In silico analysis of miRNAs Targeting Genes of Sulphur Assimilation Pathway in *Brassica juncea*

Sadia Iqrar[1], Kudsiya Ashrafi[2], Monica Saifi[3] and Prof. M.Z. Abdin[4]

*Centre for Transgenic Plant Developement, Dept. of Biotechnology, School of Chemical and Life
Sciences, Jamia Hamdard, Hamdard Nagar, New Delhi-110062
E-mail: [1]sadiaiqrar@gmail.com, [2]kudsi18@gmail.com,
[3]monica.saifi@gmail.com, [4]mzabdin@rediffmail.com*

Abstract—*Brassica juncea(Indian mustard) is the third important oilseed crop in the world after soybean (Glycine max). It has a high demand of sulphur (25 to 50kg/ha) as compare to other crops (15 to 30kg/ha). It is one of the most susceptible crop to sulphur shortage, and that it responds well to sulphur fertilization in terms of yield. A recent trend in fertilizer is the use of high analysis urea, diammonium phosphate and triple superphosphate resulting in very little addition of sulphur to the soil. These changes have resulted deficiency of sulphur in mustard crop but the application of fertilizers always is not a remedy for this problem. To overcome deficiency of sulphur in Indian mustard we can manipulate sulphur assimilation pathway using microRNA approach. MicroRNAs (miRNAs) are a class of short endogenous non-coding small RNAs. Increasing evidence shown that miRNAs play multiple roles in biological processes,including development, metabolism and stress responses. However, whether miRNAs are involved in the sulphate deficiency in Brassica juncea is unknown. In this study, we did computational prediction of the target genes for miRNAs involved in Sulphur uptake and assimilation pathway using psRNAtarget analyser. A total 39 miRNAs belonging to 10 conserved families, which were found to be targted the genes of sulphur uptake and assimilation obtained from psRNAtarget analyser and 100 miRNA attain from miRBAse were again targeted against those genes using miRanda database tool with detailed stastical study of minimum free energies (MFEs). The prediction was made using miRanda with default parameters. This study provides a set of miRNAs targeting genes of sulphur uptake and assimilation pathway which can further utilize to manipulate sulphur assimilation pathway in Brassica juncea.*