

B-09

Profile analysis: an excellent tool for breeding seed saponin composition in soybean
*Chigen Tsukamoto**, Department of Applied Biological Chemistry, Iwate University,
Iwate, Japan

Yuya Takahashi, Department of Applied Biological Chemistry, Iwate University, Iwate,
Japan

Ayaka Ito, Biological Chemistry and Food Sciences, Iwate University, Iwate, Japan

Kejing Wang, Chinese Academy of Agricultural Sciences, Beijing, China

Soyasaponins, a group of triterpene glycosides, consist of more than 200 natural secondary metabolites in soybean seeds and affect to the taste and health promoting attributes of soyfoods. Seed saponin composition shows genetic polymorphism and genetic modification is possible, but biosynthetic pathways of soyasaponins are not completely revealed. Profile analysis is an attractive tool not only to elucidate the chemical structures of new and unknown saponin components accumulated in mutant seeds but also to estimate their biosynthetic pathways. Profile analysis has been used to identify some mutant phenotypes and estimate their biosynthetic pathways from soybean (*Glycine max* (L.) Merr.) seeds treated with a chemical mutagen Ethyl-methanesulfonate (EMS) in Japan and Korea. Profile analysis of 3,805 wild soybean (*Glycine soja* Sieb. and Zucc.) accessions collected in China identified additional 7 different phenotypes. They accumulated large amounts of; 1) group E saponin E-ag (soyasaponin Bd) (2 accessions); 2) Sg-6 saponin H-ag without I-ag nor J-ag (16 accessions); 3) Sg-6 I-ag without H-ag nor J-ag (69 accessions); 4) Sg-6 J-ag without H-ag nor I-ag (66 accessions), new saponins; 5) K-ag (29-acetyl H-ag; 22 accessions); 6) HAb-ag (29-hydroxyl Ab; 1 accession), and group A saponin precursor; 7) A-ag with its acetyl derivative KA-ag (29-O-acetyl A-ag; 1 accession). A total of 177 mutant accessions corresponded to 4.65% of Chinese wild soybean collections. From crossing these mutant lines, we have identified 21 different seed saponin phenotypes, which can be used to clarify saponin biosynthetic pathways and to breed new soybean varieties having different saponin composition.