Supplementary Material for

Lignocellulosic fraction-induced niche differentiation within dissimilatory iron reducing bacterial groups in a paddy soil

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Table S1 List of bacterial genera to which the reported DIRB strains belong in alphabetical order.

Genus	Reference	Genus	Reference
Acidicaldus	Esther et al. 2015	*Geobacter*	Esther et al. 2015
Acidiphilium	Esther et al. 2015	*Georgfuchsia*	Esther et al. 2015
Acidocella	Esther et al. 2015	*Geothrix*	Zhan et al. 2021
Acidithiobacillus	Tekin et al. 2013	*Geothermobacter*	Esther et al. 2015
Acinetobacter	Zhan et al. 2021	*Geovibrio*	Esther et al. 2015
Aeromonas	Wang et al. 2010	*Klebsiella*	Li et al. 2009
Alicyclobacillus	Esther et al. 2015	*Lactobacillus*	Gonzalez et al. 2017
Alkaliphilus	Esther et al. 2015	*Lactococcus*	Freguia et al. 2009
Anaeromyxobacter	Esther et al. 2015	*Lysinibacillus*	Ye et al. 2019
Bacillus	Esther et al. 2015	*Methanococcus*	Bond and Lovley 2002
Burkholderia	Peng et al. 2015	*Micrococcus*	Tiwari et al. 2014
Citrobacter	Liu et al. 2016	*Moorella*	Poehlein et al. 2018
Clostridium	Dobbin et al. 1999	*Natranaerobaculum*	Esther et al. 2015
Comamonas	Wu et al. 2009	*Pantoea*	Liu and Wang 2015
Corynebacterium	Wu et al. 2013	*Pelobacter*	Esther et al. 2015
Deferrisoma	Esther et al. 2015	*Proteus*	Esther et al. 2015
Deferribacter	Esther et al. 2015	*Pseudomonas*	Peng et al. 2015
Desulfosporosinus	Esther et al. 2015	*Raoultella*	Sklodowska et al. 2018
Desulfitobacterium	Esther et al. 2015	*Rhodobacter*	Dobbin et al. 1996
Desulfuromonas	Esther et al. 2015	*Rhodoferax*	Esther et al. 2015
Desulfobulbus	Holmes et al. 2004	*Serratia*	Esther et al. 2015
Desulfovibrio	Liu et al. 2010	*Shewanella*	Esther et al. 2015
Enterobacter	Liu and Wang 2016	*Sporomusa*	Peng et al. 2015
Escherichia	Gescher et al. 2008	*Sulfobacillus*	Esther et al. 2015
Ferrithrix	Esther et al. 2015	*Tepidimicrobium*	Esther et al. 2015
Ferrimicrobium	Esther et al. 2015	*Thermincola*	Esther et al. 2015
Ferribacterium	Esther et al. 2015	*Thermoanaerobacter*	Esther et al. 2015
Frateuria	Esther et al. 2015	*Thermoterrabacterium*	Esther et al. 2015
Geoalkalibacter	Esther et al. 2015	*Tolumonas*	Akob et al. 2008

Table S2 Three-way ANOVA for the effects of Fh addition (Fh), substrate species (Substrate), and incubation time (Time) on the abundances of soil total bacteria and DIRB.

		Total bacteria		DIRB	
	DF	*F*	*P*	*F*	*P*
Fh	1	1.869	0.184	4.766	0.039
Substrate	2	3.679	0.040	18.10	< 0.001
Time	1	6.159	0.020	0.735	0.400
Fh × Substrate	2	2.555	0.099	4.981	0.016
Fh × Time	1	3.503	0.073	0.213	0.649
Substrate × Time	2	4.623	0.020	0.230	0.797
Fh × Substrate × Time	2	2.080	0.147	0.074	0.928

Table S3 Three-way ANOVA for the effects of Fh addition (Fh), substrate species (Substrate), and incubation time (Time) on the diversity of soil bacterial community.

