

Title Differentially expressed genes associated with post-harvest processing in *Lolium temulentum* L.

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Abstract

Forage and turf grasses are utilized as feed in livestock production, lawns, erosion prevention and recreational surfaces. During grass seed production, grasses in the field are cut while still green and physiologically active. The cut grass is allowed to cure in the fields for 1–2 weeks prior to harvesting the seed. After seed harvest, a large portion of the generated biomass is left as unused or as low value agricultural residue, such as straw. Such biomass is not suitable as animal feedstock and its biochemical composition limits its utility in biofuel conversion efforts. One potential approach to improve the utility of grass residues as feed or biofuels feedstock would be to modify the biochemical or molecular processes within the plant during the period after swathing and prior to seed harvesting. Unfortunately, little knowledge exists regarding post-harvest gene expression in grasses. To this end, we utilized the model grass *Lolium temulentum*, a diploid self-fertile species with a short life cycle (2–3 months), to characterize post-harvest gene expression. A PCR based subtractive suppression hybridization library of a simulated grass straw harvest was prepared and after sequencing a total of 598 unique sequences were identified. Many of these sequences corresponded to orthologs of previously identified genes. The expression patterns of seven genes were evaluated by Northern blot analysis in post-harvest leaf and stem tissues. These preliminary studies support the concept of utilizing of *L. temulentum* as a model forage grass for molecular genetic analyses of post-harvest stress.