P70 – NAC family's cis-regulatory elements atlas in grapevine

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Abstract

The grapevine (*Vitis vinifera*) is one of the oldest known plants and at the same time represents an important fruit crop that is used in various productions such as wine, jams, juices and jellies, grape seed extracts, raisins, vinegar, and oil of grape seeds. In consideration of the huge importance that the vine represents, much genomic research has been conducted in the last decades. These studies were also conducted thanks to the sequencing of the entire genome and the accurate knowledge that is possessed about it. Today, based on published sequence data, it is possible to perform a complete analysis of a special gene family to discover their functions, evolution, and expression profiles as accurately as possible.

On this trend, we place our work which aims to develop the knowledge related on one of the largest family of the transcription factor and most important ones for grapevine: NAC (NAM, no apical meristem, ATAF and CUC). Moreover, it is believed that the NAC family of transcription factors (TFs) is among the plant TFs, in general but especially for the grapevine, which play significant roles in the growth, development, stress and defence responses of plants and therefore, offers the critical regulatory functions of the plant in the plant at various stresses. In studies conducted on grapevine it has been observed that NAC genes can represent important signalling components especially in the control of grape ripening processes such as late development of the berries and senescence of the leaves.

With a view to identify transcription factor binding site (TFBSs) and describe the grapevine cistrome, we used a novel high-throughput TF-DNA-binding assay called DAPseq (DNA Affinity Purification and sequencing) that combines next-generation sequencing of a genomic library with in vitro expression of affinity-purified TFs to generate cistrome and epicistrome maps. DNAseq libraries have been constructed using native genomic DNA from Cabernet franc young leaves by preserving tissue-specific cytosine methylations that are known to impact TF binding.

The data collected from DAPseq analysis will be combined with other new analysis methodologies based on next-generation sequencing (NGS) such as RNASeq for gene expression, ATACSeq for chromatin accessibility, BSSeq for DNA methylation, ChIPSeq for histone modifications in order to obtain the most exhaustive knowledge possible about gene regulation in grapevine.

Our study provides new useful information on NAC with the aim of obtaining a better understanding of the mechanisms of genetic regulation and more information on the signalling mechanisms of transcription factors in the different physiological processes.

Keywords: DAPseq, grapevine, NAC, gene regulation, cistrome