

Transcriptomic and metabolomic responses to wounding and grafting in grapevine

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Abstract (250 words)

Grafting plants uses intrinsic healing processes to join two different plants together to create one functional organism. To further our understanding of the molecular changes occurring during graft union formation in grapevine, we characterized the metabolome and transcriptome of intact and wounded cuttings (with and without buds to represent scions and rootstocks respectively), and homo- and heterografts at 0 and 14 days after wounding/grafting. As over-wintering, dormant plant material was grafted, we also characterized the gene expression changes in the wood during bud burst and spring activation of growth. We observed an asymmetrical pattern of gene expression between above and below the graft interface, auxin and sugar related genes were up-regulated above the graft interface, while genes involved in stress responses were up-regulated below the graft interface. Many genes were differentially expressed between wounded cuttings and homografts, and between the different scion/rootstock combinations. By combining MapMan and gene ontology analysis, we identified several genes families potentially involved in grafting. Our results were consistent with previous work on other plant species, but we were able to identify some specificities linked to grafting in grapevine. By comparing the scion of homo- and hetero-grafts, we also show that grafting with a non-self-rootstock can influence scion gene expression 14 days after grafting. The combination of metabolomics and transcriptomics shows that the changes in gene expression were accompanied by corresponding changes in tissue metabolite concentrations.

Keywords: scion, rootstock, grafting, callus, transcriptome, metabolite analysis.