

**THE GRAPEVINE (VITIS VINIFERA L., PINOT NOIR) FLORAL ATLAS:
IDENTIFICATION OF WHORL-RELATED MOLECULAR NETWORKS AND TISSUE
SPECIFIC GENES IN PRE- AND POST-ANTHESIS**

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The comprehension of molecular processes underlying the development and progression of flowering in grapevine is a hot topic, because flower gene expression regulation at both temporal and spatial level is the cornerstone for achieving the specification of morphology and physiology of the berry. Despite the abundance of transcriptomic data relating to grape berry and its sub-tissues, most of the upstream aspects related to flower development remain still unclarified. In order to identify hub genes that unequivocally distinguish the different tissues and that contribute to whorls development, we produced a grapevine flower transcriptome by dissecting calyx, calyptra, filament, anther, stigma, ovary and embryo in both pre- and post-anthesis phases. The RNA-seq data were then analyzed using both methodologies well consolidated in transcriptomic plant studies (such as the weighted gene co-expression network analysis, WGCNA) and analytical approaches previously used only in studies on animals or human's genomics (such as the tau (t) analysis aimed at isolating highly and absolutely tissue-specific genes). By intersecting the WGCNA and tau analysis data we were able to highlight some of the molecular mechanisms occurring in tissues involved in reproductive processes, such as anther and stigma, and we provided new insights into the role of other whorls not directly related to reproduction, such as calyptra and calyx. The great amount of data relating to whorls specific genes and the identification of molecular networks underlying floral tissues determination could represent an important genomic resource for the scientific community of the vine.