

Additional File 8. Comparative analyses within *Ceratocystis* genomes and *Huntiella moniliformis*.

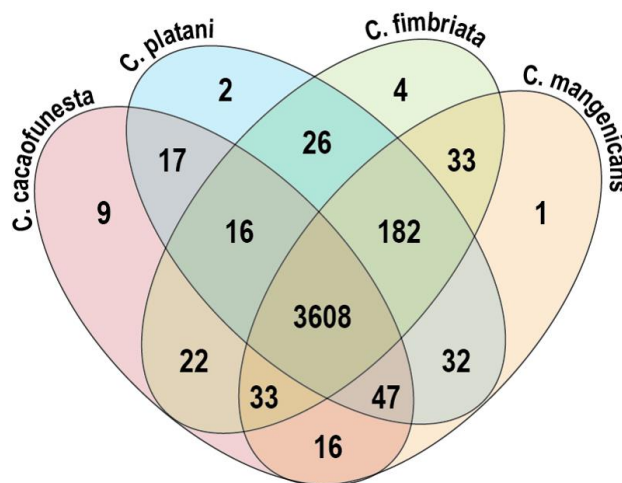


Figure 1. Venn diagram comparing the number of gene clusters shared and exclusive among *Ceratocystis* species.

Table 1. Genome descriptive statistics for *C. cacaofunesta* compared with other *Ceratocystis* species genomes and *Huntiella moniliformis*.

	<i>Ceratocystis cacaofunest</i> ¹	<i>Ceratocystis fimbriata</i> ²	<i>Ceratocystis manginecans</i> ³	<i>Ceratocystis platani</i> ⁴	<i>Huntiella moniliformis</i> ³
Life style	Necrotrophic	Necrotrophic	Necrotrophic	Necrotrophic	Saprophytic
Natural hosts	Cacao	Multiple	Multiple	Platanus	Multiple
Genome size (Mbp)	30.50	29.41	31.71	29.18	25.43
Number of scaffolds	229	2,641	980	1,213	365
N50 (kbp)	386	428	77	77	191
GC content (%)	48.1	48.1	47.9	48.2	48.0
Number of gene models	7,382	7,200	7,494	5,622	6,832
Gene density (/Mbp)	242	245	236	193	269
Assembly software	Velvet	Newbler	Velvet	GLC	AbySS
Genome coverage	103X	20.0X	22X	655X	38X

1 This study; 2 Wilken et al. 2013; 3 Van der Nest et al. 2014; 4 Belbahri L. 2015.

References:

2. Wilken, P.M. et al., 2013. IMA Genome-F 1: *Ceratocystis fimbriata*: Draft nuclear genome sequence for the plant pathogen, *Ceratocystis fimbriata*. IMA fungus, 4(2), pp.357–8.

3. van der Nest, M.A. et al., 2014. Draft genome sequences of *Diplodia sapinea*, *Ceratocystis manginecans*, and *Ceratocystis moniliformis*. *IMA Fungus*, 5(1), pp.135–140.
4. Belbahri, L. (2015). Genome sequence of *Ceratocystis platani*, a major pathogen of plane trees. URL <http://www.ncbi.nlm.nih.gov/nuccore/814603118>.