

## Inter-variatal variability of transcription factor WRKY in *Vitis vinifera* based on transcriptomic data

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**Motivation and Aim:** WRKY is plant specific transcription factors which involved in responses to stress and development. WRKY is a multigene family with a complex evolution and the specific roles of each gene are not yet fully understood. *Vitis vinifera* is one of the most widely cultivated plant species for commercial purposes. Previously we identified 62 WRKY genes in grape based on genomic data, determining their chromosomal positions and revealing intraspecific genetic variability across different grapevine cultivars. This study is devoted to exploring WRKY genes variability across grape cultivars to analyse possibility of indirectly influence on the resistance of different varieties to stress factors.

**Materials and Methods:** Transcriptomic data from 50 cultivars in the NCBI database, along with cultivars from the Nikita Botanical Gardens, were analyzed. Data preprocessing was performed using SRATools and FastQC, while RNA QUAST and BUSCO were used to evaluate assembly quality. Bowtie2 was used for alignment, and TransDecoder for transcript quantification. Functional annotation was carried out with InterProScan. For sequence alignment and phylogenetic analysis, MAFFT and IQ-TREE were used.

**Results:** Transcriptomic data of 50 cultivars were analyzed to investigate WRKY genes variability. In some transcriptomes not all 62 WRKY genes were not identified. This may be explained by low sequencing coverage or specific gene expression patterns in various samples. Genetic distance among WRKY genes across grape cultivars varied from 0 to 0.117, reflecting differing levels of genetic variability within this gene family. WRKY genes were grouped into three categories based on evolutionary pressures: positive selection, neutral evolution, and negative selection. Negative selection is prevalent among the WRKY genes analyzed, suggesting conserved functions. A small portion of genes are under positive selection, and an even smaller subset exhibits neutral evolution. No significant relationship was observed between variability and selection type.

**Conclusion:** This study revealed the genetic variability and selection pressures on some WRKY genes among *Vitis vinifera* cultivars, that suggesting potential cultivar-specific functions. It is required additional investigations.

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