

Agricultural Science: Crop breeding, Genetics and Genomics Discovery of Novel Oleate Desaturase Gene in Genus *Crambe*- A Wild Relative of Brassica

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Abstract

In higher plants, fatty acids, such as oleic acid (C18:1), stearic acid (18:0) etc. are synthesized *de novo* inside plastids. After its synthesis it is exported outside of plastids and 18:1 may undergo desaturation and/ or elongation by ER resident enzymes. During desaturation the 18:1 gets converted into 18:2 (Linoleic acid) by oleate desaturase (FAD2) and subsequently to 18:3 (Linolenic acid) by omega-3 desaturase (FAD3). Based on the function of oleate desaturase, the silencing of the *FAD2* gene is expected to enhance the levels of 18:1. *Crambe* genus has much higher level of erucic acids (22:1) and low level of oleic acid in their seed oil. The high erucic acid in seed is nutritionally undesirable property. To enhance the level of nutritionally important oleic acid, an understanding of *FAD2* gene is important to modulate the level of 18:1 in oilseed of *Crambe*, which is a wild relative of brassica. The full length coding sequences (CDS) of *FAD2* were amplified from different *Crambe* germplasm and cloned subsequently. The sequence verified clones of *FAD2* gene revealed ORFs of 1152 and 1155 bp in accessions of *C. abyssinica*, *C. kralikii* and *C. filiformis*. However in *C. glabrata* ORF of only 1152 bp was found. The *FAD2* ORFs of 1155 bp was not reported earlier and thus constitute novel finding. The sequences of twenty five full length CDS of putative functional oleate desaturase gene were submitted to NCBI (KJ573471 to KJ573495). The sequence analyses have also revealed several SNPs among *FAD2* of various accessions of *Crambe* germplasm. In addition to above functional oleate desaturase gene, several pseudogene were also identified. Such results indicate that mining valuable natural genetic variation in *FAD2* is a promising approach to breed lines with a changed oil composition.