Part II

Histological analysis of promoter activity of *XSP30* in transgenic cucumber root

Promoter sequence of XSP30

XSP30 genomic DNA (2242 bp), including promoter sequence, was cloned by TAIL-PCR (Accession No: AB095906). The promoter contained sequence motifs encoding ARFT (-745 to -740 and -393 to -388), which is the auxin-response-factor binding site (Ulmasov *et al.* 1999), GTCONSENSUS (-634 to -630), which is often found in light-regulated genes (Terzaghi *et al.* 1995), ERE (ethylene-responsive element) (-593 to -586) (Montgomery *et al.* 1993), MYBGAHY (-278 to -273), which is a central element of the gibberellin response complex (Gubler *et al.* 1995), and CIACADIANLELHC (-222 to -213), which is necessary for circadian expression of the tomato *Lhc* gene (Piechulla *et al.* 1998) (Fig. 10).

Promoter activity of *XSP30* in the transgenic hairly roots

An 820-bp DNA fragment of the *XSP30* promoter was introduced upstream of GUS in pBI121. GUS activity was analyzed in the hairy roots that emerged from the cut surface of cotyledon transformed with P_{XSP30}::*GUS* (Fig. 11). Strong GUS staining was observed in the vascular system of mature roots (Fig. 12A). The staining intensity gradually decreased in younger portions of the roots (Fig. 12A). No GUS staining was detected at the root cap or in emerging lateral roots (Fig. 12A). Cross sections revealed that *GUS* expression was restricted to the xylem parenchyma and pericycle cells in the central cylinder; GUS staining was not seen in the phloem (Fig. 12, B and C).