

Preliminary analysis of Dicer-like genes in *Cucumber* genome

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Cucumber (*Cucumis sativus*) is one of the major vegetable crops worldwide, and in Brazil with an annual production that exceeds 200 tons. Its probable center of origin is in the mountainous regions of India, and there are currently more than 100 varieties of cultivable cucumber worldwide. Recent studies have shown the importance of gene regulation involving small RNAs, the processing system and their performance at the cellular level. MicroRNAs (miRNAs) are considered one of the most important small non-coding RNAs silencing mRNAs and controlling gene expression. There are multiple proteins responsible for the generation of miRNAs, among them the Dicer-like (DCL) protein stands out as one of the main protein. This work aimed to identify, using in silico analysis, genes involved in gene silencing pathway mediated by miRNAs in the genome of *C. sativus*. The sequences of the genome and transcriptome of *C. sativus* were obtained from public database Phytozome (<https://phytozome.jgi.doe.gov/pz/portal.htm>). The orthologous proteins from *Arabidopsis thaliana*, obtained from the RefSeq database of NCBI (<http://www.ncbi.nlm.nih.gov/>) were used as reference for the search using the BLASTp tool. The conserved domains and active site amino acid residues were recovered through the predicted proteins using the database PFAM and CDD. The phylogenetic analysis was conducted by Mega5.2 program. We were able to predict 17 DCL proteins divided into 4 subfamilies DCL1, DCL2, DCL3 and DCL4 in the genome of *C. sativus*. The putative protein DCLs were highly conserved at the amino acid level showing conserved domains such as RIBOc, PAZ super family, Dicer_dimer, DEXDc, Helicase_C, DSRM, Rnc and SrmB, these containing significant residues and conserved in critical positions on the protein. The putative active site of RIBOc domain was highly conserved at amino acid level showing the conserved amino acids glutamine, glutamic acid, aspartic acid / aspartic acid, glutamic acid in the similar positions when compared with orthologs proteins from plant species. The putative *C. sativus* DCL proteins were grouped in distinct clades in the phylogenetic tree corroborating the planned paralogs subfamilies. Thus, the results allow us to expand the study of miRNAs in cucumber, providing new challenges for understanding the biology of this organism.

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