

Table S1. Genome statistics for *Mycetohabitans* sp. B13 and *Mycetohabitans* sp. B14 as well as previously sequenced *Mycetohabitans* included for comparison.

	<i>Mycetohabitans</i> sp. B13	<i>Mycetohabitans</i> sp. B14	<i>M. rhizoxinica</i> HKI454	<i>M. endofungorum</i> HKI 456
DNA, total number of bases	3579262	3653645	3750138	328408
DNA coding number of bases	87.50%	87.08%	88.73%	85.75%
DNA G+C number of bases	60.59%	60.56%	60.71%	61.27%
DNA scaffolds	2	3	3	76
Genes total number	3292	3465	3938	3051
Protein coding genes	3219	3394	3870	2631
Pseudo Genes	404	417	NA	369
RNA genes	73	71	68	62
rRNA genes	9	9	9	5
5S rRNA	3	3	3	3
16S rRNA	3	3	3	1
23S rRNA	3	3	3	1
tRNA genes	47	47	59	43
Other RNA genes	17	15	NA	5
Reference	This study	This study	(1)	(2)
GenBank accession number	FTPM01000000	FTPJ01000000	FR687359 FR687360 FR687361	GCA_002927045
Fungal host	ATCC 52813	ATCC 52814	ATCC 62417	CBS 112285

1. Lackner G, Moebius N, Partida-Martinez L, Hertweck C. 2011. Complete genome sequence of *Burkholderia rhizoxinica*, an endosymbiont of *Rhizopus microsporus*. *Journal of Bacteriology* 193:783-784.
2. Estrada-de Los Santos P, Palmer M, Chavez-Ramirez B, Beukes C, Steenkamp ET, Briscoe L, Khan N, Maluk M, Lafos M, Humm E, Arrabit M, Crook M, Gross E, Simon MF, Dos Reis Junior FB, Whitman WB, Shapiro N, Poole PS, Hirsch AM, Venter SN, James EK. 2018. Whole genome analyses suggests that *Burkholderia* sensu lato contains two additional novel genera (*Mycetohabitans* gen. nov., and *Trinickia* gen. nov.): Implications for the evolution of diazotrophy and nodulation in the Burkholderiaceae. *Genes* 9:389.