

## Poster

## Improvement of nutritional properties of Cassava (*Manihot esculenta*) through massive analysis of gene expression



Miriam Santos Valdera, Antonio J. Pérez Pulido (1), Enrique Martínez Force (2) and Mónica Venegas Calerón (3)

(1)Centro Andaluz de Biología del Desarrollo (CABD); Universidad Pablo de Olavide, Ctra. de Utrera, Km 1, 41013 Sevilla

(2)Instituto de la Grasa; Campus Universitario Pablo de Olavide, Edificio 46, Ctra. de Utrera, Km. 1, 41013 Sevilla.

(3) Edificio Cabimer, Parque Científico y Tecnológico Cartuja, Calle Américo Vespucio, s/n, 41092 Sevilla

**Keywords:** gene expression; oil; cassava root

### ABSTRACT

**Motivation:** Currently, the cassava is the basis of food for more than 1 billion people in the world. In this instance, the modification of the nutritional composition of plant foods is an urgent matter, since the basic nutritional needs of the world population are not yet covered. The identification of the transcription factors that regulate oil biosynthesis could give tools to re-direct sucrose to oil in the root of tuberculous cultures. In cassava, most of the research that has been done has focused on the tuber, with little study of the seeds and their characteristics.

In Cassava the factors that direct the flow of carbon towards the different reserve tissues and determine the final composition of the tissue in the plant are not known. The proposed research line aims to deepen the knowledge of the fatty acid biosynthesis in cassava and increase the oil content of the roots. Fundamental knowledge to be able to reach the final objective of increasing the oil content. In addition to improving its nutritional value, while the amount of nutrients that contribute to the body.

**Methods:** There are two lines of research. The computer methods are based on searching for genes involved in the biosynthesis pathway of lipid substrates through databases such as Uniref and UniProt. After a series of genes obtained from other trials, we compared their presence in the *Manihot Esculenta* genome and verified their function. With homologous genes, we can expand the number of candidate genes.

The laboratory methods aim to develop the method of genetic transformation of cassava (Ima M Zainuddin et al., *Plant Methods* 2012, 8:24) in combination with *Agrobacterium*. From a horizontal cuttings and an in vitro culture of their apical buds, we get a mother plant from which we can obtain somatic embryos and create new seedlings to be able to transform with different

**Results:** The following results were obtained after a first search for genes obtained from a compilation base don papers previously made in other related organisms. From that list of candidates genes, there are genes that cease to be candidates because they are not found in *Manihot esculenta*, these being *susy*, *ATP-PFK* and *FBAGenes* that continue as candidates, for being in the genome of cassava, being *PK*, *GPT2* and *PPT1*. And for the latter, new genes can be obtained, such as *APE2* with identifier 16G010700.1 in JGI Phytozome. It is a translocator of triose-phosphate located in the chloroplast.

**Conclusions:** There is a vision of the future in this line of research to be able to start from a new and broader list of genes involved in the synthesis routes of sucrose and oil that are susceptible to modification.

There is still a lot to study to reach the goal, but positive results will come out.

### REFERENCES

1. Consortium, I. U. (2004) UniProt: the universal proteome knowledgebase. *Nucleic Acids Res.* 32, 115-124
2. Goodstein, D. M. et al. (2012) Phytozome: a comparative platform for green plant genomics. *Nucleic Acids Res.* D1178-D1186