

Transcriptional and metabolic analysis of potato tubers during endo-dormant to eco-dormant shift and after exposure to the sprout regulating compound 1,4-dimethylnaphthalene

Michael Campbell^{AB} Emily Dobry^C

^A Lake Erie Regional Grape Research and Extension Center, 662 Cemetery Road, North East, PA, USA

^B Penn State Behrend School of Science, 4205 College Drive. Erie, PA

^C Agricultural and Environmental Plant Science, Penn State University, University Park, PA, USA

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Abstract

Potato is the third largest food crop in the world and is grown in over 100 countries. One of the advantages of potato as a crop, outside the highly nutritional value, is that tubers are harvested in an endo-dormant state, which enables storage. Enhancing storage is possible using controlled environments that suppress sprouting through establishment of an eco-dormant condition but sprout control agents are often used to prolong storage. Many of the commercially available sprout control agents prevent sprouting by damaging the meristematic tissues making treated tubers usable for food but impractical for seed. The compound 1,4-dimethylnaphthalene (DMN) has been used commercially to maintain eco-dormancy and facilitate stored tubers for food and as seed. Transcriptional profiling of tubers transitioning from the endo-dormant to eco-dormant state, and following treatment with DMN, was undertaken to establish gene expression responses. Changes in gene expression were also measured in tissues allowed to recover for 2 weeks after exposure to the sprout inhibitor. Metabolic profiles were measured in identical treatments to ascertain the molecular changes associated with changes in dormancy status and after exposure to DMN. Overall gene expression responses suggest that DMN has a greater effect on eco-dormant compared to endo-dormant tuber meristems.