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Epigenetic control of transgenerational memory reset of drought stress in potato

Drought is one of the major threats to plants worldwide that limits plant growth, development and productivity. It is a consequence of serious destructive processes at all levels form biochemical, molecular, physiological to whole plant. Potato (*Solanum tuberosum* L.) is the fourth most important food crop and is considered to be sensitive to drought stress. High yields of good quality require sufficient water availability during the entire growing season. Insufficient water availability will become more important in the next decades for potato production. Potato yields are predicted to decrease by up to 30% in the coming decades. Therefore for science and breeding, a challenge is to understand mechanisms involved in drought tolerance in the cultivated potato. The response to drought is the complex quantitative trait controlled be several genes. Although numerous physiological and molecular aspects of drought stress resistance have been conducted on potato, research is lacking in the area of drought stress resistance on the whole plant and organ level which takes into account drought acclimation and recovery. Understanding these mechanisms in potato is critical to develop drought-tolerant cultivars. Potato tubers are organs of vegetative propagation. Stress memory transmitted to the non-stressed progeny, but very little is known about mechanisms governing transgenerational stress memory in vegetatively propagated crops. It is postulated that heritable epigenetic effects result in gene expression, particularly the effects of DNA methylation patterns. Genetic variability exists within potato which can be exploited to improve drought tolerance. It seems that transgenerational memory is highly genotype-dependent future. At present, various “omics” approaches are being used globally to understand plant response to drought stress and to identify potato genotypes that exhibit high tolerance to drought. In this project we hypothesize that epigenetic states determine resetting of potato yielding potential in plants developed from tubers of drought stressed mother plants. We postulate that transposable elements may be involved in this process. A group of Katahdin-derived cultivars will be screened for expression profiling and methylation analysis to gain new insight into transcription factors and epigenetic mechanisms controlling tolerance to drought stress in potato. Identification of genes underlying this trait will be an innovative success on a global scale.