

Fungal extracellular lipases from coffee plantation environments for the sustainable management of agroindustrial coffee biomass

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Table S1. Degenerate primers designed for Fungal lipases

Genus	Primer ID	Sequence (5'-3')
<i>Apergillus</i>	As_F1	ATGTTCTCTGGACGGBTTGG
	As_R1	CTATAGCAGRCASTCKGR
	Pc_AspF_LipF	ATARGAAAGGATAAAGCAA- GATGGT
	Pc_AspF_LipR	ATACACTAYTAGCACCCAACCTCAA
	Pc_AspF_LipF3	AGAGGWCCTGGMTTCTACCACA
	Pc_AspF_LipR3	AGAGAKGTCACCATGGAGTCTC
<i>Fusarium</i>	Fu_F1	ATGCTTCTTCTACCACTYCTC
	Fu_R1	TTAAGWGC GGCGCTGGTTA
	Pc_Fu_F1	TCTTCTACCACTYCTCTCRGCC
	Pc_Fu_R1	GCGGGCCTGGTTATTCTT
	Pc_Fu_F2	GCCCTGTAGCTCTCGAYGAC
	Pc_Fu_R2	TMACATACTCCTTATCCATCTGGA
	Fu_So_F1	ATGATGCTCATCCTATCTATTC
	Fu_So_R1	CTAAGTCATCTGCTTAACAAAT
<i>Penicillium</i>	Pe_F1	ATGTTGTTCAACTRCCARTCTTTRC
	Pe_R1	GCCACARCCAGCAGTAAGC
	Pc_Pe_F2	CTKTCTGCACCTRTTTTGGAG
	Pc_Pe_R1	AAGCTTGMGAWGTGACCG
<i>Mucor</i>	Mu_F1	GGTSTCWTTACWWCYATCAC
	Mu_R1	TTAAAGRCAAAGWCCTTSATTRAT

Table S2. ITS-based DNA barcoding of fungal isolates

	IDTAXA UNITE v2020 February2020		IDTAXA Warcup_v2 March 2018		RDP UNITE Fungal ITS 07/04/2014		RDP Warcup 2		BLAST NCBI Internal transcribed spacer region (ITS)				
	Assignment	Confidence	Assignment	Confidence	Assignment	Confidence	Assignment	Confidence	Bit- score	Pairwise Identity (%)	E value	Accession	Genus
C-1	<i>Aspergillus westerdijkiae</i>	72%	<i>Aspergillus</i>	83%	<i>Aspergillus ochraceus</i> SH231999.06FU	100%	<i>Aspergillus</i>	100%	966.918	99.1	0.0	NR_135389	<i>Aspergillus westerdijkiae</i>
12-C	<i>Rhizopus arrhizus</i>	90%	<i>Rhizopus</i>	90%	<i>Rhizopus arrhizus</i> var._arr-hizus SH225968.06FU	100%	<i>Rhizopus</i>	100%	1055.56	99.0	0.0	NR_103595	<i>Rhizopus arrhizus</i>
2-5E	unclassified_ <i>Nectriaceae</i>	98%	<i>Gibberella</i>	90%	<i>Fusarium oxysporum</i> SH217297.06FU	100%	<i>Fusarium oxysporum</i>	80%	911.519	99.0	0.0	NR_120263	<i>Fusarium circinatum</i>
C-2	<i>Penicillium</i>	99%	<i>Eupenicillium</i>	86%	<i>Penicillium chrysogenum</i> SH214177.06FU	100%	<i>Eupenicillium</i>	100%	1009.39	100.0	0.0	NR_111815	<i>Penicillium rubens</i>
2-1B	<i>Fusarium</i>	69%	<i>Gibberella</i>	90%	<i>Fusarium oxysporum</i> SH217297.06FU	100%	<i>Fusarium oxysporum</i>	86%	911.519	99.2	0.0	NR_152941	<i>Fusarium inflexum</i>
2-8A	<i>Penicillium</i>	96%	<i>Eupenicillium</i>	84%	<i>Penicillium</i>	100%	<i>Eupenicillium</i>	100%	1016.78	100.0	0.0	NR_077153	<i>Penicillium crustosum</i>
2-5B-1	<i>Hypocreales_sp</i>	90%	unclassified_ <i>Nectriaceae</i>	77%	<i>Ascomycota</i>	100%	<i>Nectria haematococca</i> mpVI	85%	915.212	99.0	0.0	NR_164415	<i>Fusarium perseae</i>
2-5A-1	<i>Fusarium</i>	72%	unclassified_ <i>Nectriaceae</i>	80%	<i>Ascomycota</i> sp. SH233666.06FU	100%	<i>Fusarium oxysporum</i> f sp psidii	81%	974.305	100.0	0.0	NR_154227	<i>Neocosmospora rubicola</i>
SL14D	<i>Aspergillus</i>	82%	<i>Aspergillus</i>	90%	<i>Ascomycota</i>	100%	<i>Aspergillus</i>	100%	1040.78	100.0	0.0	NR_163668, NR_137513, NR_111348, NR_077143	<i>Aspergillus</i> sp.
2-2B	<i>Papiliotrema flavescens</i>	82%	<i>Cryptococcus</i>	79%	<i>Tremellomyces_sp</i> SH219359.06FU	100%	<i>Cryptococcus flavescens</i>	100%	887.512	99.2	0.0	NR_130696	<i>Papiliotrema flavescens</i>
2-5B-2	<i>Aspergillus</i>	91%	<i>Aspergillus</i>	89%	<i>Ascomycota</i>	100%	<i>Aspergillus</i>	100%	1038.94	99.8	0.0	NR_163668, NR_137513,	<i>Aspergillus</i> sp.

