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GENOMIC CHARACTERIZATION OF PHOSPHOPROTEIN PHOSPHATASE GENE FAMILY IN *VITIS VINIFERA*

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Abstract:

Phosphoprotein phosphatases (PPPs) play a crucial role in phosphorylation-dependent signal transduction pathways and the regulatory control of plant immunity. Evolutionarily, the PPP family is highly conserved, responsible for about 80% of the dephosphorylation of phosphoserine and phosphothreonine residues of phosphorylated proteins. In plants, this family is composed of proteins PP1, PP2A, PP4, PP5, PP6, and PP7, with most dephosphorylation events attributed to PP1 and PP2A. Studies involving the action of PPPs on grapevines are still scarce. Thus, the objective was to identify and characterize genes that encode PPP family proteins in the *V. vinifera* genome. The putative *V. vinifera* proteome annotations were retrieved from the Phytozome database. The identification of PPP proteins was performed via BLASTp, using the cured PPP proteins from *Arabidopsis thaliana* as seed sequences, and by HMMER3, using the PF00149 domain, available at Pfam. The conserved domains of candidate PPPs were analyzed by CD-Search and Pfam, being selected only the sequences with the presence of the PPP catalytic domain in both algorithms. Molecular weight (m.w.) and isoelectric point (p.I) were predicted by JVirGel 2.0 and subcellular localization by the BUSCA tool. Multiple sequence alignment was performed by MUSCLE using MEGA X software, with default parameters. The phenetic tree was constructed using the Neighbor-Joining method (bootstrap 1000) with the Jones-Taylor-Thornton substitution model. The loci associated with the VvPPP genes were retrieved from the Phytozome GFF files, and the VvPPP were renamed according to their chromosomal location. Twenty candidate proteins presented specific domains of the PPP family. The length and MW of the VvPPP proteins ranged from 298 aa and 33.85 kDa to 1134 aa and 126.92 kDa, with 85% of the proteins having an average of 324 aa. All proteins showed acidic p.I, ranging from 4.59 to 6.37. The majority (75%) of VvPPP candidates exhibited cytoplasmic localization. The phenetic analysis of VvPPP and AtPPP proteins revealed the formation of eight subfamilies (PP1, PP2A, PP4, PP6, PP7, PPKL, ??SLP, and RLPH) with adequate bootstrap values. The PP1 (bootstrap=100%) and PP2A (bootstrap=100%) subfamilies were the most abundant, with nine and five members, respectively. Otherwise, the PP4, PP6, PP7, RLPH, and SLP subfamilies had only one member. No members of *V. vinifera* clustered in the PP5 subfamily, whose only member was AT2G42810 in *Arabidopsis*, suggesting that gene loss events occurred in *Vitis*. The VvPPP genes are anchored in 13 of the 19 pseudochromosomes of V. vinifera, with the pseudochromosomes 6 and 14 presenting the largest number of genes, with four and three, respectively, while the remaining pseudochromosomes showed one to two associated genes. Our results revealed high structural conservation of VvPPP with their AtPPP homologs. In addition, we provide a broader knowledge about the physicochemical and structural characteristics of PPP family members in grapevine.

Palavras-chave: Grapevine; PPP; Bioinformatics; ;

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