Supplementary material

Article title

Local Competition and Enhanced Defense: How *Metarhizium brunneum* Inhibits *Verticillium longisporum* in Oilseed Rape Plants

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Table S1. Primers used for qPCR amplification of genes of *Brassica napus* root tissues

ID	Gen/accession	Gene description	Sequence 5' --> 3'	Reference
ABA2	LOC106300040	Xanthoxin dehydrogenase	GCATCGCTCGTCTGTTCCAC	Karssemeijer et al., 2021
	XM_013736089.1		CGGCGAAGTCAACAGCGTTA	
ERF2	At5g47220	Ethylene Response Factor 2	ATGTACGGACAGAGCGAGGT	Yang et al., 2010
			AAGCTTCGAAACCAACAAGTAACTG	
ACO	EV102889	ACC oxidase	TCCGTCTGGGCTATCACTCT	Maag 2014
			GTGAGTGGGTCGATGTTCCT	
PR1	XM_013877950.1	Pathogenesis-related protein 1	AAAGCTACGCCGACCGACTACGAG	Alkooranee 2017
			CCAGAAAAGTCGGCGCTACTCCA	
PAL	LOC106342153 ?	phenylalanine ammonia-lyase 1	TCGCTATGGCTTCTTACTGCTCTG	Karssemeijer et al., 2021
	XM_013781008.1		GAGGTCTTACGAGATGAGATGAGTCC	
AOS	LOC106327419	Allene oxide synthase	ACCGCTTGCGACTAGGGATC	Karssemeijer et al., 2021
	XM_013765565.1		CAAAGTCCTTACCGGCGCAC	
PDF1.2	EV163328	Defensin-like protein 16	TCCATCACCCTTCTCTTTGC	Maag et al., 2014
			TTTTGGCACGCATAGTCGTA	
ACTIN	AF111812	Housekeeping gene	ATCGTCCTCAGTGGTGGTTC	Maag et al., 2014
			TTGATCTTCATGCTGCTTGG	
CYP79B2	At4G39950	CYTOCHROME P450, FAMILY 79, SUBFAMILY B, POLYPEPTIDE 2	AAGAGGTTGTGCTGCTCCG	Tytgat et al., 2013 Also in Marthur
			TCCAAGTGAAACCTTGAAGAAGTC	
CYP83A1	At4G13770	CYTOCHROME P450, FAMILY 83, SUBFAMILY A, POLYPEPTIDE 1	CTCCTTATCCCTCGTGCTTG	Mathur et al., 2013
			TGTCGTAACCAGCGATCTTG	
ICS2Bn	XM_022690315	Brassica napus isochorismate synthase 2, chloroplastic	GAATGATGCTCTTCCTCGCAGTT	This study
	LOC106431819		TCGGAGACAGAAACCTTCGGAT	

Table S2. Summary statistics of fungal colony area, and colony growth inhibition percentage of *M etarhizium brunneum* and *Verticillium longisporum* when growing in dual culture

	Df (1/8)			
Fungus	**dpi**	**F value**	**Pr (>F)**	Inhibition (% ± SE)
Metarhizium brunneum Cb15	14	1.5843	0.2436	
	17	3.6803	0.0913.	-8.48% ±1.68
	23	0.7325	0.417	
Verticillium longisporum Vl43	14	21.203	0.0017**	12.97% ±1.90
	17	13.419	0.0064**	19.75% ±2.05
	23	44.798	0.0002***	41.84% ±4.49

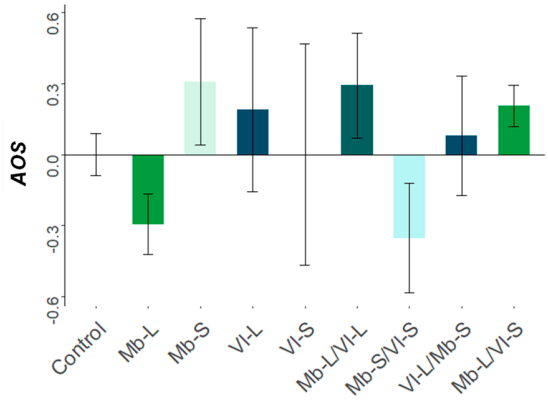


Figure S1. Expression of allene oxide synthase *AOS* gene