SUPPLEMENTARY INFORMATION FOR

Large-scale phenotyping of 1,000 fungal strains for the degradation of non-natural, industrial compounds

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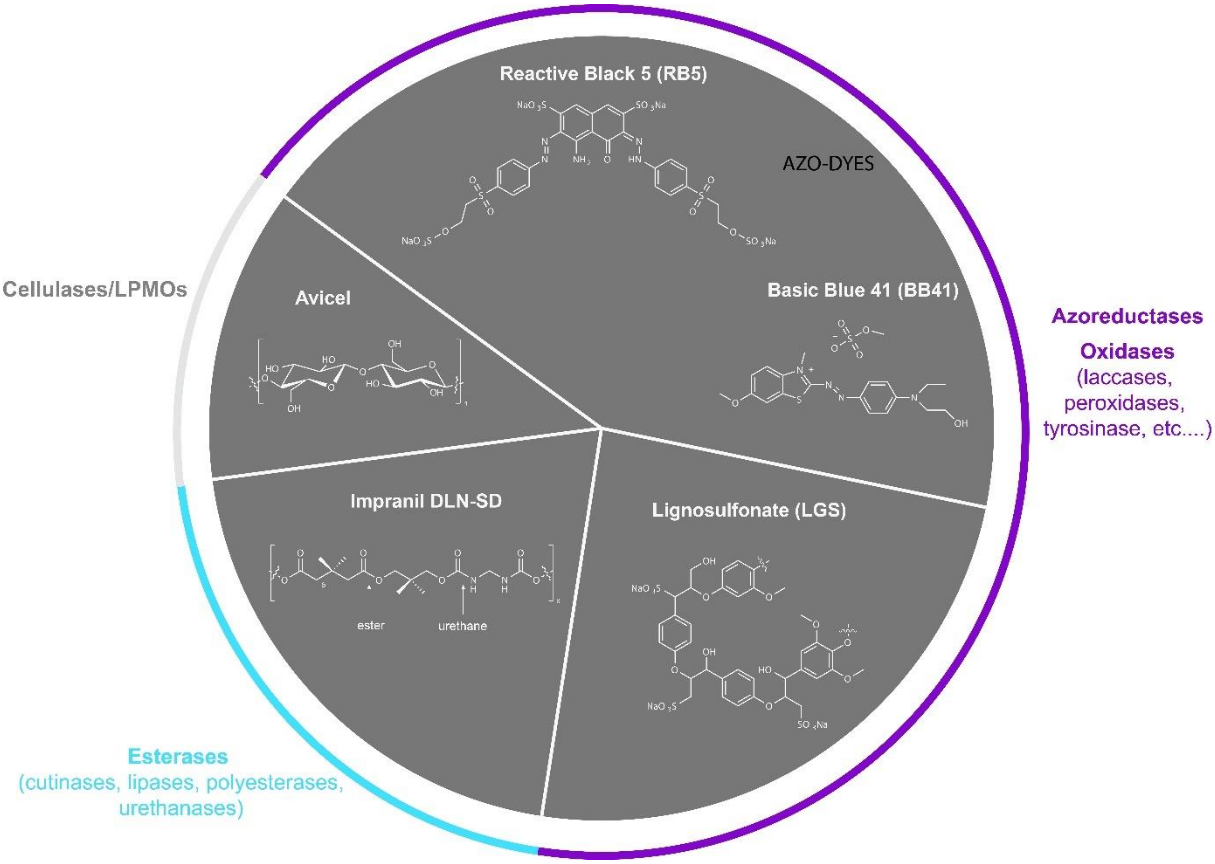
1. Supplementary Figures



Supplementary Fig. 1. Chemical structures of the 5 targeted non-natural, industrial compounds. Enzymatic activities suggested to be involved in degradation of the different compounds are indicated in the figure.

