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## GENOME-WIDE IDENTIFICATION, EXPRESSION, AND PROTEIN INTERACTION OF LYSM-RLKS IN GRAPE

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Chitin is the main component of fungal cell walls and is a well-known pathogen-associated molecular pattern (PAMP) that triggers defence responses in several plant species. The PAMPs can be recognized by plant receptors named LysM receptor-like kinase (LYK) proteins localized in plasma membranes and able to activate the plant innate immunity. This study aimed to study the phylogenetic relationships of the LYK family in the *Vitis vinifera* genome, their expression upon fungal infection and their protein-protein interactions. To this end we used 11 grape varieties ( *V.vinifera* cv. Aglianico, *V. vinifera* cv. Cabernet Sauvignon, *V.vinifera* cv. Carmenere, *V.vinifera* cv. Chardonnay, *V. vinifera* cv. Falanghina, *V.vinifera* cv. Merlot, *V.vinifera* cv. Zinfandel, *Muscadinia rotundifolia, V. riparia, V. sylvestris, V. vinifera Pinot Noir* cl. PN40024*).* The grapevine LYK family was annotated using bioinformatic tools. The phylogenetic analysis clearly distinguished 14 *V. vinifera* LysM-RKs (VvLYKs) with high orthologue variability in different genotypes. Among the 11 grape varieties used, the highest numbers of orthologues was found in Carmenere (25), the lowest in Aglianico (10). Among the studied varieties, Aglianico was the most susceptible to fungal infection, therefore it was selected for transcriptional analysis of the identified VvLYKs. We report a quantitative analysis of the expression level of LYK genes in Aglianico (as susceptible) and *V. riparia* (as resistant) at 0,4,8 12 and 24 hours post powdery mildew infection (hpi). This analysis showed that the pattern of expression of different LYK genes after infection is different between

resistant and susceptible. A down-expression of VvLYK1-2 and VvLYK4-2 has been observed in Aglianico as opposed to *V. riparia* at 24 hpi while the expression trend VvLYK3-1 was opposite. Among the other VvLYKs, VvLYK1-3 expression was 2-fold lower in Aglianico than in *V. riparia* at 24 hpi (0.3-fold versus 1.5-fold change). In order to find a possible interaction between VvLYKs, a Yeast two hybrid (Y2H) assay was used among the main actors of the activation of the response to chitin. We fused in frame N-terminal and C-terminal domains of each protein with the activation domain (AD) or the binding domain (BD) of GAL4, respectively. Yeast cells co-transformed with either N-terminal domain of VvLYK1-1 and N-terminal domain of VvLYK4-2 or VvLYK5-2 were able to grow on selective media lacking tryptophan, leucine, histidine and adenine, indicating that VvLYK1-1 interacts with both of them. These results allow us to hypothesize a three-way interaction model and a folding of the VvLYK5-2 protein in the membrane, that will be confirmed or not using an ongoing fluorescence polarization assay. This analysis represents the first investigation of VvLYKs in different varieties and a valuable raw material for future breeding goals.