International Journal of Advance Research in Science and Engineering
Vol. No.4, Special Issue (01), September 2015
www.ijarse.com
IJARSE
ISSN 2319 - 8354

DIVERSITY IN OLEATE DESATURASE GENE OF INDIAN MUSTARD (BRASSICA JUNCEA)

Rajesh Kumar[1], J Radhamani[2], S Rajkumar[3]

[1,2,3]*ICAR-NBPGR (National Bureau of Plant Genetic Resources), New Delhi (India)*

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). The final composition of fatty acids in seed oil is determined by interplay above enzymes together with FAE1 which synthesizes erucic acids (22:1). Based on the function of oleate desaturase, the silencing of the *FAD2* gene is expected to enhance the levels of 18:1. In the present work, the full length coding sequences (CDS) of *FAD2* gene of released varieties of *Brassica juncea* was amplified and cloned in TA vector. The expected size (~1.1 kb) of cloned *FAD2* gene was verified by pcr using vector-born primers. Further analyses of their sequence revealed typical *FAD2* gene (1155 bp) types i.e. *FAD2*-A and *FAD2*-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 *FAD2* gene in the Indian mustard varieties was not surprising. In addition, a novel type of *FAD2* gene was also identified which was longer (12 bp more) than typical *FAD2* and predicted to encode functional protein of 388 amino acids. It would be interesting to explore the role of such novel *FAD2* gene. Besides functional *FAD2* gene, pseudogenes were also identified among the varieties whose predicted protein contained internal stop codons. However, the present finding does indicate insignificant allelic variation in *FAD2* gene among the varieties.