Name: JERE::GUS

Accessions: H18

Map position:

Gene function: Jasmonic acid (JA) response element (AGACCGCC) fused to gusA gene

Gene effect: Transgenic MT-*JERE::GUS* tissue develops the GUS staining (upon treated with x-gluc substrate) if the tissue accumulates or becomes more sensitive to the hormone JA.

Phenotypes: The plants are resistant to kanamycin, which is the selectable maker in the vector used.

Comments:

Description of accessions available: MT-*JERE::GUS* is derived from genetic transformation (Pino et al. 2010) using the pGPTV-GUS-KAN vector (Rushton et al. 2002), which contains the *gusA* gene under control of the wound and JA inducible promoter.

Figures:



GUS staining of leaf disks excised from MT and three MT-*JERE::GUS* lines. Note the enhanced staining of the disk borders, which correspond to wounded areas.

Bibliography

Pino LE, Lombardi-Crestana S, Azevedo MS, Scotton DC, Borgo L, Quecini V, Figueira A, Peres LEP (2010) The *Rg1* allele as a valuable tool for genetic transformation of the tomato 'Micro-Tom' model system. Plant Methods 6:23.

Rushton PJ, Reinstädler A, Lipka V, Lippok B, Somssich IE (2002) Synthetic plant promoters containing defined regulatory elements provide novel insights into pathogen- and wound- induced signaling. Plant Cell 14:749-762.