

IDENTIFICATION, CLASSIFICATION, AND EXPRESSION ANALYSIS OF LYSM GENE FAMILY IN VARIETIES OF VITIS VINIFERA

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Plants evolved lysine motif (LysM) receptors to recognize fungal elicitors and drive intracellular signalling. They are proteins occurring in a range of complex structural domains. One type of them has been characterized in rice, *Arabidopsis* and grape, where it has been named VvLYK1. It contains three LysM domains that directly bind chitin oligosaccharides at the apoplast level of infected cells. Regarding the other LysM, very little is known about their function and variability. This study aimed to exploit the LysM family in different grape species, differentiate in resistant and susceptible basing on their response to powdery mildew (*Erysiphe necator*) infection. The availability of genomic and transcriptomic resources enabled the identification of LysM genes, transcripts and proteins in three wild grape species (*Muscadinia rotundifolia*, *Vitis riparia*, *V. vinifera* subsp. *Sylvestris*) and seven cultivated varieties (*V. vinifera* subsp. *Vinifera*). Our results highlighted a highly variability of this gene family at both inter- and intra-specific level. The nucleotide sequences were translated into aminoacids sequences to see whether the SNPs found in the different cultivar genes could bring deleterious mutations. Then, the CDS sequences were cloned and sequenced to confirm the mutations found. Interestingly, we found seven VvLYK1-1 orthologs lacking one domain out of three. The transcript abundance of such candidates has been investigated in public RNASeq databases to understand whether these variations could alter the protein function. Interestingly, a variable behavior of VvLYK1-1 orthologs in response to biotic and abiotic stressors was observed. It is attempting to speculate that high levels of genetic and aminoacidic variations are present in this gene family, suggesting a strong specialization of each member. The Aglianico VvLYK1-1 ortholog will be part of a genome editing

approach to increase grape resistance to fungi attack among our candidates.