



Figure S1. Bar charts of mycobiomes detected in the three sorghum cultivars (PAN8706W, PAN8816, N5511) at different taxonomic ranks: (A) Phyla, (B) Classes, (C) Orders, (D) Families. The asterisks (*) denote the mostly abundant group for each of the cultivars at the different taxonomic levels.

Table S1. Summary of the relative abundance (%) of Molecular Operational Taxonomic Units (MOTUs) taxa that were assigned at Phyla level for the different sorghum cultivars (above and below ground niche).

Phylum	Aboveground									Belowground								
	Seed			Leaves			Stems			Roots			Rhizosphere soils			Bulk soils		
	PAN8076W	PAN8816	NS5511	PAN8076W	PAN8816	NS5511	PAN8076W	PAN8816	NS5511	PAN8076W	PAN8816	NS5511	PAN8076W	PAN8816	NS5511	PAN8076W	PAN8816	NS5511
Ascomycota*	61.6	56.9	77.5	73.9	83.4	68.2	29.8	80.1	63.2	67.6	65.3	63.2	54.4	45.7	70.3	72.1	69.8	61.5
Basidiomycota	19.7	10.7	9.5	16.5	6.7	16.5	27.0	8.2	22.6	20.3	13.2	20.6	28.7	31.9	20.4	19.0	10.4	26.7
Unidentified	1.9	2.0	5.1	7.4	5.0	10.1	0.2	1.2	2.1	3.5	5.9	6.1	3.0	3.4	4.9	6.0	9.2	8.1
Zygomycota	16.8	30.4	7.9	2.2	4.9	5.2	43.1	10.5	12.1	8.6	15.6	10.0	13.9	18.9	4.2	2.7	9.4	3.5
Chytridiomycota																0.1	0.9	0.1
Glomeromycota														01	0.1		0.2	0.1

¹ Phylum followed by an asterisk and bold indicate the most abundant in relative abundance, whilst MOTUs with zero % were left blank in the table. Names are used as assigned by the UNITE database.

Table S2. Summary of the relative abundance (%) of Molecular Operational Taxonomic Units (MOTUs) taxa that were assigned at Class level for the different sorghum cultivars (above and below ground niche).

[illegible]

Glomeromycota																		
Glomeromycetes															0.1		0.2	0.1
Unidentified														0.1	0.1		0.1	0.1
Zygomycota																		
Incertae sedis	16.8	7.9	30.4	2.2	4.9	5.2	10.5	43.1	12.1	8.6	15.6	10.0	13.9	18.9	4.2	2.7	9.4	3.5
Unidentified	1.9	5.1	2.0	7.4	5.0	10.1	1.2	0.2	2.1	3.5	5.9	6.1	3.0	3.4	4.9	6.0	9.2	8.1

Class followed by an asterisk and bold indicate the most abundant in relative abundance, whilst MOTUs with zero % were left blank in the table. Names are used as assigned by the UNITE database.

Table S3. Summary of the relative abundance (%) of Molecular Operational Taxonomic Units (MOTUs) taxa that were assigned at Order level for the different sorghum cultivars (above and below ground niche).

