E229 Marmesin, a UV Absorbing Compound from Barks of Thanakha

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From barks of Thanakha(*Hesperethusa crenulata* L.), an active compound for absorbing UV A(320-360㎚) was isolated as a crystal by solvent extractions, SiO_2 column chromatographies and HPLC. Analyses of low and high resolution FAB MS revealed that the molecular weight of the active compound is 246 whose formula is $C_{14}H_{14}O_4$. To determine the chemical structure of the active compound, 300㎒ NMR analyses using various probes, ^1H, ^{13}C, DEPT ^{13}C, ^1H-^1H COSY and ^1H-^{13}C COSY were carried out. NMR data provided that the structure of the active compound is 2,3-dihydro-2(1-hydroxy-1-methyl)-furocoumarin, marmesin. Marmesin contained UV absorbing chromophores, an aromatic ring, a double bond at C3-C4 and a carbonyl at C2 in the structure. The λmax of marmesin was 335㎚, indicating that marmesin could be commercially useful for a natural UV A filtering compound as it is. Also, it is thought that marmesin can be used as a leading compound to synthesize more strong UV A filtering compounds by structural modifications.

E230 Isolation and charactrization of cDNA encoding proteins which interacts with a novel bZIP protein STF1 using yeast two hybrid system

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The hypocotyl elongation of dicotyledonous seedlings is widely used as a mode of the physiological study of the mechanism of cell elongation and a vareity of biological events that participate in its control. Light is a key determinat that control hypocotyl elongation causing rapid inhibition of hypocotyl elongation of dark grown seedlings. Arabidopsis *hy5* is a mutant defective in a bZIP factor involved in the activation of light regulated genes and the inhibition of hypocotyl elongation by light. We have previously reported a novel bZIP factor, STF1, which carries a zinc-finger motif and a bZIP domain which can heterodimerize with GBF proteins of soybean. The identification of two separate domains in STF1 which show identity to the N-terminus of cellulose synthase and HY5 protein led us to study proteins interacting with STF1 in soybean.
Using STF1 as bait in a yeast two-hybrid screen, we identified 14 distinct classes of soybean genes that interact with STF1. Among them one class, SIF1(STF1 interacting protein 1) comprise major SIFs and showed high sequence identity to a salt induced Arabidopsis zinc-finger protein STO and CONSTANS. Further analysis will be directed to the understanding of molecular mechanism of STF1 and SIF1 interaction and functional significance involved in this molecular interaction.