a

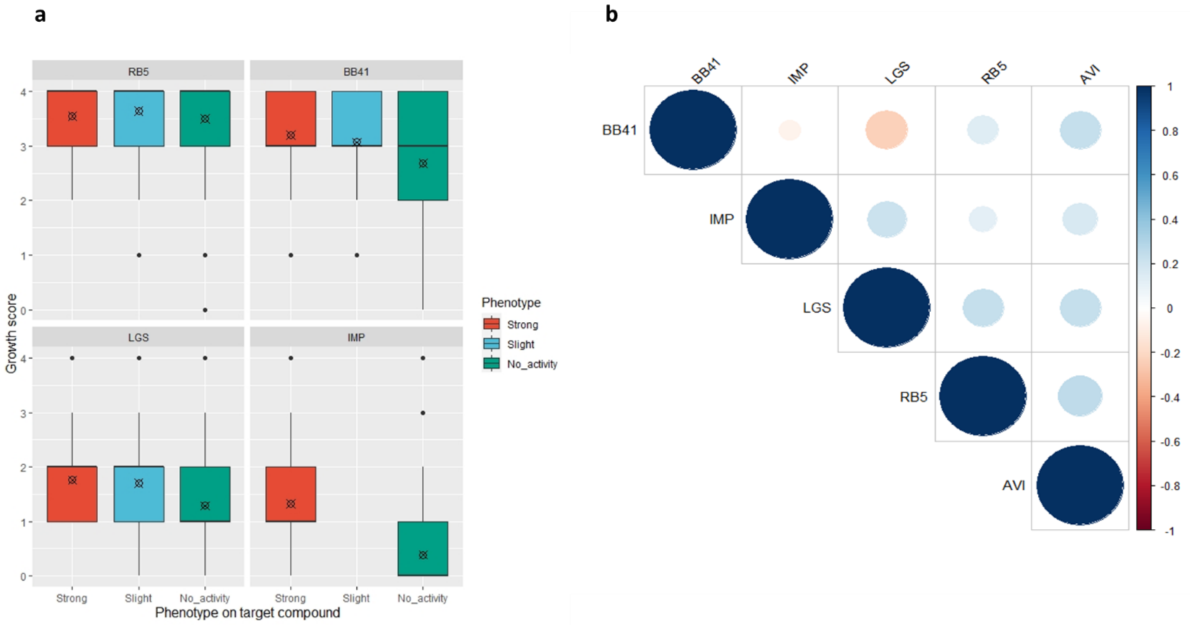
	supplemented with malt as carbon source				as a sole carbon source				
	RB5		**BB41**		**LGS**		**IMP**		**AVI**
	Growth	Decolorization	Growth	Decolorization	Growth	Oxidation	Growth	Clearing	Growth
Strong (3-4)	975	217	731	123	135	157	20	233	154
Slight (1-2)	55	133	205	87	819	449	445	na	420
None (0)	1	681	95	821	77	425	566	798	457

b

	RB5		**BB41**		**LGS**		**IMP**		**AVI**
%	Growth	Decolorization	Growth	Decolorization	Growth	Oxidation	Growth	Clearing	Growth
Strong (3-4)	95	21	71	12	13	15	2	23	15
Slight (1-2)	5	13	20	8	79	44	43	na	41
None (0)	0	66	9	80	7	41	55	77	44

c

Supplementary Fig. 2. Global phenotype scoring of the 1,013 filamentous strains. The figure shows for each substrate the number of strains displaying growth and either decolorization (for RB5 and BB41), or oxidation (for LGS) or clearing (for IMP), clustered by score intensity (strong, slight or none), and displayed as (**a**) total number of strains, (**b**) percentages (100% = 1,031) and (**c**) diagram. Abbreviations: AVI, Avicel; BB5, Basic Blue 41; IMP, Impranil; LGS, lignosulfonate; na, not applicable; RB5, Reactive Black 5.



Supplementary Fig. 3. Correlation analysis between (a) growth and functional phenotypes and (b) between the functional phenotypes. In panel a, the box plots show the distribution of growth scores (y-axis) for each phenotype levels: strong (scores 4-3; red color), slight (scores 2-1 ; blue color) and inactive (score 0 ; green color). Boxes show the interquartile range (i.e. data comprised between the first and last quartile, 25<x<75%), black bars show the median and crossed-circles show the mean. The figure shows clearly that there is no correlation between growth and functional phenotypes. In panel b, the color scale on the right-hand side indicates the correlation coefficient, from 1 (perfect positive correlation) to -1 (perfect negative correlation). The diameter of circles represents the absolute value of correlation for each pair of functional phenotypes. The figure shows the absence of correlation in between most functional phenotypes. Raw data are available in the **Supplementary Data 1**.

2. Supplementary Tables

Supplementary Table 1. Geographic origin, ecological information and authentication method used of the phenotyped 1,031 fungal strains. The Table is available as attached file (**supp_table_1.xlsx**).

Supplementary Table 2. Overview of the taxonomic diversity of phenotyped strains.

Order	Family	Number of families	Number of genera	Number of species	Number of strains
Basidiomycota	**Agaricales**	**15**	**33**	**58**	**181**
	Boletales	5	5	6	6
	Atheliales	1	1	1	1
	Polyporales	**9**	**68**	**126**	**392**
	Russulales	**6**	**10**	**13**	**27**
	Gloeophyllales	**1**	**4**	**8**	**20**
	Corticiales	1	1	1	2
	Hymenochaetales	**2**	**8**	**15**	**49**
	Cantharellales	2	4	4	9
	Microstromatales	1	1	1	1
Ascomycota	**Eurotiales**	**2**	**4**	**22**	**66**
	Chaetothyriales	1	1	1	1
	Pleosporales	**4**	**9**	**9**	**18**
	Capnodiales	1	3	3	4
	Dothideales	1	1	1	1
	Helotiales	1	3	2	4
	Chaetomellales	1	1	1	1
	Hypocreales	**8**	**46**	**73**	**147**
	Coniochaetales	1	1	1	1
	Sordariales	3	3	3	3
	Pezizales	1	1	3	3
	Xylariales	**5**	**16**	**41**	**83**
	Rhinotrichum spp.				1
	Saccharomycetales	2	2	1	2
Mucoromycota	Mucorales	2	3	4	6
	Umbelopsidales	1	1	1	1
	Mortierellales	1	1	1	1
		78	231	400	1031