Order	Aboveground									Belowground								
	Seed			Leaves			Stems			Roots			Rhizosphere soils			Bulk soils		
	PAN8076 W	PAN 8816	NS55 11	PAN8076 W	PAN88 16	NS55 11	PAN8076 W	PAN88 16	NS55 11	PAN8076 W	PAN88 16	NS55 11	PAN8076 W	PAN88 16	NS55 11	PAN8076 W	PAN88 16	NS55 11
Ascomycota																		
Capnodiales	0.2	7.8	26.5	6.4	2.7	5.0		1.3	6.4	63	10.0	16.4	2.8	8.2	22.1	6.8	3.3	32
Dothideales		0.1		2.5	2.2	2.6		0.4	0.3	0.8	0.2	1.1	1.6	0.9	1.7	1.5	0.3	1.0
Pleosporales*	12.3	15.3	16.2	19.8	21.2	14.5		3.6	8.1	13.2	15.5	10.8	13.4	14.6	17.6	30.5	27.4	26.2
Pezizales															0,1	0,1	1,0	0,3
Saccharomycetales	4.3	3.6	1.3	5.4	2.5	1.5	29.3	15.8	4.8	22.3	5.4	8.8	24.3	6.0	7.3	1.6	0.3	0.1
Sordariomycetes;Other															0,2	0,6	0,5	0,1
Hypocreales*	11.3	19.0	16.2	34.1	30.6	17.9		57.7	39.6	19.5	28.6	21.4	4.4	6.3	10.8	16.6	24.5	19.5
Incertae_sedis				0.1	0.1					0.1	0.1					0.5	1.3	0.1
Sordariales												0.1			0.2	1.2	2.0	0.1
Trichosphaeriales		0.1			0.2	0.2		0.6			1.0				0.2		0.1	
Unidentified	33.4	10.8	16.8	5.3	23.5	26.3		0.4	3.6	4.7	3.9	4.2	7.3	8.8	9.2	10.8	6.7	7.8
Basidiomycota																		
Other																0,2	3,4	
Cantharellales	10.4	0.2	3.0	15.3	1.8	4.6	0.5	0.9	0.5	0.2	0.7	0.8	6.7	1.9	3.5	4.8	0.2	0.6
Sporidiobolales	0.2	0.6	0.2	0.2	0.7	0.9	5.0	0.4	0.3	1.8	1.4	3.4	2.7	4.3	1.1	0.8	0.7	2.4
Tremellomycetes;Other		0,2	0,1		0,5	0,7	0,1		0,2	0,2	1,1	1,9	0,3	3,0	0,5	0,5	0,4	1,0
Cystofilobasidiales										0,3			0,6					
Filobasidiales	8.7	8.8	4.3	0.8	3.5	9.9	20.1	6.0	21.3	17.0	5.9	11.0	18.0	20.0	12.9	11.9	4.4	21.2
Tremellales			0.1	0.1	0.1	0.1			0.1	0.0	0.1	0.1	0.1	0.5	0.1		0.2	0.6
Ustilaginales	0.3	0.6	0.9					0.1	0.1					0.1		0.1	0.1	0.1
Unidentified			0.9			0.3					0.6	2.4		0.1	0.7		0.1	0.1

Chytridiomycota																			
Rhizophydiales																		0.5	
Spizellomycetales																		0.1	0.1
Glomeromycota																			
Glomerales																		0.2	
Unidentified																		0.1	0.1
Zygomycota																			
Mortierellales													0,1		0,2		0,2	0,3	2,9
Mucorales	16.8	30.4	7.9	2.2	4.9	5.2	43.1	10.5	12.1	8.6	15.5	9.9	13.9	18.8	4.2	2.5	9.1	0.6	
Unidentified																			
Unidentified	1.9	2.0	5.1	7.4	5.0	10.1	0.2	1.2	2.1	3.5	5.9	6.1	3.0	3.4	4.9	6.0	9.2	8.1	

Order followed by an asterisk and bold indicate the most abundant in relative abundance, whilst MOTUs with zero % were left blank in the table. Names are used as assigned by the UNITE database.

Table S4. Summary of the relative abundance (%) of Molecular Operational Taxonomic Units (MOTUs) taxa that were assigned at Family level for the different sorghum cultivars (above and below ground niche).