	DF	*F*	*P*
Fh	1	61.162	< 0.001
Substrate	2	156.896	< 0.001
Time	1	2.922	0.100
Fh × Substrate	2	32.268	< 0.001
Fh × Time	1	51.373	< 0.001
Substrate × Time	2	0.200	0.820
Fh × Substrate × Time	2	93.328	< 0.001

Table S4 PERMANOVA for the effects of Fh addition (Fh), substrate species (Substrate), and incubation time (Time) on the composition of soil bacterial community.

	DF	R^2	*P*
Fh	1	0.124	0.001
Substrate	2	0.246	0.001
Time	1	0.031	0.004
Fh × Substrate	2	0.147	0.001
Fh × Time	1	0.030	0.006
Substrate × Time	2	0.050	0.003
Fh × Substrate × Time	2	0.055	0.001

Table S5 Keystone taxa in bacterial co-occurrence networks in lignocellulose-amended soils without (–Fh) or with Fh addition (+Fh).

Network		ASV ID	Role	Degree	*Zi*	*Pi*	Phylum	Genus	Abundance (%)[a]
–Fh	Xylan	ASV23	Module hub	23	2.99	0	Chloroflexi	*UTCFX1*	0.24 ± 0.05
		ASV110	Module hub	21	2.60	0.44	Methylomirabilota	Unclassified Rokubacteriales	0.21 ± 0.10
	Cellulose	ASV355	Module hub	19	2.77	0.46	Chloroflexi	Unclassified JG30-KF-CM45	0.06 ± 0.04
		ASV544	Module hub	24	3.12	0.67	Actinobacteriota	Unclassified Micrococcaceae	0.07 ± 0.03
		ASV1003	Module hub	18	2.54	0.35	Firmicutes	*Effusibacillus*	0.05 ± 0.03
	Lignin	ASV1441	Module hub	17	3.29	0.47	Proteobacteria	Unclassified Steroidobacteraceae	0.06 ± 0.02
+Fh	Cellulose	ASV23	Module hub	52	2.91	0.52	Chloroflexi	*UTCFX1*	0.31 ± 0.11
		ASV49	Module hub	46	4.17	0	Chloroflexi	*UTCFX1*	0.16 ± 0.08
		ASV114	Module hub	35	2.89	0	Proteobacteria	Unclassified Xanthobacteraceae	0.21 ± 0.05
		ASV167	Module hub	8	2.60	0	Acidobacteriota	Unclassified Vicinamibacterales	0.14 ± 0.08
		ASV191	Module hub	32	2.54	0.59	Gemmatimonadota	Unclassified S0134	0.07 ± 0.04
		ASV243	Module hub	52	2.91	0.38	Desulfobacterota	*Citrifermentans*	0.18 ± 0.07
		ASV330	Module hub	48	2.60	0.07	Acidobacteriota	Unclassified 11-24	0.07 ± 0.03
	Lignin	ASV205	Module hub	23	2.67	0.44	Actinobacteriota	*Conexibacter*	0.14 ± 0.05

[a] Average relative abundances of ASVs across the nine soil samples used for network construction (Mean ± SD).

Table S6 Relative abundances (%) of DIRB-associated genera detected in lignocellulose-amended soils without (–Fh) or with Fh addition (+Fh) after three (3w) and six weeks (6w) of incubation and non-amended control at the beginning of incubation.

