ABSTRACT

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Title: BIOINFORMATIC ANALYSIS OF SOME PLANT GLUTAMATE RECEPTOR LIKE GENES FROM FAMILY BRASSICACEAE

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Plant Glutamate receptor like channels (GLRs) are homologous to Ionotropic glutamate receptors (iGluRs) that mediate neurotransmission in mammals. GLRs are nonselective cation channels involved in various physiological processes. Thus, knowledge about *GLR* genes is crucial which can lead to effective way of improving agronomic traits in crop plants. The plant family Brassicaceae possess the model plant *Arabidopsis thaliana* as well as some major crops of the genus *Brassica*. *A. thaliana* possesses 20 *GLR* genes (*AtGLR*s) in its genome which are involved in many functions including light signal transduction and calcium homeostasis. This study reports the physico-chemical, structural and functional aspects of GLRs of *A. thaliana* as well as three important crops *i.e. B. napus*, *B. rapa* and *B. oleracea*. Gene ontology analysis showed the participation of AtGLRs in various biological processes including different stress responses. This study have identified 11, 27 and 65 *GLR* genes in *B. oleracea*, *B. rapa* and *B.napus*, respectively showing an expansion of this gene family in *B. napus*. Chromosomal locations revealed several tandemly duplicated *GLR* genes in all the three species. The phylogenetic analysis showed that the GLRs are classified into three main groups. The exon-intron structures of these genes are not very conserved and showed wide variation in intron numbers. However, protein sequences are much conserved as shown by the presence of ten short amino acid sequence motifs. Predicted *cis*-acting elements in promoters of *GLR* genes are mainly involved in light, stress and hormone responses. RNA-seq analysis showed that in *B. oleracea* and *B. rapa*, some *GLRs* are more tissue specific than others. In *B. napus*, some *GLRs* are differentially expressed under cold stress. The three-dimensional structure of GLRs has been developed *in silico* by homology modeling. The modeled proteins were predicted to be membrane bound homo tetramers with a three-layer domain architecture. This bioinformatic study will act as a platform to gain knowledge about the structure-function relationship of plant GLRs.

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