Family	Aboveground									Belowground								
	Seed			Leaves			Stems			Roots			Rhizosphere soils			Bulk soils		
	PAN8076	PAN88	NS551	PAN8076	PAN88	NS551	PAN8076	PAN88	NS551	PAN8076	PAN88	NS551	PAN8076	PAN88	NS551	PAN8076	PAN88	NS551
	W	16	1	W	16	1	W	16	1	W	16	1	W	16	1	W	16	1
Ascomycota																		
Mycosphaerellaceae	0.2	7.8	27.0	6.4	2.7	5.0		1.2	6.4	6.3	10.0	16.0	2.8	8.2	22.0	6.8	3.3	3.2
Dothioraceae		0.1		2.5	2.2	2.6		0.4	0.3	0.8	0.2	1.1	1.6	0.9	1.7	1.5	0.3	1.0
Pleosporales;Other	0.9	3.0	2.6	11.2	11.0	8.6		0.7	2.7	5.9	8.6	5.3	7.5	9.0	10.0	21.9	21.0	17.0
Incertae sedis	6.1	11.0	11.0	7.5	9.5	5.2		2.6	5.2	6.8	6.6	5.3	5.5	5.1	7.1	7.9	5.2	8.2
Pleosporaceae	5.3	1.2	2.3	1.1	1.1	0.6		0.4	0.1	0.4	0.2	0.2	0.4	0.4	0.5	0.7	1.2	0.9
Unidentified													0.1		0.2	0.5	0.7	1.3
Pezizaceae															0.1	0.1	1.0	0.3
Debaryomycetaceae	2.5	2.4	0.1	0.1	0.1	0.1	4.0	2.7	0.1	0.3	0.3	0.1	0.2	0.3		0.6		
Incertae sedis	1.4	1.1	1.1	4.3	2.2	1.2	12.7	2.3	2.0	20.6	2.8	6.6	24.0	5.5	6.3	0.8	0.2	0.1
Pichiaceae		0.1	0.1	1.0	0.1		4.8	8.4	2.6	0.8	2.3	1.4	0.1	0.2	0.7	0.1		
Saccharomycodaceae	0.3					0.1	5.4		0.1	0.5		0.7						
Trichomonascaceae							2.5	2.4	0.1	0.1								
Bionectriaceae				0.6						0.1								
Nectriaceae*	11.3	19.0	16.0	33.3	31.0	18.0		58.0	40.0	19.4	28.0	21.0	4.4	6.3	11.0	16.5	25.0	19.5
Incertae_sedis				0.1	0.1					0.1						0.5	1.3	0.1
Sordariales;Other																0.8	0.6	
Incertae sedis		0.1			0.2	0.2		0.6		0.2	1.0				0.2		0.1	
Unidentified	33.4	10.8	17.0	5.3	23.5	26.3		0.4	3.6	4.7	3.9	4.2	7.3	8.8	9.2	10.8	6.7	7.8

Basidiomycota																		
Marasmiaceae					0.1			0.6		0.3	3.2	0.2	0.2	1.5	1.0			0.1
Ceratobasidiaceae	10.4	0.2	3.0	15.3	1.8	4.6	0.5	0.9	0.5	0.2	0.7	0.8	6.7	1.9	3.5	4.8	0.2	0.6
Other						0.1		0.3	0.1	0.1	0.2	0.3		0.1	0.1	0.3	0.3	0.9
Incertae sedis	0.2	0.6	0.1	0.2	0.7	0.8	5.0	0.1	0.2	1.8	1.2	3.1	2.6	4.2	1.0	0.5	0.5	1.5
Unidentified		0.1					1.3	0.1	0.2							0.1		0.1
Cystofilobasidiaceae										0.3			0.6					
Filobasidiaceae	8.7	8.8	4.3	0.8	3.5	9.9	20.1	6.0	21.3	17.0	5.9	11.0	18.0	20.0	12.9	11.9	4.4	21.2
Ustilaginaceae	0.3	0.6	0.9					0.1	0.1					0.1		0.1	0.1	0.1
Unidentified			0.9			0.3					0.6	2.4		0.1	0.7		0.1	0.1
Chytridiomycota																		
Rhizophydiales																	0.5	
Spizellomycetales																	0.1	0.1
Glomeromycota																		
Glomerales																	0.2	
Unidentified																	0.1	0.1
Zygomycota																		
Mortierellaceae												0.1		0.2		0.2	0.3	2.9
Mucoraceae	16.8	30.4	7.9	2.2	4.9	5.2	43.1	10.5	12.1	8.5	15.4	9.9	13.9	18.8	4.2	2.5	8.9	0.6
Unidentified	1.9	2.0	5.1	7.4	5.0	10.1	0.2	1.2	2.1	3.5	5.9	6.1	3.0	3.4	4.9	6.0	9.2	8.1

Family followed by an asterisk and bold indicate the most abundant in relative abundance, whilst MOTUs with zero % were left blank in the table. Names are used as assigned by the UNITE database.