

Dissecting the *Sinapis alba* L. defense transcriptome, a potential donor of resistance to *Alternaria* blight

Reshma Ahmed and *Priyadarshini Bhorali

Department of Agricultural Biotechnology, Assam Agricultural University, Jorhat-785013,
Assam, India

*Presenting and corresponding author email: priyadarshini.bhorali@aau.ac.in

Crop wild relatives (CWRs) are close weedy relatives of plant species which are generally underestimated because of their undesirable characters and lesser yield potential. However, these species carry many useful alleles and agronomic traits and therefore, could serve as significant resources for transfer of such genes to cultivated germplasms. *Sinapis alba* L. or white mustard is a member of the *Brassicaceae* family and a CWR of the oilseed *Brassica* spp., that possesses resistance to biotic/abiotic stresses like *Alternaria* blight and drought. The attempts to introgress such traits from *S. alba* to cultivated rapeseed and mustard germplasms have largely been unsuccessful, which necessitates the utilization of modern biotechnological tools to develop resistant cultivars. In our study, we validated the resistance in *S. alba* against the common and serious necrotrophic fungal pathogen *Alternaria brassicicola*, and characterized the interaction between the two. Subsequently, we performed a transcriptomic analysis to dissect the defense responses in *S. alba*, against the pathogen. The study established *S. alba* to be resistant to the *Alternaria* pathogen and presented new insights into its defense machinery in the form of a comprehensive dataset of genes and transcription factors modulated specifically in response to *A. brassicicola*, paving a way towards the development of *Alternaria* resistant oilseed Brassicas.