

Functional characterization of the oil palm type 3 metallothionein-like gene (MT3-B) promoter.

ABSTRACT

In silico analysis showed that the differentially expressed type 3 oil palm metallothionein-like genes MT3-A and MT3-B share at least 11 common putative promoter regulatory elements. The identified motifs include W-boxes, TATCCA element, binding element for cytokinin response regulators and pollen-specific elements. A high degree of conservation was observed in their genomic organisation where the coding regions are divided at two identical positions in both genes by two AT-rich introns. Promoter activity of the MT3-B gene was analysed using a transient assay by bombarding oil palm tissue slices with a β -glucuronidase (GUS) gene construct and a stable reporter assay by analysing GUS expression in transformed *Arabidopsis thaliana* plants. Transient expression analysis revealed MT3-B promoter activity in oil palm root tissues but not in fruit mesocarp at 12 weeks after anthesis and spear leaves. The T3 homozygous transgenic *Arabidopsis* plants, harbouring the MT3-B promoter/GUS construct, showed reporter activity in cotyledons and mature leaves with lower expression levels in root tissues. The expression levels in the roots of the T3 homozygous transgenic plants increased five- and 2.5-folds when treated with 80 μ M of Zn²⁺ and Fe²⁺, respectively. Altogether, these results indicate that the MT3-A and MT3-B promoter activities may be regulated by a variety of abiotic factors and MT3-B promoter may potentially be manipulated for use in plant genetic engineering for induced synthesis of gene product.

Keyword: *Elaeis guineensis*; Metallothioneins; Promoter analysis; Zn binding; Fe binding.