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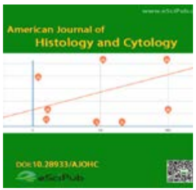

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In Silico Characterization of Nbs-Irr Gene Family in Vitis Vinifera Genome

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ABSTRACT

Introduction: During evolution, plants developed defense mechanisms against pathogen attack, including an infinity of molecular processes that are triggered by pathogen exposure, such as resistance gene synthesis (R). The NBS-LRR gene family is known as one of the most representative families in the R gene class, in which its protein domains are related to one form of plant defense mechanisms. Objective: To identify and characterize candidate sequences of the NBS-LRR gene family in the Vitis vinifera genome. Methodology: Initially, a seed sequence was selected from those curated in the NBS-LRR family and deposited in the UniProt database. This sequence was aligned via tBLASTn against the V. vinifera genome deposited in the NCBI, by adopting a cut-off of e-value ≥ e-10. The sequences were annotated, translated and had its conserved protein domains identified by both ORF Finder and CD-search tools, respectively. Finally, the prediction of the isoelectric point was performed, and the molecular weight was also estimated using the JVirGel 2.0 software. Moreover, the subcellular localization was carried out by the Cell-PLoc 2.0 software. Results and Discussion: A total of 40 candidate sequences were retrieved that are related to the gene of interest. The translated proteins showed a variation from 338 to 944 aa in size. A total of 33 complete NBS domains were found, from which 16 sequences had a whole RX-CC_like domain, while only two sequences have a full-length LRR domain. The candidate proteins had an isoelectric point from 5.25 to 9.46, a molecular weight varying from 38.47 and 108.14 kDa. All proteins showed cytoplasmatic subcellular localization, from which, 21 % also displayed an cellular membrane localization, in agreement with the data described in the literature. Conclusions: The results described here can contribute to a better understanding of the molecular characteristics of the NBS-LRR gene family and their role in defense mechanisms of grapevines to pathogens.

Keywords: Bioinformatics; Biotic stress; Grapevine; Plant defense; Resistance Genes

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