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# OIL REGULATORY GENES OF BRASSICA JUNCEA (INDIAN MUSTARD): A REVIEW

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**Abstract**

Improvement in seed oil content is a major target of plant breeders and biotechnologists worldwide. Import of edible oil in our own country to meet our demand-supply gap cost several thousands of crores in valuable foreign exchange. Therefore development of strategies to increase oil content of oilseed crops is of paramount importance. Brassica species comprise oilseed and a variety of vegetable crops. In the Indian subcontinent, Brassica juncea (Indian mustard) is the major oilseed crop after groundnut.Oil is mostly accumulated in seeds in the form of Triacylglycerols (TAGs). These TAGs are synthesized from fatty acyl-CoA and glycerol-3-phosphate in the endoplasmic reticulum of the cell. Fatty acids are exclusively synthesized in the plastids from acetyl-CoA and then transported in the form of fatty acyl-CoA to the cytoplasm. TAGs are synthesized by the stepwise acylation of glycerol-3-phosphate in the endoplasmic reticulum, (Kennedy pathway). Phosphatidic acid is formed from glycerol-3-phosphate with the help of two enzymes, glycerol-3-phosphate acyltransferase and lyso-phosphatidic acid acyltransferase, which add fatty acyl moieties to the sn-1 and sn-2 positions of glycerol-3-phosphate respectively. Phosphatidic acid is hydrolysed by the enzyme phosphatidate phosphahydrase to give diacylglycerol (DAG). TAGs are synthesized by the addition of a third acyl chain to DAG by the enzyme diacylglycerol acyltransferase.

**Key words**: Brassica juncea, GL2, DAG, TAG

## Introduction

Brassicajuncea, Indian oilseed mustard, is an important oilseed crop of the country. This crop is grown in the north-western region of India in around six million hectares of land during the winter growing season either under completely rainfed or with limited irrigation. The average yields of the best check varieties in India are around 2.2 tonnes per hectare. Therefore even minor improvement in the quality and yield of this crop would markedly improve the income of our farming community. B. juncea (AABB genome) is an allopolyploid species produced by crosses between two diploid species viz.B. rapa (AA genome) and B. nigra(BB genome). The existence of two distinct and genetically diverse gene pools namely, the east European and the Indian gene pools in B. juncea, has been reported earlier[1] had shown that the lines belonging to the Indian gene pool show B. rapa (AA) like characters whereas those belonging to the east European gene pool show closeness to B. nigra (BB) for many agronomic and yield influencing traits. However, the east European lines, which are generally tall and late in maturity, are poor yielders as they are ill adapted to winter growing conditions of the Indian subcontinent.

Recent studies on QTL mapping of oil content under zero-erucic conditions in B. juncea, identified two novel loci on linkage groups A2 and A3 that explain ~19% phenotypic variance for oil content.Using a syntenous map developed between the model plant, Arabidopsis, and B. juncea[3] comparative analysis of the above QTL regions had identified two potential candidate genes for oil content WRI1 and GLABRA2[2].

Extensive studies done previously in Arabidopsisshowed that the GL2 gene is involved in the development of normal trichomes, atrichoblasts, seed coat epidermal cells and limits hair formation in roots in addition to controlling seed oil content[3][4][5][6]. Studies on gl2 mutant plants showed deviation from the normal expansion of trichomes. Most trichomes found on the mutant plant were either enlarged abortive epidermal cells that expanded in the plane of the leaves or they were un-branched spikes. The trichome wall did not appear to be thickened and neither did they acquire papillae[5].

A number of genes upstream to GL2 gene have been identified that positively regulate the expression of GL2 thus controlling trichome and root hair development. For normal trichome initiation, a myb-type transcription factor encoded by GLABRA1 (GL1) gene and a WD40 protein encoded by TRANSPARENT TESTA GLABRA 1 (TTG1) gene are required. Complete loss of leaf trichome initiation resulted due to loss of function mutations in gl1 and ttg1 mutants of Arabidopsis[7]. The double mutants, gl2 gl1 and gl2 ttg also lack trichomes showing that the GL2 gene acts downstream to GL1 and TTG genes. Further, the level of GL2 expression in ttg roots was reduced, suggesting that the TTG gene plays a role in up-regulating GL2 expression [8]. Similarly GLABRA 3 (GL3) and ENHANCER OF GLABRA 3 (EGL3) are two homologous genes encoding bHLH transcription factors and gl3/egl3double mutants showed a complete loss of trichome development [5].

In addition to the above, GL2 is also required in the development of seed coat epidermis, and seed coat mucilage biosynthesis. The latter role is executed through positive control of the MUCILAGE MODIFIED 4 (MUM4/RHM2) gene [9], which encodes the rhamnose synthase enzyme required to produce rhamnose, a key substrate for mucilage biosynthesis. Recent studies showed that mucilage deficient gl2 seeds of Arabidopsis produce more oil and MUM4 is a downstream target of GL2 gene. MUM4 activity along with GL2 is required for normal seed oil accumulation in the seed coat. However, loss of function of MUM4 resulted in mucilage deficiency leading to higher seed oil content. The phenotype of gl2/mum4 double mutant was similar to that of both parents suggesting that both GL2 and MUM4 function in the same pathway influencing seed oil biosynthesis. These studies strengthen the concept that GL2 negatively regulates seed oil content by positively regulating MUM4. However it is still not clear whether GL2 directly targets and regulates MUM4 or other downstream intermediate genes are also involved in seed oil biosynthesis. Shi et al. (2012)

studied the seed oil content of various mutants like TTG1, TTG2, MYB5, TT2, EGL3, TT8, GL2 and MUM4, which were disrupted in components of the regulatory pathway for mucilage production. Their results showed that the oil content of ttg2 seeds was comparable to that of the wild type, suggesting that it is not just the deficiency or loss of mucilage that results in over production of seed oil but in fact, is the loss of MUM4 function that is responsible for higher seed oil content.

