

Table S1. Genome sequencing data generated and final genome assembly statistics.

	<i>C. floricola</i> DSM27421			<i>C. wingfieldii</i> CBS7118		
Sequencing run	# Nanopore (run1)	# PacBio (run1)	# PacBio (run2)	# Nanopore (run1)	# Nanopore (run2)	# PacBio (run1)
All reads						
Number of reads	1,339,621	635,351	487,986	110,824	538,185	482,124
Total bases	2,146,305,526	3,375,565,303	3,899,299,184	436,059,915	2,405,382,444	3,465,771,589
Median read length	863	4,455	3,368	2,185	3,039	3,560
Mean read length	1,602.17	5,312.91	7,990.60	3,934.71	4,469.43	7,189
Read length N50	2,590	8,315	18,192	7,398	6,950	14,102
Reads > 10 kb						
Number of reads	18,492	91,597		10,234	52,563	
Total bases	290,900,125	1,229,014,728		159,602,101	775,673,444	
Median read length	13,510	12,531		13,718	13,217	
Mean read length	15,731	13,418		15,595	14,757	
Read length N50	15,491	13,193		15,475	14,532	
Assembly statistics						
No. contigs	16 (15 nuclear + 1 mtDNA)			15 (14 nuclear + 1 mtDNA)		
Assembly size (bp)	21,699,837			20,813,371		
Coverage	252x			165x		
GC%	53.35			53.23		
tRNA genes (nuclear)	167			183		
tRNA genes (mtDNA)	18			14		
Telomeric repeats	17			2		

read data used to generate the final genome assembly is highlighted in bold