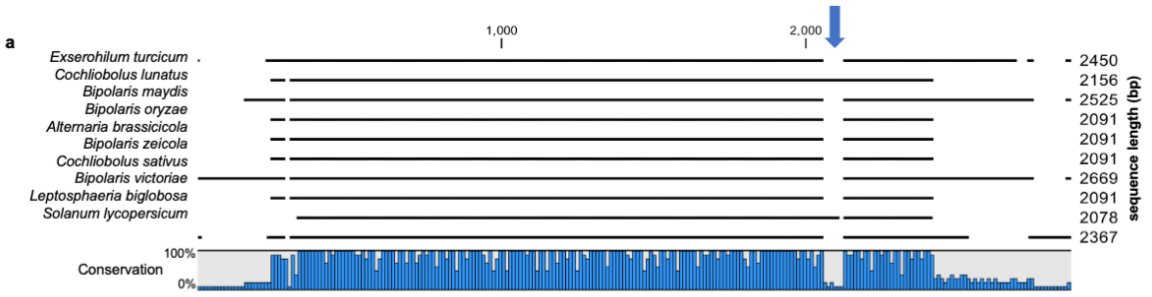
Supplementary Figures



b

Organism	Total score[a]	Query cover[b]	E-value[c]	Identity[d]	Accession number[e]
Exserohilum turcicum	3663	97%	0.0	100%	XM_008026943.1
Cochliobolus lunatus	2390	100%	0.0	85%	EU111681.1
Bipolaris maydis	2323	97%	0.0	85%	XM_014224556.1
Bipolaris oryzae	2307	97%	0.0	85%	XM_007689856.1
Alternaria brassicicola	2247	97%	0.0	85%	AB506083.1
Bipolaris zeicola	2276	97%	0.0	85%	XM_007716203.1
Cochliobolus sativus	2278	97%	0.0	85%	XM_007696136.1
Bipolaris victoriae	2269	97%	0.0	85%	XM_014698353.1
Leptosphaeria biglobosa	1889	99%	0.0	80%	FO905875.1
Solanum lycopersicum	2153	97%	0.0	84%	AK320781.1

[a] Total alignment score
[b] Percentage query covered by the alignment
[c] Expect value of the alignment
[d] Percentage identity of the aligned sequences
[e] GenBank accession number

Fig. S1 The conserved nature of the *cpr1* gene in other fungal orthologs. BLASTn analysis, with the predicted *E. turcicum cpr1* gene as query, revealed a highly conserved nature in other fungal species. **a** Multiple sequence alignment of the top ten BLAST hits, which includes the *E. turcicum* (XM_008026943.1) sequence. Sequences are indicated with black horizontal lines. The percentage of conservation for each base pair between the aligned sequences is indicated by the blue bar graph and the sequence length in base pairs (bp) of each sequence is shown next to the sequences. The only region of the predicted *E. turcicum cpr1* gene that showed less conservation when compared to the other *cpr1* orthologs was the intronic region (indicated by the blue arrow). **b** Table with alignment information that includes total score, percentage query cover, E-value, percentage of identity as well as the accession number for each sequence