The GL2 gene encodes a homeodomain (HD) transcription factor, belonging to the class IV homeodomainleucine zipper (HD-ZIP) gene family, based on its protein sequence[4]. Homeodomain proteins are transcription factors which function during diverse developmental processes, to coordinate the expression of several target genes (reviewed by Kessel and Gruss, 1990; Gehring et al., 1994). At least fifteen homeodomain proteins are known to be present in Arabidopsis[4]. The HD-Zip group, to which GL2 geneis most closely related, contains towards its N terminus, a homeodomain which is then followed by an amphipathic alpha helical domain [10]. Under in vitro conditions, the alpha helical region of GL2 is capable of interacting with itself. GL2 encodes an additional 527 amino acid residues towards the C-terminal of the helical domain. Although this region does not contain any recognizable motifs, other genes that show significant similarity to the C-terminal domain of GL2 have been identified. For example, GL2 and Arabidopsis Thaliana Meristem Layer 1 (ATML1) genes are 37% identical throughout their sequence but 60% identical in the homeodomain[11]. GL2 also shares C-terminal sequence similarity to homeodomain genes from Phalenopsis, Helianthus and Panicum.

**Conclusion**

The expression of GL2 gene in each cell type is activated by a transcription complex which includes polypeptides from three classes of transcriptional regulators. A WRKY transcription factor TRANSPARENT TESTA GLABRA 1 (TTG1), a basic helix-loop-helix (bHLH) transcription factor and a MYB transcription factor[9][11].

**References**

1. Srivastava A, Gupta V, Pental D, Pradhan AK (2001). AFLP-based genetic diversity assessment amongst agronomically important natural and some newly synthesized lines of Brassica juncea. TheorAppl Genet 102:193–199.
2. Jagannath A, Sodhi Y.S., Gupta V., Mukhopadhyay A., Arumugam N., Singh I., Rohatgi S., Burma P.K., Pradhan A.K., Pental D. (2011). Eliminating expression of erucic acid-encoding loci allows the identification of “hidden” QTL contributing to oil quality fractions and oil content in Brassica juncea (Indian mustard). TheorAppl Genet 122:1091-1103.
3. Koornneef, M., Dellaert, L.W. and van der Veen, J.H. (1982). EMS- and radiation-induced mutation frequencies at individual loci in Arabidopsis thaliana (L.) Heynh. Mutat. Res. 93, 109–123.

4. Rerie, W.G., Feldmann, K.A. and Marks, M.D. (1994) The GLABRA2 gene encodes a homeo domain protein required for normal trichome development in Arabidopsis. GenesDev. 8, 1388–1399.
5. Szymanski, D.B., Jilk, R.A., Pollock, S.M. and Marks, M.D. (1998) Control of GL2 expression in Arabidopsis leaves and trichomes. Development, 125, 1161–1171.
6. Masucci, J.D., Rerie, W.G., Foreman, D.R., Zhang, M., Galway, M.E., Marks, M.D. and Schiefelbein, J.W. (1996). The homeobox gene GLABRA2 is required for position-dependent cell differentiation in the root epidermis of Arabidopsisthaliana. Development, 122, 1253–1260.
7. Shen, B., Sinkevicius, K.W., Selinger, D.A. and Tarczynski, M.C. (2006) Thehomeobox gene GLABRA2 affects seed oil content in Arabidopsis. PlantMol. Biol. 60, 377–387.
8. Di Cristina, M., Sessa, G., Dolan, L., Linstead, P., Baima, S., Ruberti, I. and Morelli, G. (1996). The Arabidopsis Athb-10 (GLABRA2) is an HDZip protein required for regulation of root hair development. PlantJ. 10, 393-402.
9. Western, T.L., Young, D.S., Dean, G.H., Tan, W.L., Samuels, A.L. and Haughn, G.W. (2004) MUCILAGE-MODIFIED4 encodes a putative pectin biosynthetic enzyme developmentally regulated by APETALA2, TRANSPARENTTESTAGLABRA1, and GLABRA2 in the Arabidopsis seed coat. Plant Physiol. 134, 296–306.
10. Kerstetter, R., Vollbrecht, E., Lowe, B., Veit, B., Yamaguchi, J. and Hake, S. (1994). Sequence analysis and expression patterns divide the maize knotted1-like homeobox genes into two classes. Plant Cell 6, 1877-1887.
11. Lu, P., Porat, R., Nadeau, J. and O'Neill, S. (1996). Identification of a meristem L1 layer-specific gene in Arabidopsis that is expressed during embryonic pattern formation and defines a new class of homeobox genes. Plant Cell 8, 2155-2168.