Genera	Control	–Fh						+Fh					
		Xylan		Cellulose		Lignin		Xylan		Cellulose		Lignin	
		3w	6w	3w	6w	3w	6w	3w	6w	3w	6w	3w	6w
Acinetobacter	ND	ND	ND	ND	ND	0.01	ND	< 0.01	ND	ND	0.02	0.02	0.01
Alicyclobacillus	< 0.01	ND	ND	ND	0.01	0.01	ND	ND	ND	0.01	ND	< 0.01	ND
Alkaliphilus	0.02	0.01	ND	ND	0.01	ND	0.02	ND	0.01	0.01	0.01	< 0.01	ND
Anaeromyxobacter	1.45	1.23	1.11	0.83	1.14	1.83	1.39	0.97	1.04	0.99	2.27	1.60	1.60
Bacillus	3.20	1.74	2.64	1.20	2.26	1.81	2.78	0.69	1.48	2.17	1.51	2.14	2.19
Brevundimonas	0.01	ND	0.02	ND	0.01	< 0.01	ND	ND	ND	ND	ND	ND	ND
Clostridium	3.66	11.39	13.13	1.13	1.25	0.99	1.48	9.51	16.70	0.75	0.70	1.24	0.88
Deferrisoma	0.08	0.14	0.16	0.19	0.15	0.42	0.33	0.50	0.36	0.61	0.37	0.41	0.29
Desulfitobacterium	0.04	0.14	0.03	0.04	0.03	0.08	0.07	0.10	0.08	0.04	0.02	0.15	0.23
Desulfobulbus	0.01	ND	0.01	ND	ND	0.14	0.10	0.01	ND	< 0.01	ND	0.02	0.05
Desulfosporosinus	0.18	ND	0.07	ND	0.03	0.39	0.16	ND	ND	0.01	ND	0.09	0.15
Desulfovibrio	0.28	0.03	0.06	0.03	0.02	0.29	0.28	0.04	0.03	0.06	0.06	0.33	0.37
Geobacter	0.09	0.05	0.19	0.24	0.43	0.25	0.16	0.02	0.03	0.12	0.25	0.13	0.12
Geothrix	0.05	ND	ND	ND	ND	0.01	0.02	ND	ND	ND	ND	ND	ND
Lysinibacillus	0.06	0.01	0.09	ND	0.03	0.08	0.04	ND	ND	0.04	0.01	0.06	0.05
Propionibacterium	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	< 0.01
Pseudomonas	0.04	ND	ND	ND	ND	0.09	ND	ND	ND	ND	ND	0.02	0.04
Sporomusa	0.65	0.09	0.03	1.17	0.46	0.06	0.04	0.01	ND	0.02	0.01	0.06	0.13
Thermincola	0.20	0.23	0.12	0.02	0.02	0.03	0.03	13.83	6.63	0.05	0.02	0.15	0.12
Sum	**10.03 ± 4.13**	**15.06 ± 4.06**	**17.66 ± 3.51**	**4.85 ± 0.57**	**5.83 ± 0.67**	**6.48 ± 0.61**	**6.90 ± 0.76**	**25.69 ± 2.54**	**26.36 ± 0.79**	**4.89 ± 0.43**	**5.26 ± 0.83**	**6.44 ± 0.13**	**6.25 ± 0.62**

Data for each genus are the means of the three replicates. Data of sum are presented as the means ± SD. ND means not detected.

