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Scientists decipher fruit tree genome for the first time

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A scientific group of the Universities of Illinois (USA), Georgia (USA), Hawaii (USA) and Nakai (China), among others, have deciphered for the first time fruit genomic sequence, in this case papaya (Carica papaya), according to the cover of the last issue of the prestigious journal Nature. One of the researchers is a scientist assigned to the group of Molecular Genetics of the Department of Genetics of the University of Granada

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This new advance involves, after sequencing other plants’ genomes such as the sample species in biological research Arabidopsis thaliana, rice, poplar and vine, the fifth vegetal genome sequenced up to now, and the first one from a fruit tree. Besides, the authors have used in their analysis the SunUp transgenic variety, virus ringspot resistant (which represents a serious threat for this species), which means that this has been the first transgenic organism to be sequenced.



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Rafael Navajas Pérez, researcher of the Department of Genetics of the University of Granada, is part of the team made up by more than 85 scientists who have participated in this research supervised by doctors Ray Ming (University of Illinois), Andrew H. Paterson (University of Georgia) and Maqsudul Alam (University of Hawaii).

Papaya is a very important crop in great part of Latin America and the USA owing to its nutritional benefits and medical applications, and provides an annual income of about 130 million dollars only in the state of Hawaii. In Europe, this crop is experiencing a boom, and Spain, and specifically the Tropical Coast of Granada, is an important producer as a consequence of the particular climatic conditions of the area.

A model to research

Apart from the relevant commercial implications, due to its position in the tree of life and the recent discovering of sexual chromosomes in its genome, Carica papaya is an excellent study model to answer a series of interesting questions related to the evolutionary history of flower plants.

From this discovery, the researchers have already identified that its genome contains fewer genes than that of the Arabidopsis (a small annual herb), in spite of being three times bigger than it. According to the researcher from Granada, the lack of recent phenomenon of gene duplication, frequent in angiosperms genomes, can be behind of this observation. Despite this, it has been detected a significant increase in the number of genes related to arboreal development, the deposition and removal of starch reserves, the attraction of agents responsible for spreading the seeds and the adaptation to the length of the day in a tropical climate.

Other important crops

Experts predict that this new genome will offer numerous advantages as a reference system for comparative genomics with other fruit trees, and will be the basis to study morphological, physiological, medicinal and nutritional properties of other plants belonging to the order of the Brassicales, where papaya is included, which includes economically important crops such as cabbage, cauliflower, whitewash brush, mustard or turnip. Likewise, they expect papaya to be a reference organism for the study of the evolution of sexual chromosomes in plants.

Dr Navajas Pérez, who at present is working on the sequencing of the determinant region of the sex in the sexual chromosomes of papaya and whose research career has been focused on different aspects of plants’ sexual determination, intends, in a near future, to implement a research work in the UGR directed to sex early diagnosis in vegetal species of economic interest for Andalusia, as well as for the study of other molecular aspects of sex Biology in plants.

Reference: Rafael Navajas Pérez. Department of Genetics of the University of Granada. Post-Doctoral Fulbright Researcher at the University of Georgia, Athens (GA, USA).

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