

A repertoire of candidate effector proteins of the fungus *Ceratocystis cacaofunesta*

Gabriela N. Ramos-Lizardo, Jonathan J. Mucherino-Muñoz, Eric R. G. R. Aguiar, Carlos P. Pirovani, Ronan X. Corrêa

Supplementary table S1. Identification of the genomes, proteomes and SRA of *Sordariomycetes* used in this analysis.

	Assembled genome size (Mb)	GC content (%)	Predicted proteome	Genome accession(s)	Proteome accession(s)	SRA accession(s)	Transcriptome accession(s)
<i>Ceratocystis albifundus</i>	26.88	48.6	7,619	GCA_000813685.1	this paper		
<i>Ceratocystis cacaofunesta</i>	30.48	48.1	7,879	GCA_002776505.1	this paper	SRR6217952	this paper
<i>Ceratocystis fimbriata</i>	30.16	47.6	7,266	GCA_000389695.3	UP000222788	SRR8599076	GCA_000389695.3
<i>Ceratocystis manginecans</i>	31.71	47.9	7,563	GCA_000712455.1	this paper		
<i>Ceratocystis platani</i>	29.18	48.2	5,622	GCA_000978885.1	UP000034841		
<i>Verticillium albo-atrum</i>	32.86	55.4	10,233	GCA_000150825.1	UP000008698		
<i>Verticillium dahliae</i>	33.9	55.6	10,530	GCA_000150675.2	UP000001611		
<i>Fusarium graminearum</i>	38.05	48.15	14,162	GCA_900044135.1	UP000070720		
<i>Fusarium oxysporum</i>	54.77	47.8	17,784	GCA_000222805.1	UP000002489		
<i>Fusarium verticillioides</i>	41.84	48.69	17,875	GCA_000149555.1	UP000009096		