

**Table S3:** Expression of selected *C. zeina* genes when grown *in vitro* and during maize gray leaf spot disease in the field (*in planta*).

Gene name	Protein accession	Gene expression (counts)*							Gene expression (counts per 100 million)#
		<i>in vitro</i> Complete medium	<i>in vitro</i> Cornmeal agar	<i>in vitro</i> PDA-AP	<i>in vitro</i> PDA-pH8	<i>in vitro</i> PDB-pH3	<i>in vitro</i> V8	<i>in vitro</i> YPD	<i>in planta</i>
<i>C. zeina DCL-1</i>	PKR99831.1	553	422	410	436	330	456	891	128
<i>C. zeina DCL-2</i>	PKR98439.1	604	2154	1921	866	848	550	2314	131
<i>C. zeina AGO-1</i> ( <i>QDE-2</i> like)	PKR99617.1	2615	2602	3109	1867	2257	1870	1401	575
<i>C. zeina AGO-2</i> ( <i>QDE-2</i> like)	PKS00983.1	577	443	493	306	217	135	484	54
<i>C. zeina AGO-3</i> (meiotic silencing suppressor like)	PKS02248.1	328	309	239	219	113	225	567	86
<i>C. zeina RdRp</i> ( <i>QDE-1</i> like)	PKS04443.1	434	497	298	562	152	395	871	137
All <i>C. zeina</i> genes expression level (90th percentile)**		4325	4334	3971	4146	4061	3916	5004	1590
All <i>C. zeina</i> genes expression level (50th percentile)**		813	767	694	682	557	591	620	376
All <i>C. zeina</i> genes expression level (10th percentile)**		67	60	55	43	27	28	35	135

\* Gene expression counts are the number of RNAseq reads which mapped to the *C. zeina* gene of interest. RNA was extracted from *C. zeina* CMW25467 grown *in vitro* in seven different media as described in Swart et al 2017. RNAseq data is from GSE90705 in the NCBI GEO database. PDA=potato dextrose agar, AP=ammonium phosphate, YDP=yeast extract peptone dextrose

\*\*The percentile expression counts of genes with > 1 count in each *in vitro* condition were used to calculate the percentile values to give an indication of the expression levels of the selected genes compared to other genes. The number of genes with > 1 count in each condition ranged from 9407 to 9492.

# Gene expression is given as counts per 100 million of RNAseq reads which mapped to the *C. zeina* gene of interest. RNA was extracted from leaves of field-grown maize inbred line B73 with GLS disease symptoms as described in Swart et al 2017. RNAseq data is from GSE94442 in the NCBI GEO database. The percentile expression counts from 6640 genes with > 100 counts per 100 million were used to calculate the percentile values to give an indication of the expression levels of the selected genes compared to other genes.

Swart, V., Crampton, B.G., Ridenour, J.B., Bluhm, B.H., Olivier, N.A., Meyer, J.M. et al. (2017) Complementation of CTB7 in the maize pathogen *Cercospora zeina* overcomes the lack of *in vitro* cercosporin production. *Molecular Plant-Microbe Interactions*, 30, 710–724.