												NR_111348, NR_077143	
2-1A	<i>Fusarium</i>	76%	<i>Gibberella</i>	86%	<i>Fusarium proliferatum</i> SH217299.06FU	93%	<i>Fusarium annulatum</i>	93%	961.378	99.8	0.0	NR_111889	<i>Fusarium fujikuroi</i>
2-5G	<i>Absidia_sp</i>	67%	unclassified_Root	26%	<i>Absidia</i>	100%	<i>Mucorales</i>	96%	348.29	91.5	5.23e-96	NR_154704, NR_103626	<i>Absidia sp.</i>
2-2A	<i>Cunninghamella echinulata</i>	88%	unclassified_Root	19%	<i>Cunninghamella</i>	100%	<i>Fungi</i>	100%	322.437	86.2	5.55e-88	NR_168760	<i>Cunninghamella gigacellularis</i>
2-6B	Unclassified <i>Nectriaceae</i>	97%	<i>Gibberella</i>	84%	<i>Fusarium oxysporum</i> SH217297.06FU	96%	<i>Gibberella</i>	100%	920.752	98.8	0.0	NR_120263	<i>Fusarium circinatum</i>
2-5F	<i>Hypocreales_sp</i>	90%	unclassified_Nectriaceae	77%	<i>Ascomycota</i>	100%	<i>Nectria haematococca</i> mpVI	85%	915.212	99.0	0.0	NR_164415	<i>Fusarium perseae</i>
2-9A-1	<i>Penicillium</i>	98%	<i>Eupenicillium</i>	77%	<i>Penicillium</i>	100%	<i>Eupenicillium</i>	100%	1014.93	99.8	0.0	NR_077153	<i>Penicillium crustosum</i>
2-9B	<i>Penicillium</i>	96%	<i>Eupenicillium</i>	78%	<i>Penicillium</i>	100%	<i>Eupenicillium</i>	100%	1016.78	99.8	0.0	NR_077153	<i>Penicillium crustosum</i>
2-6	<i>Mucor nidicola</i>	92%	<i>Mucor sp</i> JJP_2009a	84%	<i>Mucor sp.</i> JJP 2009a SH202371.06FU	100%	<i>Mucor sp</i> JJP_2009a	100%	776.713	90.4	0.0	NR_172288	<i>Mucor irregularis</i>
2-9A-2	<i>Penicillium</i>	98%	<i>Eupenicillium</i>	84%	<i>Penicillium polonicum</i> SH231333.06FU	82%	<i>Eupenicillium</i>	100%	1011.24	100.0	0.0	NR_077153	<i>Penicillium crustosum</i>
2-5A-2	<i>Penicillium</i>	76%	<i>Eupenicillium</i>	73%	<i>Penicillium</i>	96%	<i>Eupenicillium</i>	96%	909.672	97.0	0.0	NR_077153	<i>Penicillium crustosum</i>
2-2	<i>Mucor nidicola</i>	99%	unclassified_Root	68%	<i>Mucor sp.</i> IN-Bio2559C SH202378.06FU	100%	<i>Mucor sp</i> JJP_2009a	99%	776.713	92.5	0.0	NR_111660	<i>Mucor fusiformis</i>
2-8D	<i>Penicillium</i>	96%	<i>Eupenicillium</i>	93%	<i>Penicillium</i>	100%	<i>Eupenicillium</i>	100%	955.838	99.8	0.0	NR_077153	<i>Penicillium crustosum</i>
2-7	<i>Mucor nidicola</i>	69%	<i>Mucor sp</i> JJP_2009a	76%	<i>Mucor sp.</i> JJP 2009a SH202371.06FU	93%	<i>Mucor sp</i> JJP_2009a	100%	765.633	90.1	0.0	NR_172288	<i>Mucor irregularis</i>
2-4B	<i>Penicillium</i>	98%	<i>Eupenicillium</i>	84%	<i>Penicillium polonicum</i> SH231333.06FU	82%	<i>Eupenicillium</i>	100%	1011.24	100.0	0.0	NR_077153	<i>Penicillium crustosum</i>
14	<i>Aspergillus westerdijkiae</i>	62%	<i>Aspergillus</i>	81%	<i>Aspergillus ochraceus</i> SH231999.06FU	100%	<i>Aspergillus</i>	100%	963.225	98.9	0.0	NR_135389	<i>Aspergillus westerdijkiae</i>
19	<i>Fusarium</i>	87%	<i>Gibberella</i>	87%	<i>Fusarium proliferatum</i> SH217299.06FU	90%	<i>Fusarium annulatum</i>	95%	953.992	99.8	0.0	NR_111889	<i>Fusarium fujikuroi</i>
20	<i>Aspergillus</i>	82%	<i>Aspergillus</i>	91%	<i>Ascomycota</i>	100%	<i>Aspergillus</i>	100%	1035.24	100.0	0.0	NR_163668, NR_137513,	<i>Aspergillus sp.</i>

