

M-131

Transcriptomic profiling of genes involved in epicatechin biosynthesis in soybean
*Myoyeon Kim**, Applied Technology and Research Division, Amorepacific, Gyeonggido,
Republic of Korea

Jungmin Ha, Department of Plant Science, Seoul National University, Seoul, Republic of
Korea

Moon Young Kim, Department of Environmental Engineering, Seoul National University,
Seoul, Republic of Korea

Min Young Yoon, Seoul National University, Seoul, Republic of Korea

Proanthocyanidins are oligomeric or polymeric end products of flavonoid metabolism starting from central phenylpropanoid pathway. Because the presence of proanthocyanidins in crop species has double-sided effects depending on their agricultural or commercial usage, regulation of proanthocyanidins has become a target of breeding and genetic modification. Epicatechin and catechin are the building blocks of proanthocyanidins, of which epicatechin is more common extension unit and starter unit in the plant species. Soybean seeds have been utilized as ingredients for healthful human diet and cosmetic formulas because they are rich in flavonoid metabolites including isoflavonoids, anthocyanins and proanthocyanidins. Although it has been shown that there are large variations in proanthocyanidin contents among soybean genotypes, genetic regulatory mechanisms in biosynthesis of proanthocyanidins in soybean still remain unclear. We evaluated interspecific and intraspecific variability in flavonoid component contents using 43 cultivated, landrace and wild soybeans. Transcriptomic profiling of genes for enzymes involved in flavonoid biosynthesis was conducted using three soybean genotypes, Hwangkeum (cultivated), IT109098 (landrace) and IT182932 (wild) at two developmental stages of R5 and R7. Among three genotypes, more genes were differentially expressed in seed sample at R5 stage, compared to leaf sample and R7 stage. Among 367 genes in flavonoid biosynthetic pathway, 153 genes were identified as differentially expressed genes (DEGs). Different homologous genes for anthocyanidin synthase (ANS), 3-O-glucosyltransferase (3GT) and anthocyanidin reductase (ANR), the enzymes that derive end products of flavonoid metabolism, were detected as DEGs between wild and cultivated soybeans and between landrace and cultivated soybeans. Our results provide primary insights on underlying genetic variations for proanthocyanidin biosynthesis between cultivated, landrace and wild soybeans.