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Comparative Analysis of *PfFAD3-1* Transgenic Soybean Seeds using LC-MS Untargeted Metabolite Profiles

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PfFAD3-1 transgenic soybean line (#10, 11, 12) accumulates higher linolenic acids by expressing omega-3 fatty acid desaturase 3-1 gene (*FAD3-1*) of *Physaria*. To assess compositional equivalence of *PfFAD3-1* transgenic soybean lines in the range of natural variation, LC-MS untargeted metabolite profiles of transgenic soybean lines were compared with those of a parental line, Kwangan, and commercial varieties grown at Gunwi and Jeonju in 2021 and 2022 year. The PLS-DA score plot by varieties revealed that *PfFAD3-1* lines grouped with Kwangan but separated from commercial varieties, indicating similar levels of metabolites of *PfFAD3-1* and Kwangan. The PLS-DA score plots by growth year at each location showed clear separation of soybean data between 2020 and 2021. These results indicate that the metabolic compositions in soybean seeds could be altered by year as well as by genotype. Besides, metabolites significantly different between transgenic lines and Kwangan except with fatty acids were different by growth location and years, exhibiting the levels of metabolites were significantly influenced by growth environments. Overall, the contents of isoflavones in *PfFAD3-1* line decreased compared to Kwangan, although the magnitudes of their differences were small. We are currently studying for the biosynthetic network between fatty acids and isoflavones in soybean seeds to explain responsible factors for the difference.

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