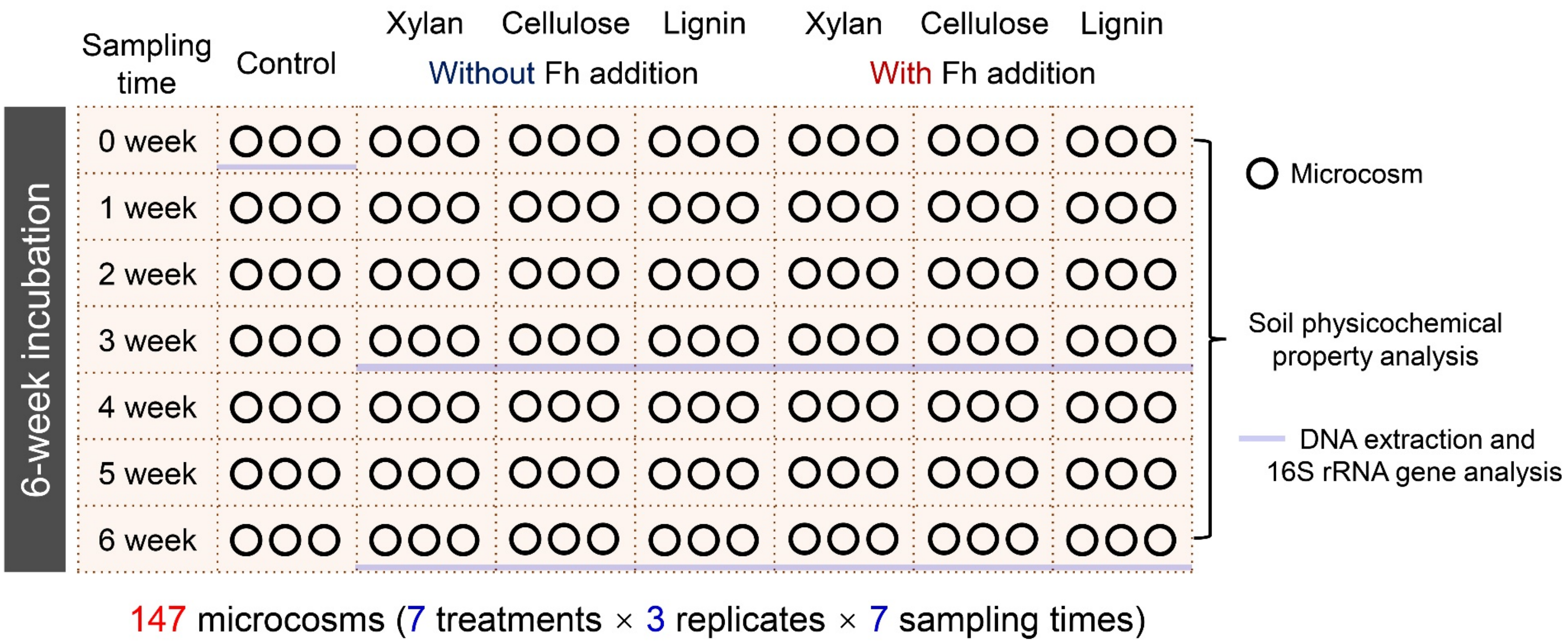

Fig. S1 Schematic diagram of the experimental design.

