

CHARACTERIZATION AND IDENTIFICATION OF MATURE miRNAs AND THEIR PRECURSORS IN THE GENOME OF CULTIVATED PEPPER

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Abstract

The cultivated pepper *Capsicum annuum* L. (Zunla-1) is a plant of Solanaceae's family, one of the crops with the largest cultivated area of Brazil according to CEAGESP, and one of the most consumed by humans. Its high nutritional, sensorial and aesthetic value for different foods worldwide are directly proportional to its economic and cultural importance. Despite the significance of this species, the knowledge about the gene regulation is still very scarce. A class of microRNAs (miRNAs) is considered the main class of small non-coding RNAs with approximately 19 to 25 nucleotides. They regulate the expression of messenger RNA (mRNAs) into cells, inhibiting their translation process. In cells, the miRNAs play several roles, including development regulation, defense, response to stress and control of cell proliferation. Therefore, this work objective was identifying and characterizing mature microRNAs and their precursors in the genome of *C. annuum* L.(Zunla-1). The precursors and mature miRNAs were identified using an optimized algorithm based on the conserved characteristics of miRNAs. The ClustalX 2.0 and RNAalifold programs were used to generate alignment while the RNAfold program was used to predict the secondary structure of the precursor. The Phylogenetic analysis was performed in the Mega5.2 software by the Kimura 2 parameters. About 91 families of miRNAs scattered in the genome, among them miR160, miR162, miR164, miR393 and miR828 were identified and characterized. Of these 5 families investigated we've found 12 real precursors with conservation at primary and secondary level. It was observed in *C. annuum* L.(Zunla-1) that families such as miR160 and miR828, showed miRNAs that were evolutionarily distant from other organisms in the Solanaceae family, leading to speculation that there is in fact evolutionary distant or missing information in the database. While in the other families it can be observed that there is evolutionary conservation among them. The miR160 family has already been described as regulating the response factors to auxin, a hormone involved in the regulation of plant cell growth, demonstrating the importance of these small RNAs in the organism. This study will open new challenges and new perspectives to understand better the biology and the genome of pepper.

Funding: FAPEMIG, UFU, CNPq and CAPES