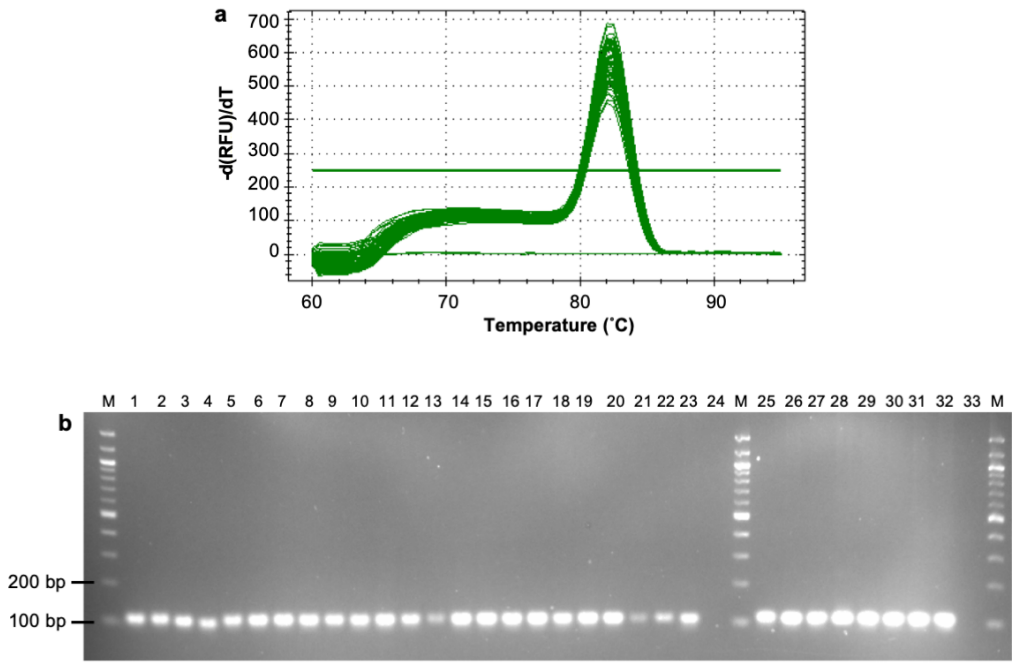


Fig. S2 Amplification efficiency of the *cpr1* primer set on *E. turcicum* isolates from sorghum and maize. The *E. turcicum cpr1* quantification primer set (EtCPR1QF and EtCPR1QR) was tested on eight sorghum and 23 maize isolates through quantitative PCR and subsequent melting curve analysis. **a** The *cpr1* amplicon from all isolates showed a single melting peak at 82.5 - 83°C and confirms that the reactions were specific. Melt curves for each of the isolates were determined by plotting the negative first derivative of fluorescence versus the temperature in degrees Celsius. **b** Selected quantitative PCR products were separated on a 2.5% agarose gel with size standard (100 bp ladder, New England Biolabs) (M) followed by the *E. turcicum* maize isolates (lane 1-23), *E. turcicum* sorghum isolates (lane 25-32) and no-template controls in lanes 24 and 33. The desired 109 bp amplification product was present in all samples. Information on the sorghum and maize *E. turcicum* isolates is in the relevant methods and materials section

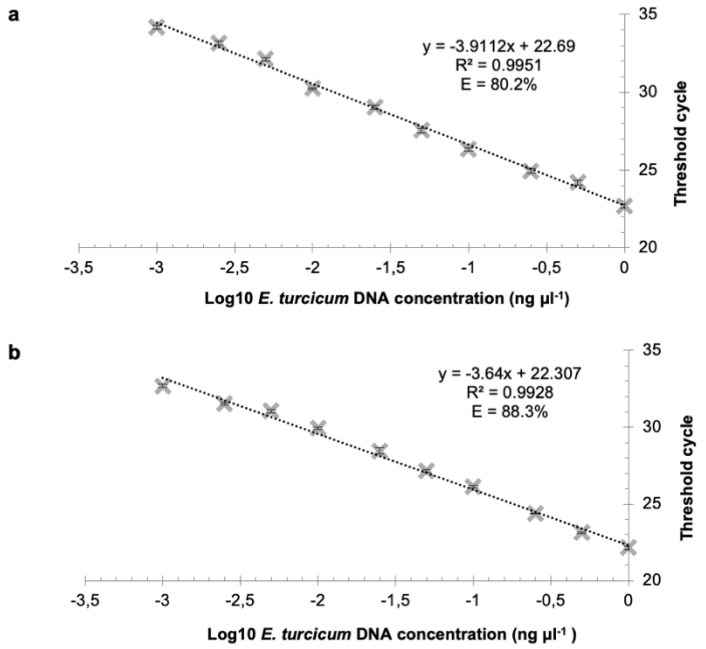


Fig. S3 Standard curves of *E. turcicum* in **a** sorghum and **b** maize simulated lesion samples. The standard curves indicate the efficiency and sensitivity of the *cpr1* primer set designed to quantify *E. turcicum in planta*. The detection limit of the *cpr1* amplicon is 1 pg *E. turcicum* DNA in both sorghum and maize. The bars on the graphs represent standard error

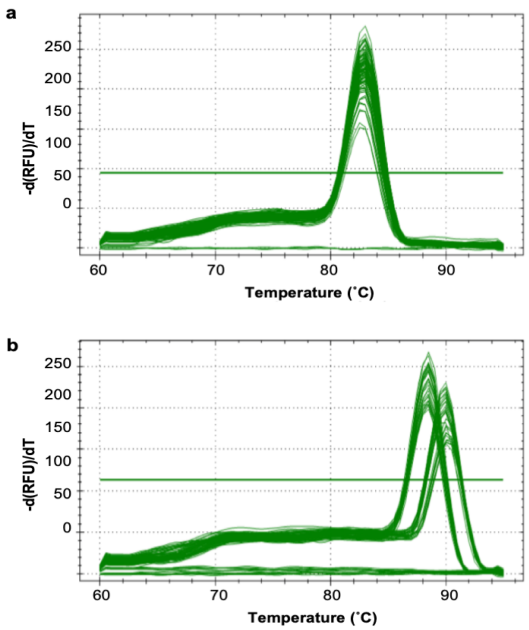


Fig. S4 The figure shows the melting curves of the *cpr1* and the *gst3* fragments amplified using the qPCR assay on the sorghum and maize diseased leaf samples showing chlorotic spot and lesion symptoms. **a** The *E. turcicum cpr1* amplicon from the sorghum and maize diseased leaf samples showed a single melting peak at 82.5 - 83°C and no differences were seen in the melting temperatures between samples from the two different *E. turcicum* isolates. **b** The *gst3* amplicon from the sorghum samples showed a single melting peak at 88.5°C, while the *gst3* amplicon from the maize samples showed a single melting peak at 90 – 90.5°C. Melt curves for each of the isolates were determined by plotting the negative first derivative of fluorescence versus the temperature in degrees Celsius