

# Agricultural Science: Crop breeding, Genetics and Genomics Allelic Diversity in FAE1 gene of Indian mustards (*Brassica juncea*)

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## Abstract

Fatty acid (FA) biosynthetic pathway in higher plant that leads to accumulation of FAs in seed oil is well studied. The oleic acid (C18:1) upon its synthesis is transported to the cytosol and activated to C18:1-CoA and then incorporated in the ER. In cytosol, C18:1 may undergo either elongation to erucic acid (C22:1) in a reaction involving a 3-ketoacyl-CoA synthase (KCS1, also known as fatty acid elongase 1, FAE1) or desaturation to linoleic acid (C18:2) and subsequently to linolenic acid (C18:3) through the action of microsomal enzymes delta-12-fatty acid desaturase (FAD2) and delta-15-fatty acid desaturase (FAD3), respectively. Therefore, final composition of FAs in seed oil is primarily determined by the activities and interplay of desaturases and elongases. Erucic acid in seed oil of *Brassica juncea* is nutritionally undesirable property because of its reported health concern. In the present work, the full length coding sequences (CDS) of *FAE1* gene of released varieties of *Brassica juncea* was amplified and cloned in TA vector. The expected size (~1.5kb) of cloned *FAE1* gene was further verified by pcr using vector-born primers. The sequence analyses revealed two different type of *FAE1* gene i.e. *FAE1*-A and *FAE1*-B in most of the varieties. *Brassica juncea* (AABB) is amphidiploid and composed of genome of both *Brassica rapa* (AA) and *Brassica nigra* (BB). Therefore, occurrence of two types of *FAE1* gene in the Indian mustard varieties was not surprising. The *FAE1* gene sequences of nine varieties have been submitted to NCBI (KP074949-KP074963). Based on present finding, among the varieties there was insignificant variation in *FAE1* gene, either at the level of nucleotide or its predicted protein level as the identities among themselves were more than ~94%. The present study suggests that among the released varieties of Indian mustard there is meager allelic variation among them based on *FAE1* gene sequence.