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UH News

UH Manoa consortium unravels genetic code of transgenic papaya

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An International Papaya Genome Consortium led by University of Hawai'i at Manoa researchers has deciphered the genetic code of the disease-resistant transgenic "SunUp" papaya. Papaya, cultivated in tropical and sub-tropical regions worldwide, ranked number one on nutritional scores among 38 common fruits. Fruit, stem, leaves, and roots of papaya are used in a wide range of medical applications including production of papain, a valuable proteolytic enzyme. This draft, which spells out more than 90 percent of the plant's gene coding sequence, sheds new light on the evolution of flowering plants. And because it involves a genetically modified plant, the newly sequenced papaya genome offers the most detailed picture regarding the impact of particle bombardment on genome structure and function.

The findings appear today as the cover article in the journal Nature.

The papaya variety sequenced was SunUp, selected for its good fruit quality and the fact that it is the original transgenic line used as a breeding line in several papaya improvement programs. Papaya is a principal fruit crop of tropical and subtropical regions worldwide. It ranks behind grapefruit in world importance of fruit crops and it is Hawaii's second most important fruit crop, after pineapple.

"Sequencing the papaya genome is the first large scale genome project done in Hawaii with international collaboration from 22 research institutes and will benefit the papaya research community, papaya farmers, and consumers for years to come" said Maqsudul Alam, Director of the Center for Advanced Studies in Genomics, Proteomics, and Bioinformatics, College of Natural Sciences, University of Hawaii- Manoa (UHM) lead institute of the International Papaya Genome Consortium.

Transgenic papaya that resists papaya ringspot virus was developed by Drs. Dennis Gonsalves, Richard Manshardt, and Maureen Fitch at the USDA Agricultural Research Service's U.S. Pacific Basin Agricultural Research Center (ARS/ PBARC) and the UH College for Tropical Agriculture and Human Resources (CTAHR), respectively and released in the mid-1990s to save Hawaii's papaya industry from collapse. It was a widely publicized success story of genetically modified crop that provides dramatic benefits for both farmers and consumers.

"The genome sequence of SunUp facilitates deregulation of transgenic papaya in Japan and other foreign countries", said Dennis Gonsalves, Director of the USDA ARS/ PBARC in Hawaii. "Papaya as a minor crop worldwide has significant contributions to science and farm production. The draft sequence will provide candidate genes for developing disease and insect resistant varieties with improved fruit quality", said Stephanie Whalen, Director of the Hawaii Agriculture Research Center (HARC). The draft genome has found that the transgenic insertions occurred in only three places in the papaya genome, and that no nuclear genes were disrupted.

The papaya genome was sequenced using a whole genome shotgun approach. It took two years to construct the physical map and to sequence the 372 million bases of the SunUp genome. An interactive website (<http://asgpb.mhpc.hawaii.edu/papaya/>) is available to collaborators to access the papaya genome sequence, which has been submitted to GenBank.

The transgenic Rainbow papaya, a hybrid between transgenic SunUp and non-transgenic Kapoho, is currently greater than 60% of Hawaii's total papaya production and nearly 70% when other transgenic varieties are included.

Currently, the transgenic papaya can be marketed in Canada and the mainland USA but not in Japan. The Japanese papaya market can be expanded significantly if the transgenic papaya were deregulated. The papaya genome has answered many technical questions for the Japanese regulatory agency and the transgenic "Rainbow" papaya may soon be available for consumption in Japan. The State of Hawaii supported the Japanese deregulation effort through a research grant to the HPIA and International Papaya Genome Consortium.

The new analysis revealed that papaya has fewer functional genes than any other flowering plant for which genome sequence is available. Papaya also contains more genes for volatile compounds, the odors that attract pollinators and animals that eat the fruit and disperse its seeds. Papaya is now the fifth angiosperm (flowering plant) for which detailed genomic information is available. "One of the implications of this study is, on a larger scale, to understand the genome evolution of angiosperms," said Ray Ming, a University of Illinois professor of plant biology and co-lead author on the study.

The PAPAYA GENOME PROJECT is the most ambitious scientific endeavor of its nature in the State of Hawaii to date and is carried out by University of Hawaii with a consortium of several local, national, and international institutions and organizations, including the Hawaii Agriculture Research Center in Aiea, USDA Agricultural Research Service's U.S. Pacific Basin Agricultural Research Center (PBARC), the Hawaii Papaya Industry Association (HPIA) and Nankai University, China.



"University of Hawaii was able to build essential genomic and bioinformatic infrastructure for the success of this project" said, Shaobin Hou, Genome leader and co-lead author on the study. "This is an excellent example of international collaboration and we are very proud to be part of this exciting project and we will continue our collaboration with ASGPB researchers", said Lei Wang, Professor Nankai University, one of the project leaders and corresponding authors of the Nature manuscript.

Link to Nature article: <http://www.nature.com/nature/index.html>