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Expression profiling of transporter genes in relation to glucosinolate accumulation in vegetative and reproductive sinks of Brassica juncea

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The phloem mobility of glucosinolates (GLSs) from vegetative to reproductive sinks require involvement of two proton dependent transporters belonging to nitrate peptide transporter family, GLS transporter 1 and 2 (GTR1 and GTR2). In the present communication, we report our efforts to assess the expression patterns of GLS transporter genes in relation to organ specific distribution of GLSs in ten genotypes of mustard with contrasting leaf and seed GLS levels. GLS content increased progressively at anthesis (11.17-24.91 µmoles/g DW), 3 days after fertilization (DAF) (16.3-35.72 µmoles/g DW) and immature siliques at 14 DAF (21.9-69.14 µmoles/g DW). These was followed by a decline in GLS content in silique walls at 21 DAF (17.63-42.69 µmoles/g DW) and 30 DAF (9.01-32.68 µmoles/g DW). GLS was maximum in mature seeds (24.32 to 123.45 µmoles/g defatted meal). A decline in GLSs in silique walls concomitant with their accumulation in mature seeds may indicate active GLSs switch from siliqua walls to the maturing seeds. Fold changes in GTR1 and GTR2 gene expressions were higher in silique walls at 21 and 30 DAF in contrast to other tissues at earlier developmental stages, underlining the potential role of transporter genes in tissue specific allocation of GLSs. The expression of GTR1 in leaves was more in high GLS lines compared to low GLS, suggesting the role of GTR1 in distribution of GLS within the leaves. Sinigrin was most abundant in leaves, whereas, gluconapin was more important GLS in seeds. Possibly, glucoerucin synthesis was maximum at the time of maturity. Our studies may help in identification of alternate pathway of GLS reduction seeds while retaining their biological function in the rest of the plant.