

## GENOMICS OF AVOCADO CRIOLLO FRUIT (*Persea americana* Mill. VAR. DRYMIFOLIA)

R. López-Gómez<sup>1</sup>, Y. Torres-Cárdenas<sup>1</sup>, M. Chávez-Moctezuma<sup>1</sup>, R. Salgado-Garciglia<sup>1</sup>, B. Jiménez-Moraila<sup>2</sup>, G. Corona-Armenta<sup>2</sup> and L. Herrera-Estrella<sup>2</sup>

<sup>1</sup> Instituto de Investigaciones Químico-Biológicas, Universidad Michoacana de San Nicolás de Hidalgo. Francisco J. Mujica s/n. Edificio B-1. Morelia, Mic. México CP58060. Correo electrónico: lgomez@zeus.umich.mx

<sup>2</sup> Unidad de Servicios Genómicos. Laboratorio Nacional de Genómica y Biodiversidad (LANGEBIO). Km 9.5 Libramiento Norte carretera León-Irapuato. Irapuato Gto. México

México is the main consumer and producer of avocado in the world with an approximate annual production of 1.127.574.3 tons. Michoacán is the most important producer with an annual production of 1.012.667.6 tons. Today, México is the main exporter of this fruit in the world. Despite of the economic importance of avocado, little information is available on its genetics. It is significant that most of the important problems of production have a genetic base. The basic knowledge of how an organism works provides invaluable information for the biotechnological development. As complement to the knowledge of plant genomes, ESTs (Expressed Sequence Tags) projects have been generated, which basically consist of sequencing a great number of obtained cDNAs obtained from cDNA libraries, generated from different structures and stages of plant development. Our group has generated cDNA libraries of fruit and seed, and also genomic libraries of creole avocado (*Persea americana* var. *Drymifolia*). The cDNA libraries are currently being sequenced and to date our preliminary results show that 42% of the sequenced genes are related to metabolism, 20% are related to unknown function, 14% are related to fruit ripening, 8% are related to lipid synthesis, 6% to pathogens response, interestingly, 6% of the genes showed no similarity to any sequence reported in the databases. Finally 4% of the genes are involved in senescence process.

