Genes associated with dormancy release of shortleaf pine auxiliary buds after topkill

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Young shortleaf pine sprouts prolifically after topkill due to a disturbance such as fire. Considerable interest has been shown in shortleaf pine restoration due to continually declining native populations. Shortleaf pine's strong sprouting ability has tremendous potential in promoting its regeneration. However, little is known about its sprouting mechanisms at the molecular level. We designed a microarray experiment to study genes responsible for sprouting ability. In this study one year old shortleaf pine and loblolly pine seedlings were mechanically topkilled, and remaining stem tissues were collected just before sprouting. The shortleaf pine showed extraordinarily strong sprouting ability. Large numbers of sprouts were seen within two days after topkill. However, loblolly pine developed only a few sprouts about one week following topkill. Using microarray gene profiling with about 2400 cDNA clones obtained from suppression subtractive hybridization, 141 differentially expressed genes were found to be associated with the sprouting response, including genes functioning in reserve (carbohydrates and fatty acid) mobilization, transcriptional regulation, stress response, plant development, signal transduction and hormone regulation. Abundant differentially expressed genes were found to be responsible for the dormancy release of auxiliary buds of shortleaf pine leading to sprouting. Far fewer differentially expressed genes were detected for loblolly pine. Shortleaf pine responds actively to topkilling at the molecular level. As reported for dormancy release of buds of other perennial plants, oxidative stress might be the major cause of dormancy release of auxiliary buds of shortleaf pine. Apparent cross talking between plant hormones (especially gibberellin and auxin), carbohydrates and other players of signal transduction leads to cooperative promotion of sprouting of shortleaf pine after topkill.

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