Supplementary Table 3. Occurrence of the PF01083 domain (cutinase domain) in the sequenced fungal genomes available in the JGI Mycocosm portal (Grigoriev *et al*., 2011; Grigoriev *et al*., 2014)[1,2]

Fungal families	Number of PF01083 domain "cutinase"	Number of sequenced genome
Ascomycota	6966	1070
Eurotiales	1448	279
Pleosporales	987	93
Hypocreales	897	98
Xylariales	793	113
Basidiomycota	1117	551
Agaricales	301	164
Gloeophyllales	0	4
Hymenochaetales	0	14
Polyporales	2	77
Russulales	12	40
Mucoromycota	0	97

Supplementary Table 4. List of primers used for the molecular authentication of candidate strains.

References	gene fragment	species	Forward		Reverse	
Stielow *et al*., 2015 [3]	TEF-1α	*Ascomycetes*	TEF1α-983-F	GCYCCYGGHCAYCGTGAYTTYAT	EF1-1567R	ACHGTRCCRATACCACCRATCTT
Rehner *et al*., 2005 [4]	TEF-1α	*Basidiomycetes*	TEF1α-983-F-CF2	GCYCCYGGHCAYCGTGAYTTYAT	TEF1α-2218-R-CR2	ATGACACCRACRGCRACRGTYTG
White *et al*., 1990 [5]	ITS1-5,8S-ITS2	*Ascomycetes*	ITS5	GGAAGTAAAAGTCGTAACAAGG	ITS4	TCCTCCGCTTATTGATATGC
	ITS1-5,8S-ITS2	*Basidiomycetes and Mucoromycetes*	ITS1	TCCGTAGGTGAACCTGCGG	ITS4	TCCTCCGCTTATTGATATGC
Parry and Nicholson, 1996 [6]	TEF-1α	*Fusarium poae*	Fp82F	CAAGCAAACAGGCTCTTCACC	Fp82R	TGTTCCACCTCAGTGACAGGTT
Nicholson *et al*., 1998 [7]	TEF-1α	*Fusarium culmorum*	Fc01F	ATGGTGAACTCGTCGTGGC	Fc01R	CCCTTCTTACGCCAATCTCG
	TEF-1α	*Fusarium graminearum*	Fg16NF	ACAGATGACAAGATTCAGGCACA	Fg16NR	TTCTTTGACATCTGTTCAACCCA
Yoder et Christianson, 1998 [8]	TEF-1α	*Fusarium crookwellense*	FcroF	CTCAGTGTCCACCGCGTTGCGTAG	FcroR	CTCAGTGTCCCATCAAATAGTCC
Wilson *et al*., 2004 [9]	TEF-1α	*Fusarium sporotrichioides*	FsporF1	CGCACAACGCAAACTCATC	LansporR1	TACAAGAAGACGTGGCGATAT
Turner *et al*., 1998 [10]	TEF-1α	*Fusarium avenaceum*	JIAf	GCTAATTCTTAACTTACTAGGGGCC	JIAr	CGTTAATAGGTTATTTACATGGGCG
Moller *et al*., 1999 [11]	TEF-1α	*Fusarium subglutinans*	61-2 F	GGCCACTCAAGAGGCGAAAG	61-2 R	GTCAGACCAGAGCAATGGGC
Picot *et al*., 2012 [12]	FUM 1	*Fusarium proliferatum*	FproF	TGCTCGTCATCCCTGATAG	FproR	GAAGATGGCATTGATTGCCTC
Aguado *et al*., 2018 [13]	FUM 1	*Fusarium verticillioides*	Fum1-654	CGGTTGTTCATCATCTCTGA	Fum1-1158	GCTCCCGATGTAGAGCTTGTT
Scauflaire *et al*., 2012 [14]	EF1- α	*Fusarium temperatum*	FtemF	AAGACCTGGCGGGC	FtemR	TCAGAAGGTTGTGGCAATGG
This study	ITS2	*Agaricus bisporus var. bisporus*	5,8 S 3'F	AYGCCTGTYYGAGYGTC	Abisp ITS2	TGTCCTTAGACGATTAGAAGC

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