The role of a grapevine-derived acetolactate synthase gene as a selectable marker for precision breeding of *Vitis.*

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Precision breeding (PB) is a newly-enabled approach to plant genetic improvement that transfers only specific desirable traits among sexually-compatible relatives via the mitotic cell division pathway to avoid the genetic disruption imposed by meiosis. PB builds upon decades of both fundamental and applied research aimed at bypassing the disruption of sexual reproduction (meiosis) by allowing gene insertion to be accomplished via the significantly more stable and predictable mitotic cell division pathway. Recent advances in the development of cell culture protocols for efficient plant regeneration combined with crop genome sequencing have opened new avenues for the movement of specific functional traits among sexually compatible crop cultivars. A grapevine derived MybA1 transcription factor was recently studied and characterized for its use as a reporter gene in plant transformation. We are currently studying the grape-derived tolerant acetolactate synthase gene, *VvALS2f*, that might potentially confer herbicide resistance and can be used as a marker gene for selection of modified events in cell culture. In the current study, the effect of different herbicides including Monument and Image, on inhibition of tobacco shoot cultures and grape embryogenic cultures will be studied to determine the optimum levels of herbicide that can be used for selection at the cell culture level. These studies will enable the use of the acetolactate synthase gene for the recovery of modified events in cell culture and regeneration of whole plants with traits of interest.

Molecular identification of rhizosphere fungi isolated from a selenium rich ecosystem

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This is an ongoing study of fungal samples collected from the rhizosphere of selenium (Se) hyperaccumulator and non-accumulator plants in the north central Wind River Basin west of Lysite, WY. Development of a consistent and reliable procedure to identify these chemically diverse species proved to be challenging. Presently each sample has been assessed for Se tolerance, total phenolics, antioxidant capacity and antibiotic production. However, these isolates still require taxonomic classification. Identifying these fungi will provide insight into their phylogenetic and ecological roles in Se tolerance, host plant and fungal interactions, and impacts of environmental Se on fungal communities. To identify fungal taxa, DNA was isolated using the E.Z.N.A. SP Fungal DNA Mini Kit. Each DNA sample was amplified using standard PCR for the internal transcribed spacer region (ITS), commonly used to identify fungi. Amplified DNA was visualized and extracted using 1% agarose gels and prepared for sequencing using Quantum Prep PCR Kleen Spin Columns. The purified DNA was sequenced in both forward and reverse directions and concatenated sequences were compared to available sequence data of other fungi using BLASTN in Geneious. Using this information, we identified a sub-set of the unknown taxa minimally to genus and report preliminary results.