												NR_111348, NR_077143	
22	<i>Meyerozyma</i>	97%	<i>Meyerozyma</i>	87%	<i>Candida smithsonii</i> SH216776.06FU	100%	<i>Meyerozyma guilliermondii</i>	94%	1033.4	99.6	0.0	NR_111247	<i>Meyerozyma guilliermondii</i>
23	<i>Metarhizium robertsii</i>	66%	<i>Metacordyceps</i>	80%	<i>Metarhizium pinghaense</i> SH201724.06FU	100%	<i>Metacordyceps</i>	100%	942.912	99.4	0.0	NR_132011	<i>Metarhizium robertsii</i>
24	<i>Fusarium</i>	83%	<i>Gibberella</i>	86%	<i>Fusarium proliferatum</i> SH217299.06FU	95%	<i>Fusarium annulatum</i>	88%	948.452	99.6	0.0	NR_111889	<i>Fusarium fujikuroi</i>
30	<i>Aspergillus puniceus</i>	96%	<i>Aspergillus puniceus</i>	87%	<i>Aspergillus monodii</i> SH227456.06FU	100%	<i>Aspergillus puniceus</i>	100%	1016.78	100.0	0.0	NR_103579	<i>Aspergillus puniceus</i>
31	<i>Aspergillus</i>	82%	<i>Aspergillus</i>	91%	<i>Ascomycota</i>	100%	<i>Aspergillus</i>	100%	1035.24	100.0	0.0	NR_163668, NR_137513, NR_111348, NR_077143	<i>Aspergillus sp.</i>
EN-13	<i>Trichoderma</i>	97%	<i>Hypocrea</i>	90%	<i>Ascomycota sp.</i> SH211670.06FU	85%	<i>Hypocrea lixii</i>	100%	1066.64	99.8	0.0	NR_137297	<i>Trichoderma simmonsii</i>
EN-15B	<i>Aspergillus</i>	88%	<i>Aspergillus</i>	91%	<i>Ascomycota</i>	100%	<i>Aspergillus</i>	100%	1026.01	99.6	0.0	NR_163668, NR_137513, NR_111348, NR_077143	<i>Aspergillus sp.</i>
EN-16B	<i>Aspergillus</i>	82%	<i>Aspergillus</i>	91%	<i>Ascomycota</i>	100%	<i>Aspergillus</i>	100%	1035.24	100.0	0.0	NR_163668, NR_137513, NR_111348, NR_077143	<i>Aspergillus sp.</i>
EN-19	<i>Hypocreales sp</i>	88%	unclassified_Nectria-ceae	74%	<i>Ascomycota</i>	100%	<i>Nectria haematococca mpVI</i>	87%	904.132	98.6	0.0	NR_164415	<i>Fusarium perseae</i>
EN-20A	<i>Penicillium</i>	94%	<i>Eupenicillium</i>	78%	<i>Penicillium</i>	99%	<i>Eupenicillium</i>	100%	996.464	99.5	0.0	NR_077153	<i>Penicillium crustosum</i>
AW-2	<i>Fusarium</i>	83%	<i>Gibberella</i>	86%	<i>Fusarium proliferatum</i> SH217299.06FU	95%	<i>Fusarium annulatum</i>	88%	948.452	99.6	0.0	NR_111889	<i>Fusarium fujikuroi</i>
AW-301	<i>Aspergillus westerdijikiae</i>	68%	<i>Aspergillus</i>	83%	<i>Aspergillus ochraceus</i> SH231999.06FU	100%	<i>Aspergillus</i>	100%	963.225	98.9	0.0	NR_135389	<i>Aspergillus westerdijikiae</i>

