Arabidopsis genes found in blueberry

galactinol synthase, beta amylase, LEAs, dehydrins, and early light-inducible protein

not found in Arabidopsis

auxin-repressed protein, protein kinase PINOID, pectate lyase-like protein, and S-adenosylmethionine decarboxylase proenzyme

PINOID is involved in auxin-mediated signaling

In Arabidopsis PINOID has been shown to work in concert with LEAFY to direct forma- tion of the Xoral meristem (Ezhova et al. 2000; Lebed- eva et al. 2005), testifying to an important role of auxin gradients in regulating expression of LEAFY. Its cold- responsiveness has perhaps not been reported before in Arabidopsis because most researchers have used leaf tissue or whole seedlings in cold stress experiments, not Xower buds. Also, the amount of polyamines such as putrescine, spermidine, and spermine increase under environmental stress conditions (Wi and Park 2002). Overexpression of S-adenosylmethionine decarboxyl- ase, a key enzyme in polyamine biosynthesis, has been shown to increase broad-spectrum tolerance to abiotic stresses in transgenic tobacco plants (Wi et al. 2006).

Examples of some of the encoded proteins associated with stress tolerance are phospholipid hydroperoxide glutathione peroxidase, glutathione-S- transferase, metallothionein-like protein type 2, ankyrin-repeat protein, and low temperature-induced 78 kD protein, among many others.

The glycolytic and TCA cycle enzymes, whose messages were upregulated under cold room conditions but not Weld conditions, include phosphoglyceromutase, glyceraldehyde-3-phos- phate dehydrogenase, enolase (induced 1.7–1.9 fold, so not shown in Table2), alcohol dehydrogenase 2 (induced 1.5 fold), malate dehydrogenase, and succi- nate dehydrogenase Xavoprotein alpha subunit (induced 1.8 fold).

Adh2 gene