencing Initiative at WSU

**Agency Name:** USDA-NRI  
**Amount awarded:** \$150,000  
**Notes:** Development of BAC library for the double haploid apple

**Total Project Funding: 32,000**

### Budget History

Item	2008		
Salaries			
Benefits			
Wages			
Benefits			
Equipment			
Supplies	30,000		
Travel	2,000		
Miscellaneous			
<b>Total</b>	32,000		

## **OBJECTIVES**

Apple scion and rootstock improvement by utilizing *genomics, genetics and breeding* has emerged as one of the highest research priorities. The ever-changing global and environmental scenarios challenge us to employ creative approaches to accelerate apple improvement. The basic foundation of genetics, genomics breeding activities is grounded in a *genome sequence*. Availability of the apple genome sequence will provide ultimate utility to all the massive body of previous research performed in apples.

This project had only one objective

1. The specific objective was to augment the Apple Genome Sequencing Initiative (AGSI) with acquisition of approximately 300 Mega bases of apple genome sequence

## **SIGNIFICANT FINDINGS**

The apple genome project is ongoing and the 300 million bases of DNA sequence generated with support from this project are expected to help in assembling of the genome information.

## **RESULTS AND DISCUSSION**

Genetically unique doubled haploid material P21 R1 A50 n°13 = clone X9273, derived from Golden Delicious was used to isolate nuclear DNA. The material was obtained from the group at INRA, Angers, France. Utilization of double haploid genotype in conjunction with next generation technologies has generated a lot of interest in several genomics research groups.

As per the proposed timeline, we have achieved 2X coverage of the double haploid genome. The data is being constantly augmented with sequence data from other sources and assembly of this information is undergoing.

## **ADDITIONAL DEVELOPMENTS**

This project has enabled establishment of several important collaborations with international groups. Some of the major developments are summarized below.

1. Formation of the international consortium of apple genome sequencing. The formal partners include researchers from INRA, France; IASMA, Italy; University of Western Cape, South Africa; HortResearch NZ.
2. Next-Generation Sequencer: The apple genome project enabled us to leverage a demo unit from Roche Inc in June 2008. Finally the University procured this equipment and it is valued at \$650,000.
3. Roche Inc: In addition to loaning the equipment, Roche Inc as part of the collaboration has agreed to provide us additional sequence information data worth over \$100,000. This will increase the coverage of the genome by an additional 2X and make the genome assembly more feasible.
4. USDA-NRI Funding: The preliminary data generated from this project further enabled to attract USDA-NRI funding worth \$150,000.
5. Collaboration with DOE-Joint Genome Institute: DOE JGI director, Dr. Dan Rokhsar has agreed to generate additional sequence information to augment the ongoing work. In addition, they will also

assist in genome assembly work. DOE-JGI has sequenced several large plant genomes like maize, poplar, and medicago to name a few.

6. Collaboration with University of Guelph: U of G has invested \$1.5 million in establishing an very well equipped post-harvest facility. The sequence information generated with this project will be linked with post-harvest biochemistry studies to devise appropriate storage conditions for apple cultivars.

## **PRESENTATIONS AND PUBLICATIONS**

### Peer-reviewed publication

1. A Dhingra, A Kalyanaraman and R Bumgarner: Plant Genomes Revealed: Unraveling the structure and function of large plant genomes with next-generation genomics. *Current Genomics* in press 2009  
*Invited Review*

### Invited Presentation

1. A Dhingra: International Consortium for Apple Genome Sequencing. 4<sup>th</sup> International Rosaceae Genomics Conference. Pucon, Chile March 2008.
2. A Dhingra: Apple Genome Project: Laying the foundation for a better apple. University of Guelph, Ontario November 2008.
3. A Dhingra: Apple Genome Project. IASMA Italy February 2009
3. A Dhingra: Rosaceae research meets next generation genomics. Department of Plant Molecular Biology, Univ of Delhi South Campus, India December 2008
4. A Dhingra: Next-generation genomics for horticultural crop improvement. National Botanical Research Institute, Lucknow, India December 2008

### Poster Presentation

1. A Dhingra, A Kalyanaraman and R Bumgarner: Laying the foundation for a better apple. Annual WSHA meeting, Yakima, December 2008
2. A Dhingra et al. Apple Genome Project: Annual PAG conference, San Diego, CA January 2009

## **EXECUTIVE SUMMARY AND FUTURE DIRECTIONS**

The blueprint of apple genome is coming together rapidly as technological advances continue in the area of next-generation genomics. The funding from this project was to seed a larger initiative. In total we have attracted over \$ 1 million in funding with this project just for the apple genome project. What this means is rapid progress towards the finish line. Importantly, this project has furthered WSU and WTFRC's mission of enhancing PNW's profile in horticultural genomics research.

Data generation is to be followed by data distillation and assimilation in a biologist's programs. While the USDA-NRI project will enable establishment of basic genomics resources, we have requested for additional funding from WTFRC to support data distillation and assimilation. The data will also serve as preliminary information for a NSF grant ready to be submitted in January and July 2008.