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Differential proteome analysis during early somatic embryogenesis in *Musa* spp. AAA cv. Grand Naine

Abstract

Banana (*Musa* spp.) is well known globally as a food fruit crop for millions. The requirement of quality planting material of banana is enormous. Although mass multiplication through tissue culture is in vogue, high-throughput techniques like somatic embryogenesis (SE) as a mass multiplication tool needs to be improved. Apart from clonal propagation, SE has extensive applications in genetic improvement and mutation. SE in banana is completely genome-dependent and most of the commercial cultivars exhibit recalcitrance. Thus, understanding the molecular basis of embryogenesis in *Musa* will help to develop strategies for mass production of quality planting material. In this study, differentially expressed proteins between embryogenic calli (EC) and non-embryogenic calli (NEC) with respect to the explant, immature male flower buds (IMFB), of cv. Grand Naine (AAA) were determined using two-dimensional gel electrophoresis (2DE). The 2DE results were validated through qRT-PCR. In total, 65 proteins were identified: 42 were highly expressed and 23 were less expressed in EC compared to NEC and IMFB. qRT-PCR analysis of five candidate proteins, upregulated in EC, were well correlated with expression at transcript level. Further analysis of proteins showed that embryogenesis in banana is associated with the control of oxidative stress. The regulation of ROS scavenging system and protection of protein structure occurred in the presence of heat shock proteins. Alongside, high accumulation of stress-related cationic peroxidase and plant growth hormone-related proteins like indole-3-pyruvate monooxygenase and adenylate isopentenyltransferase in EC revealed the association with the induction of SE.

Keywords

Somatic embryogenesis Embryogenic callus Non-embryogenic callus 2DE Protein expression qRT-PCR