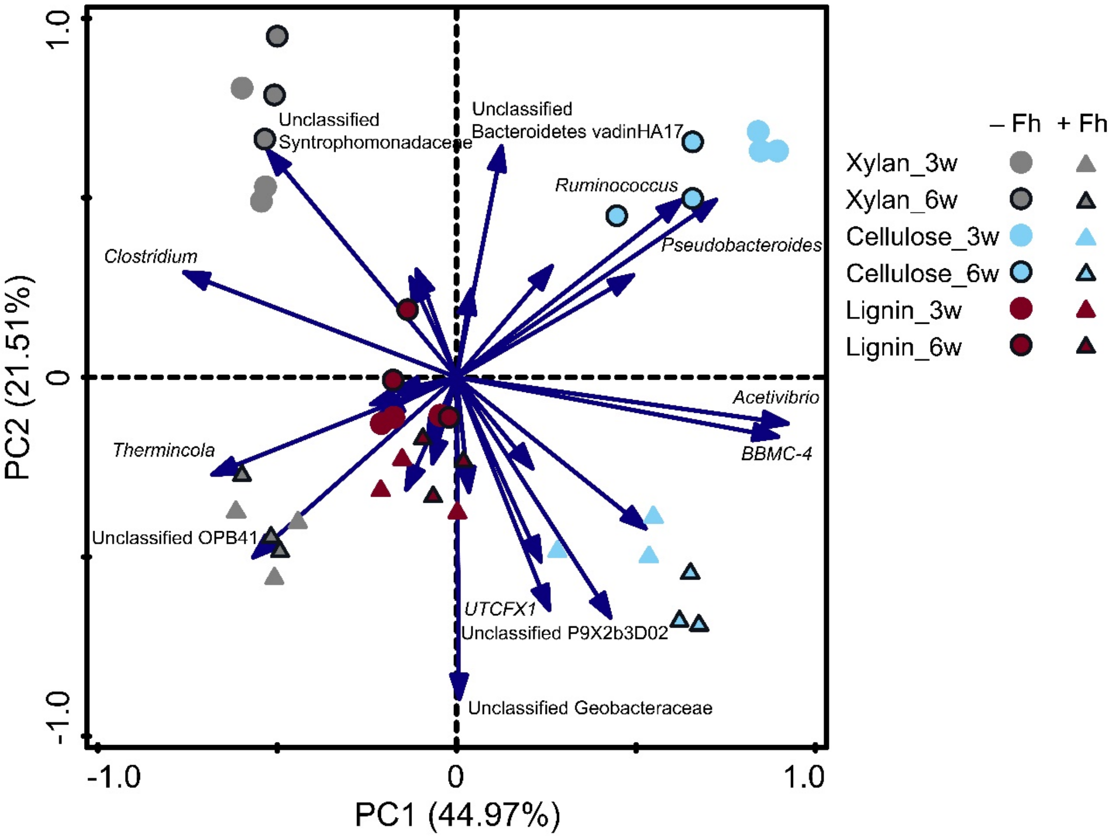

Fig. S2 Principal component analysis of the bacterial genera (relative abundance ≥ 2% in at least one soil sample) in lignocellulose-amended soils without (–Fh) or with Fh addition (+Fh) after three (3w) and six weeks (6w) of incubation.

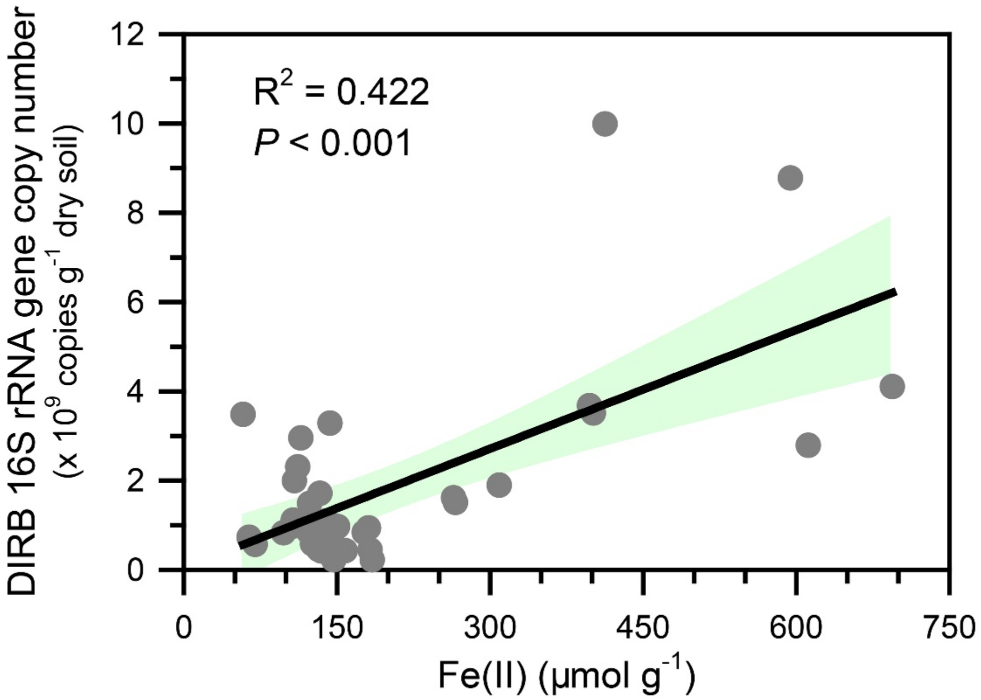

Fig. S3 Linear regression analysis between DIRB abundance and soil Fe(II) content.

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