

improved root growth in plants supplied with insufficient boron. These findings suggest that root growth inhibition resulting from boron deficiency, aluminum and chlorosulfuron toxicity may be a consequence of disrupted ascorbate metabolism.

E207 Salt Tolerance In Spinach Beet

Seung-Gyu Kim^{*}, Yeon-Sik Choo, In-Jung Lee¹ and Seung-Dal Song²

Dept. of Biology, Dongeui University; Dept. of Agriculture, Kyungpook National University¹;
Dept. of Biology, Kyungpook National University²

Growth and photosynthetic activity of spinach beet (*Beta vulgaris* var. *cicla*) and the patterns of glycinebetaine (GB) were studied under different salt conditions. Plants of forty-three days old were assessed by growing for 10 and 20 days at four NaCl concentrations (0, 100, 200, 300 & 400 mM). Shoot biomass was greatest for plants grown at control to 100 mM, and after 10d it was decreased slightly at salinities of 200 mM or higher. In spite of very low tissue K⁺:Na⁺ ratios, however, there were not significant differences in photosynthetic activity in response to NaCl. Salt stress led to a preferential accumulation of GB in shoot of spinach beet, especially at 200 mM NaCl treatment with 10 mM Ca²⁺. These findings suggest that high degree of NaCl tolerance of spinach beet is resulted from the accumulation of GB - known to act as osmoprotectant - in parts, and show that studies on solute compartmentation at the cellular level are required to elucidated the mechanisms by which this plant tolerates very low tissue K⁺:Na⁺ ratios.

E208 Does Transgenic Expression of a Grape UDP-glucose Flavonoid Glucosyl Transferase Gene Affect the Colour Development of Flowers in Tobacco ?

Woo Hyun Jeon^{*}, Horim Lee, Sook Lee, Miok Lee and Jaeho Pyee

Department of Molecular Biology, Dankook University

Anthocyanin is flavonoid, a phenolic compound, responsible for most of the colours in various plant organs and the enzymes and genes involved in the biosynthetic pathway have been isolated and characterized in maize, petunia, snapdragon, apple and grape. However, the regulation of the anthocyanin biosynthesis has not been fully understood. Grape berry was chosen as a system to elucidate the mechanism of regulation of gene expression, in which the pigment accumulates only in berry skin. Of seven genes, only the UDP-glucose flavonoid glucosyl transferase(ufgt) -encoding gene was reported to be differentially regulated in grape berries: the ufgt gene was expressed only in berry skin, while the others in both skin and flesh. We isolated a ufgt cDNA clone from grape berries and analyzed its expression profiling in red and yellow grape varieties. The open reading frame of the ufgt cDNA was ligated in pBI121 vector in a sense or an antisense orientation under the control of the CaMV 35S promoter and the recombinant constructs were incorporated into tobacco. Several transgenic lines are being selected and characterized to test whether over-expression or repression of the ufgt gene affects the anthocyanin content. We also isolated a genomic clone and analyzed the nucleotide sequence of the promoter region in order to determine the regulatory elements involved in the environmental response and skin-specific expression of the ufgt gene.

E209 Molecular cloning and complementation of nif V gene from Frankia EulK1 strain

Chang Jae Oh^{*} and Chung Sun An
School of Biological Science, Seoul National University, Seoul 151-742, Korea

Frankia, a gram-positive actinomycete, can establish a nodule symbiosis with eight families of angiosperms, collectively called actinorhizal plants. Among the genes involved in the nitrogen fixation, *nif V* encodes the homocitrate synthase and its catalytic product, homocitrate, is associated with the FeMo-cofactor, the component of the nitrogenase complex. Although many *nif* genes from *Frankia* EuK1 strain, a symbiont of *Elaeagnus umbellata*, were cloned and characterized, *nif V* was not. So, in this study, *nif V* from *Frankia* EuK1 strain was cloned and functional complementation was designed. The *nif V* ORF, consisting of 1245bp, started at ATG and terminated at TGA. Unusually, it wasn't organized in clusters with other *nif* genes and a putative promoter, the Shine-Dalgarno sequences were not found, either. The deduced amino acid sequence revealed high similarities with NifV proteins from other organisms available in database, with values ranging from 60.43% (*Azospirillum brasilense*) to 80.42% (*Frankia* sp. FaC1) and also had two conserved regions of NifV proteins. The phylogenetic tree based on amino acid sequence similarities supported the possibilities that three *Frankia* species would be closely related and be grouped with other γ -class Proteobacteria. To verify its function, the complementation test using *Klebsiella pneumoniae* mutants is in progress.

E210 Expression patterns of two ω -3 fatty acid desaturases from hot pepper and overexpressed plants analysis under cold and heat stresses.

Jeom A Kim* and Chung Sun An
School of Biological Science, Seoul National University, Seoul 151-742, Korea

ω -3 fatty acid desaturases (FAD) are enzymes that increase the content of trienoic fatty acid by introducing double bonds into fatty acyl chains. Trienoic fatty

acids have been known to be important not only for low temperature acclimation, but also for precursors of plant pathogen defense-related signaling molecules. These imply that regulation of trienoic fatty acid level is involved in the defense response of higher plant cells to environmental stresses. In this study, To know the expression patterns of chloroplast ω -3 fatty acid desaturase (chFAD) and microsomal ω -3 fatty acid desaturase (mFAD), isolated from *Capsicum annuum*, we treated environmental stresses such as cold and heat. Benzyl alcohol (membrane fluidizer) and dimethyl sulfoxide (membrane rigidifier) were also used to examine the relationship between membrane fluidity and induction of the desaturase synthesis. ChFAD transcription level was decreased under heat and benzyl alcohol treatments but increased under light. mFAD transcription level was not changed under heat and light. ChFAD and mFAD was not affected by cold (4?) treatment during short times. Moreover, To know the functions of two genes, we overexpressed two fatty acid desaturase genes in *Arabidopsis thaliana* and will investigate the responses to cold or heat of transgenic plants.

E211 Salt 스트레스가 근대의 내생 Gibberellins, Abscisic acid 및 Jasmonate 함량에 미치는 영향

김미향¹, 남재원¹, 장수원¹, 송승달², 추연식³, 이인중¹

¹경북대학교 농학과; ²경북대학교 생물학과; ³동의대학교 생물학과

Salt 스트레스에 대한 식물체의 적응 메커니즘을 구명하기 위한 일환으로 내염성 식물로 알려져 있는 근대(*Beta vulgaris* subsp. *cicla* L.)를 이용하여 식물체내의 내생호르몬 생합성(Gibberellins(GA), Abscisic acid(ABA), Jasmonic acid(JA))에 미치는 salt의 영향을 조사하였다. Salt처리를 한 근대의 지상부 생체시료에 내부표준물질로 (ω)-3,5,7,7-d₆ ABA와 [9,10-²H₂]JA 및 [²H₂ GA₁, ²H₂ GA₁₂, ²H₂ GA₁₉, ²H₂ GA₂₀, ²H₂ GA₅₃]를 일정량 첨가하여 각각의 호르몬을 분리한 후