

## *Proteomics: Method for Studying Vascular Connection Proteins between Scions Grafted on Rootstock*

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Grafting is widely used in the agriculture of fruit crops and vegetables [1, 2]. The grafting is made of two genotypes, the rootstock and scion. A successful grafting is a complex biochemical and structural process that starts with the union of two organisms, followed by callus development and the formation of a functional vascular system [3]. The use of rootstocks, in which entire root system of a plant is replaced, has profound effect on scion developments. Indeed rootstocks are known to alter physiological processes in scions such as biomass accumulation [4], fruit quality [5] and response to biotic and abiotic stress as described above [6]. Quite a few recent studies have described significant factors underlying graft union formation at both the gene expression and protein translation levels [1, 2, 7]. However, how the two organisms can share a vascular connection after successful grafting remains unclear. A possible mechanism at the proteome level can advocate crucial information about the proteins/genes involved in the vascular connections of grafted plants.

The proteomic approaches encompass studying protein content, which include identification of proteins by sequencing amino acids, a possible evaluation of post-translational modifications and functional pathways in cells. A classical proteomic method is usually performed by comparative analysis of proteins expressed by organisms under different conditions (biotic/abiotic stress conditions and healthy organisms). Two Dimensional gel Electrophoresis (2DE) method is widely used to generate maps of proteins that shows changes in protein expression levels, post translational modifications. Proteomic study also analyze structural analysis by various mass spectrometer methods such as tandem Time Of Flight Mass Spectrometer (MALDI-TOF/TOF) and further also generate cleaved peptides by Peptide Mass Finger printing (PMF) and tandem MS (MS/MS) fragmentation. Proteomic analysis of the vascular connections between the rootstock and the scion can reveal interesting proteins that might be involved in strong connections of two organisms during the healing process to provide tolerance against stress conditions. Moreover, deeper proteomic analysis of vascular connection level can disclose the mechanism by which two organisms share a single transport route of nutrients and minerals for successful grafting.

## References

1. Cookson SJ, José M, Moreno C, Hevin C, Mendome LZN, et al. (2013) Graft union formation in grapevine induces transcriptional changes related to cell wall modification, wounding, hormone signaling, and secondary metabolism. *Journal of Experimental Botany* 64: 2997-3008.
2. Cookson SJ, Clemente Moreno MJ, Hevin C, Mendome LZN, Delrot S, et al. (2014) Hetrografting with nonself rootstocks induces genes involved in stress response at the graft interface when compared with auto grafted controls. *Journal of Experimental Botany* 65: 2473-2481.
3. Pina A, Errea P (2005) A review of new advances in mechanism of graft compatibility-incompatibility. *Scientia Horticulturae* 127: 93-105.
4. Tandonnet JP, Cookson S, Vivin P, Ollat N (2010) Scion genotype controls biomass allocation and root development in grafted grapevine. *Australian Journal of Grape Wine Research* 16: 290-300.
5. Jones TH, Cullis BR, Clingeleffer PR, Ruhl EH (2009) Effects of novel hybrid and traditional rootstocks on vigour and yield components of Shiraz grapevines. *Australian Journal of Grape Wine Research* 15: 284-292.
6. Yang Y, Wang L, Tian J, Li J, Sun J, et al. (2012) Proteomic study participating the enhancement of growth and salt tolerance of bottle gourd rootstock-grafted watermelon seedlings. *Plant Physiology and Biochemistry* 58: 54-65.
7. Zheng BS, Chu HL, Jin SH, Huang YJ, Wang ZJ, et al. (2010) cDNA-AFLP analysis of gene expression in hickory (*Caryacathayensis*) during graft process. *Tree Physiology* 30: 297-303.