Erratum to: Development of Vascular Tissue and Stress Inducible Hybrid–Synthetic Promoters Through Dof-1 Motifs Rearrangement

Rajiv Ranjan · Nrisingha Dey

Published online: 7 December 2012
 © Springer Science+Business Media New York 2012

Erratum to: Cell Biochem Biophys (2012) 63:235–245
DOI 10.1007/s12013-012-9359-9

Unfortunately the legends of Fig. 6 and the Fig. 8d were furnished incorrectly in the original publication of the article by mistake. These errors are corrected in this erratum as follows:

1. Corrected legend of Fig. 6:

CLSM assay. **a** Superimposed (bright field and fluorescent) images of transverse section of tobacco petiole expressing GUS in vascular tissue under the control of CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 promoter constructs. **b** Fluorescence images of transverse section of transgenic tobacco petiole expressing GUS in vascular tissue under the control of CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 promoter constructs. **c** Bright field confocal images of transverse section of transgenic tobacco petiole expressing GUS in vascular tissue under the control of CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 promoter constructs

2. Corrected Fig. 8d is presented below.

Fig. 8 JA induction. **a** Tobacco whole seedlings (21 days old) were treated with JA as described in ‘Method’ section. The GUS expression activities from control seedlings (transformed with no GUS), CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 promoter constructs were monitored at 0 and 48 h of post-treatment. The data were presented as mean of three-independent experiments for each construct. Statistical analysis showed a *P* value of <0.003, indicating highly significant. **b** Real-time PCR-based relative of *GUS* transcript accumulation (*uidA*-mRNA) in whole seedlings expressing CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 promoter constructs, 0 and 48 h post-treatment with JA. The data were presented as an average fold differences of *GUS* transcript of two-independent experiments. Each bar represents fold difference in transcript level of the *GUS* gene in transgenic plants in comparison to that obtained in transgenic plants expressing CaMV35S (taken as 1) promoter. **c** Electrophoresis of RT-dependent PCR amplifications of *GUS* transcripts from total RNA (*DNaseI* treated) obtained from transgenic plant expressing CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 constructs. **d** Electrophoresis of RT-dependent PCR amplifications of *GAPDH* transcripts from total RNA (*DNaseI* treated) from transgenic plant expressing CaMV35S, EFCFS, EFCFS-HS-1, EFCFS-HS-2 and EFCFS-HS-3 promoter constructs

The online version of the original article can be found under doi:10.1007/s12013-012-9359-9.

R. Ranjan · N. Dey (✉)
 Division of Gene Function and Regulation, Institute of Life Sciences, Department of Biotechnology, Govt. of India, Nalco Square, Chandrasekherpur, Bhubaneswar 751 023, Orissa, India
 e-mail: dey@ils.res.in; nrisinghad@yahoo.com

R. Ranjan
 e-mail: rajivranjanbt@gmail.com