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Shikimate representatives and Catalase (CAT2) are possible determinants of resistance to mustard aphid infestation in Brassica fruticulosa

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Brassica fruticulosa, a wild crucifer, is a known source of resistance against cabbage aphid (Brevicoryne brassicae) and mustard aphid (Lipaphis erysimi) infestation. Lack of aphid resistance in cultivated Brassicas led our group to introgress genomic fragments responsible for aphid resistance from B. fruticulosa into the susceptible background of B. juncea (RLC-1). These introgression lines (ILs) showed excellent variation for resistance to mustard aphid infestation. Deep analysis of this resistance necessitates identification of defensive genes and development of functional markers for marker assisted gene transfer into superior agronomic backgrounds. To facilitate this, we employed mRNA sequencing and de novo RNA-Seq technologies for identification of defensive transcripts that were unique between B. fruticulosa and B. juncea cv. RLC-1. Leaves at vegetative stage of both the speciesand ten ILs (categorized as resistant or susceptible) were collected and outsourced for transcriptome sequencing. The clean reads were assembled and sequences of novel transcripts were subjected to gene prediction, mapping, annotation and KEGG analysis. A total of 28,427 genes in B. fruticulosa and 26, 484 genes of RLC1 were predicted with Arabidopsis thaliana as reference. Annotation revealed that two species shared 4231 genes (63.8%). B. fruticulosa and RLC 1 possessed 1362 (20.5%) and 1042 (15.7%) unique genes, respectively. B. fruticulosa appeared to harbor interesting defensive genes such as catalase 2 (CAT2), Shikimate kinase like 1 (SKL1) and Quinolinate synthase (QS).These genesare representative of NAD biosynthesis and shikmic acid pathways. These act as integral regulator of reactive oxygen species and production of secondary metabolites against biotic and abiotic stresses. Identified B. fruticulosa exclusive defensive genes encouraged us to determine their presence selected ILs. In silico transcriptional analysis/results encompassing successful transfer of resistance genes in ILs will be presented. The information generated laid foundation for effective deployment of fruticulosa resistance in mustard breeding.

Keywords: Lipaphis erysimi, RNA-Seq, CAT2, Shikmic Acid Pathway, biotic stresses, introgression lines