

**New Phytologist Supporting Information**

**Comprehensive microarray profiling of cell wall related polymers and enzymes in the parasitic plant *Cuscuta reflexa* and the host *Pelargonium zonale***

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The following Supporting Information is available for this article:

**Table S1** RT-qPCR primer sequences

**Table S2** Gene expression levels in individual biological replicates

**Table S3** Mean gene expression levels of biological triplicates

**Table S1** Sequences of gene-specific primers used for RT-qPCR with respective amplicon sizes and PCR efficiencies

<b>Gene</b>	<b>Forward primer (5' → 3')</b>	<b>Reverse primer (5' → 3')</b>	<b>Amplicon size</b>	<b>Efficiency</b>	<b>R<sup>2</sup></b>
<b>Cr-Actin</b>	atggaagctgctggaatccac	ttgctcatacggtcagcgatg	140 bp	96,3 %	0,999
<b>Cr-SF2</b>	cgaggattgtttacaagtatgg	cgaccacgaatagcgtcttcc	126 bp	102,3 %	0,998
<b>Cr-PL-1</b>	gaactatggcttcgggatca	cacagtccggagctgcaaata	113 bp	99,7 %	0,992
<b>Cr-PL-2</b>	ttgacctaccgcattacc	atccgtgaggcagatcgaag	128 bp	101,1 %	0,995
<b>Cr-PL-3</b>	accactttggggaaggctctg	acatctcccagtgcgtgtag	93 bp	90,3 %	0,983
<b>Cr-PL-4</b>	ggaactggagatcagagggg	agcttgaggctctcgcatag	96 bp	105,9 %	0,999
<b>Cr-PL-5</b>	cgatgtcagcaaagctggag	accacaccactcgaaatccc	142 bp	106,6 %	0,998

**Table S2** Mean normalized relative transcript abundances (RTA) in individual biological replicates with respective standard deviations (SD) of technical duplicates

<b>Gene</b>	<b>Stem 1 (RTA ± SD)</b>	<b>Stem 2 (RTA ± SD)</b>	<b>Stem 3 (RTA ± SD)</b>	<b>Infective tissue 1 (RTA ± SD)</b>	<b>Infective tissue 2 (RTA ± SD)</b>	<b>Infective tissue 3 (RTA ± SD)</b>
<b>Cr-PL-1</b>	1,00 ± 0,072	0,87 ± 0,589	0,76 ± 0,046	51,41 ± 4,585	53,30 ± 3,592	33,07 ± 0,540
<b>Cr-PL-2</b>	1,00 ± 0,093	1,38 ± 0,050	1,19 ± 0,728	12,54 ± 1,989	4,39 ± 1,400	6,88 ± 0,771
<b>Cr-PL-3</b>	1,00 ± 0,132	0,58 ± 0,177	0,87 ± 0,197	1,30 ± 0,123	2,58 ± 0,170	0,71 ± 0,073
<b>Cr-PL-4</b>	1,00 ± 0,330	0,16 ± 0,013	0,14 ± 0,010	1,71 ± 0,323	0,84 ± 0,849	1,26 ± 0,348
<b>Cr-PL-5</b>	1,00 ± 0,229	2,32 ± 0,768	0,90 ± 0,148	3,52 ± 0,424	3,94 ± 1,208	3,59 ± 0,547

**Table S3** Mean normalized relative transcript abundances (RTA) with respective standard errors (SEM) of biological triplicates

<b>Gene</b>	<b>Stem (RTA ± SEM)</b>	<b>Infective tissue (RTA ± SEM)</b>
<b>Cr-PL-1</b>	1,00 ± 0,080	51,57 ± 7,408
<b>Cr-PL-2</b>	1,00 ± 0,094	6,13 ± 2,044
<b>Cr-PL-3</b>	1,00 ± 0,157	1,68 ± 0,691
<b>Cr-PL-4</b>	1,00 ± 0,991	4,28 ± 0,879
<b>Cr-PL-5</b>	1,00 ± 0,358	2,87 ± 0,103