Table S1. The species used for Phylogenetic analysis.

Species	Family	Order	Genbank accession number
Coniothyrium glycines	*Coniothyriaceae*	Pleosporales	NC_040008
Corynespora cassiicola	*Corynesporascaceae*	Pleosporales	NC_056323
Didymella pinodes	*Didymellaceae*	Pleosporales	NC_029396
Phaeosphaeria nodorum	*Phaeosphaeriaceae*	Pleosporales	NC_009746
Pithomyces chartarum	*Astrosphaeriellaceae*	Pleosporales	NC_035636
Shiraia bambusicola	*Shiraiaceae*	Pleosporales	NC_026869
Stemphylium lycopersici	*Pleosporaceae*	Pleosporales	NC_036039
Paraconiothyrium sp.	*Didymosphaeriaceae*	Pleosporales	OM617730
Bipolaris sorokiniana	*Pleosporaceae*	Pleosporales	NC_047242
Bipolaris oryzae	*Pleosporaceae*	Pleosporales	NC_057095
Bipolaris cookei	*Pleosporaceae*	Pleosporales	NC_036417
Rhynchosporium orthosporum	*Ploettnerulaceae*	Helotiales	NC_023127

Table S2. Base composition and skew of the mitochondrial genome.

	A%	T%	G%	C%	AT%	GC%	AT skew	GC skew
whole genome	35.84	36.29	13.78	14.09	72.13	27.87	-0.006	-0.01
PCGs	32.93	38.33	14.78	13.96	71.26	28.74	-0.07	0.03

Table S3. The genome size and the number of introns of four species from Pleosporales.

Species	Mitochondrial genome size (bp)	Number of introns
Shiraia bambusicola	39,030	1
Phaeosphaeria nodorum	49,761	5
Didymella pinodes	55,973	15
Bipolaris cookei	135,790	33

Shiraia bambusicola

Didymella pinodes