Table S3. Predicted proteins alignments to the homologous families in the LED and NCBI nr databases.

Lipase	Isolate	Protein sequence producing significant alignment (LED)			Protein sequence producing significant alignment (NCBI nr)			Max Ident (%)
			Score (bits)	E value		Max score	E value	
1	SL14D	abH23.01 triacylglycerol lipase	579	1e-166	alpha/beta-hydrolase, XP_025452468.1	582	0.0	100
2	2-1B	abH23.01 lipase	681	0.0	lipase, ABR12479.1	681	0.0	99
3	2-5E	abH23.01 lipase	673	0.0	hypothetical protein FOZG_04142, EWZ48645.1	674	0.0	100
4	2-5B	abH23.01 lipase	599	1e-172	probable triacylglycerol lipase precursor, XP_023428998.1	636	0.0	100
5	2-5F	abH23.01 lipase	634	0.0	probable triacylglycerol lipase precursor, XP_023428998.1	671	0.0	100
6	C-2	abH23.01 lipase	461	1e-130	Pc13g14030, XP_002559811.1	545	0.0	100
7	2-8A	abH23.01 lipase	495	1e-141	alkaline lipase, AAF82375.1	495	3e-176	100
8	2-4B	abH23.01 lipase	493	1e-140	alkaline lipase, AAF82375.1	493	4e-175	100
9	2-9A	abH23.01 lipase	489	1e-139	alkaline lipase, AAF82375.1	489	8e-174	100
10	C-1	abH23.02 lipase	170	1e-42	extracellular triacylglycerol lipase, XP_024702282.1	589	0.0	78
11	AW-301	abH23.01 hypothetical protein	383	1e-107	alpha/beta-hydrolase, XP_024707445.1	449	1e-157	86
12	2-5A	abH23.01 lipase	647	0.0	lipase, AAB34680.1	647	0.0	97
13	EN-19	abH23.01 lipase	617	1e-177	uncharacterized protein, XP_003040342.1	618	0.0	96
14	2-6	abH23.01 lipase	494	1e-140	lipase, AGV00787.1	620	0.0	84