

# GM papaya to reveal gene modification effects

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Last Updated: 7:01pm BST 23/04/2008

A food crop has had its entire genetic code read to reveal the precise effects of genetic modification on its DNA for the first time.

The pioneering feat could be exploited to allay concerns about the effects of gene tinkering.

The SunUp papaya was created by bombarding young plants with gold particles coated in a gene that would make the resulting plants resistant to a serious pest, the ringspot virus.

Today, in the journal *Nature*, a team of scientists led by Prof Maqsoodul Alam produces the first detailed look at the entire genetic code of the "transgenic" plant that resulted from this gene bombardment.

The International Papaya Genome Consortium led by the University of Hawaii researcher has deciphered the genetic code of the disease-resistant SunUp papaya.

The draft plant genetic code - genome - consists of 372 million "letters" and reveals that the insertions of new DNA occurred in only three places in the papaya genome.

This reveals the "transgene" responsible for resistance to papaya ringspot virus and the feat shows that now it is possible to study the effects of GM in unprecedented detail.

advertisement The GM papaya was developed by the USDA Agricultural Research Service's US Pacific Basin Agricultural Research Centre and released in the mid-1990s to save Hawaii's papaya industry from collapse.

"The draft sequence will provide candidate genes for developing disease and insect resistant varieties with improved fruit quality", says Stephanie Whalen, Director of the Hawaii Agriculture Research Centre.

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

Currently, the transgenic papaya can be marketed in Canada and the mainland USA but not in Japan. The team says 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.

Comparing the genome sequence with that of a distant relative, the grass *Arabidopsis*, the authors find that the papaya genome is three times larger but in fact contains fewer genes - which could provide clues about the evolution of seed-producing plants.

As well as having fewer working genes than any other flowering plant for which equivalent data are available, papaya also contains more genes for volatile compounds, the odours 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," says Prof Ray Ming, University of Illinois.

Fruit, stem, leaves, and roots of papaya are used in a wide range of medical applications including



Papaya is one of the most nutritious fruits

production of papain, a valuable proteolytic enzyme.

"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," says Prof Alam, Director of the Centre for Advanced Studies in Genomics, Proteomics, and Bioinformatics, College of Natural Sciences.

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