

News Section / [Genomics](#)

Melon genome may help improve production of disease resistant varieties

Tuesday, July 3rd, 2012

A consortium of nine research centres has obtained the complete genome of melon, a horticultural specie with high economic value around the world.

Besides the complete melon genome, scientists have obtained the particular genomes of seven melon varieties.

The scientific Project has been lead by Pere Puigdomenech, at the Spanish National Research Council (CSIC), and Jordi Garcia Mas, at the Institute for Research and Technology in Food and Agriculture (IRTA). Both scientists work at the Center for Research in Agricultural Genomics (CRAG), in Barcelona.

Also, the team lead by Roderic Guigo, at the Genomic Regulation Center has made an important contribution to the project.

The Melonomics project was launched by the Spanish Genome Foundation. Nine research centres have been involved in it, having the support of 5 companies and of five Spanish autonomous communities.

Results have shown that the melon genome has 450 millions of base pairs and 27.427 genes. It is much bigger than the genome of its nearest “relative”, the cucumber that has 360 millions base pairs.

“This difference is due mainly to the amplification of transposable elements. We didn’t find recent duplications within the genome, which are very common in plant species,” Puigdomenech stated.

“We have identified 411 genes that can be related in disease resistance. They are few but, nevertheless, the melon has a high capacity of adaptation to different environments,” explained the CSIC scientist.

During the work, when comparing this genome with others that are near phylogenetically, they have observed how changes occur to the genome of this species, which is known for its high variability.

Another question of interest is that related to the ripening of the fruit, a process that determines fruit characteristics such as taste and flavour. Scientists have identified up to 89 genes related with some aspects of this process: 26 genes related to the carotenoid accumulation -which gives the colour to the melon flesh- and 63 related to the sugar accumulation and the taste of melon. 21 genes out of the last 63 had never been described before.

“Knowing the genome and the genes related to the characteristics of value for agriculture will allow us to improve this species for obtaining more disease resistant varieties and with better organoleptic properties,” highlighted the IRTA scientist Jordi Garcia Mas.

Melon belongs to the family of cucurbits, which also includes species such as cucumbers, watermelons and squashes. Cucurbits have relatively small genomes.

“These are species of high financial interest, especially in the Mediterranean, Asian and African countries. Diseases that affect them, such as the mosaic virus in the case of cucumber or fungi can cause high financial losses. Therefore, we hope the genome sequentiation will have an important impact on improving this crop,” said Pere Puigdomènech.

The study has been published in the magazine Proceedings of the National Academy of Sciences (PNAS).

Disclaimer: Bioscholar is not intended to provide medical advice, diagnosis or treatment. The articles are based on peer reviewed research, and discoveries/products mentioned in the articles may not be approved by the regulatory bodies.

Related News Stories

1. [Melon genome may help improve production of disease resistant varieties](#)