Genome-wide analysis of Cation/Proton exchanger (CAX) gene family in *Vitis vinifera* L.

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Cation/proton exchangers (CAX) are proteins that export cations from the cytosol to maintain optimal ionic concentrations in cells. Being associated to calcium homeostasis and signalling, CAX are essential for plant growth, development, and environmental stress response. CAX family members are grouped into three subfamilies named CAX type I, type II, and type III. Plants are characterized by the presence of members only belonging to CAX type I (similar to *Arabidopsis thaliana* CAX1) subfamily.

In *Vitis vinifera* L., genome-wide analysis allowed the identification of five CAX genes (VviCAX) homologous of AtCAX sequences (sequences retrieved from *A. thaliana* were here used as queries at grapevine genome databases and the resulting sequences as secondary queries). Analysis of sequences revealed a conservation of gene structure with three VviCAX genes exhibiting the most common structure composed by eleven exons, while the other two genes presented twelve and fourteen exons due to events of intron gain.

To classify the identified five VviCAX sequences, a phylogenetic tree was constructed using CAX sequences of different Magnoliophyta species, and *Saccharomyces cerevisiae*'s and *Escherichia coli*'s CAXs as outgroup sequences. Phylogenetic tree showed a clear separation of VviCAX sequences in the two main clusters of plant CAXs: type I-A and type I-B. As expected, the CAXI-A cluster integrates AtCAX1, AtCAX3, and AtCAX4, and I-B integrates AtCAX2, AtCAX5, and AtCAX6. While two VviCAX members were clustered in the CAXI-A, three members were grouped in the CAXI-B.

Aiming to correctly classify the VviCAX members, a comparison with the known members integrated in the same cluster was done. However, a lack of consistency in the labelling of CAXs genes was noted. With the goal of establishing a consistent standard pipeline for CAX gene annotation, we here propose a new classification scheme according to identified trends, based on protein phylogenies and sequence harmony method.

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