

HARNESSING GENOME EDITING TO ELUCIDATE THE ROLE OF HISTONE VARIANT H2A.Z IN GRAPEVINE

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Plants continually encounter various environmental stresses that represent significant challenges to their growth, development, and survival. In particular, grapevine, which is a perennial plant of great economic importance, is subjected to both abiotic stresses, such as drought and extreme temperatures, and biotic stresses, including diseases like powdery (Erysiphe necator) or downy (Plasmopara viticola) mildew. Lastly, due to a long history of breeding programs, crops have developed the "domestication syndrome". This involves an imbalance in the plant use of resources towards growth and productivity, at the expense of resistance to pathogens and the ability to recruit beneficial microorganisms, such as mycorrhizae.

Epigenetic modifications, such as DNA methylation and histone modifications, play an important role in stress responsiveness. Histone variants can be incorporated into nucleosomes in a targeted and replication independent manner thus influencing nucleosome structure and properties, gene transcription, DNA repair mechanisms and finally genome stability. Despite this, there is still much to be discovered about histone variants, especially on their role during plant-microorganism interactions. Currently, H2A.Z, one variant of the canonical histone H2A, seems to be the most involved in these mechanisms. Indeed, in plant, H2A.Z enrichment in the nucleosome occurs at Transcription starting site (TSS) of active genes and in the gene body of silent inducible genes. Plant mutants of histone

H2A.Z variants that have been produced so far are viable, and therefore can reveal the function of these chromatin regulators throughout the life of the plant.

Recent advances in genome editing techniques have provided powerful tools for precise modification of the genome. Our study aim is to investigate the application of genome editing (CRISPR-Cas9) techniques to modulate the expression of H2A.Z genes in grapevine and elucidate their role in in the interaction between plant and microorganisms, both beneficial and pathogenic. Target genes of interest for editing have been identified and transformation efforts are underway, aimed at both downregulation and overexpression of the H2A.Z genes. This will provide a wider knowledge of the role of H2A.Z in biotic interactions in grapevine.