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A critical role for AtGDSL1 lipase gene in *Sclerotinia sclerotiorum* resistance and functional identification of its rapeseed homologue that underwent selection during breeding

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Sclerotinia stem rot (SSR) caused by *Sclerotinia sclerotiorum* is a devastating disease of rapeseed (*Brassica napus* L.). To date, the genetic mechanism of rapeseed' interaction with *S. sclerotiorum* is not fully understood, and molecular breeding is still the most effective strategy to control this disease in rapeseed. Here, *Arabidopsis thaliana* AtGDSL1, a novel defence-related GDSL lipase gene, was characterized as functioning in *Sclerotinia* resistance. Overexpression of AtGDSL1 in *B. napus* displayed increased resistance to *S. sclerotiorum*. Further studies reveal that AtGDSL1 is an extracellular protein and functions in rapeseed early defense against *S. sclerotiorum* infection by increasing the expression levels of salicylic acid (SA)-related genes and suppressing the expression of jasmonic acid (JA)-related genes. However, the sequence closest rapeseed GDSL homologue (BnGDSL1) had no effect on SSR resistance. Candidate gene association study revealed that only one of rapeseed GDSL lipase homologues, BnaC07g35650D (BnGLIP1), was significantly contributed to resistance traits in a natural *B. napus* population and the resistance function was also confirmed by transient expression assay in tobacco leaves. Moreover, genomic analyses showed that BnGLIP1 locus was embedded in selected regions related to SSR-resistance trait during the breeding process, and its elite allele type was ascribed to minor allele in the population. Thus, BnGLIP1 is the functional counterpart of AtGDSL1 and has a broad application prospect in rapeseed *S. sclerotiorum*-resistance breeding.

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