

Exploring the Strategy to Identify Seed-Specific Acyl-Hydrolases from *Arabidopsis thaliana* by Activity-Based Protein Profiling

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Abstract : Vegetable oils mainly triacylglycerol (TAG) are an essential nutrient in the human diet as well as one of the major global commodity. There is a pressing need to enhance the yield of oil production to meet the world's growing demand. Oil content is controlled by the balance between synthesis and breakdown in the cells. Several studies have established to increase the oil content by the overexpression of oil biosynthetic enzymes. Interestingly the significant oil accumulation was observed with impaired TAG hydrolysis. Unfortunately, the structural, as well as the biochemical properties of the lipase enzymes, is widely unknown, and so far, no candidate gene was identified in seeds except sugar-dependent1 (SDP1). Evidence has shown that SDP1 directly responsible for initiation of oil breakdown in the seeds during germination. The present study is the identification of seed-specific acyl-hydrolases by activity based proteome profiling (ABPP) using *Arabidopsis thaliana* as a model system. The ABPP reveals that around 8 to 10 proteins having the serine hydrolase domain and are expressed during germination of *Arabidopsis* seed. The N-term sequencing, as well as LC-MS/MS analysis, was performed for the differentially expressed protein during germination. The coding region of the identified proteins was cloned, and lipases activity was assessed with purified recombinant protein. The enzyme assay was performed against various lipid substrates, and we have observed the acylhydrolase activity towards lysophosphatidylcholine and monoacylglycerol. Further, the functional characteristic of the identified protein will reveal the physiological significance the enzyme in oil accumulation.

Keywords : lipase, lipids, vegetable oil, triacylglycerol

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