

# Microbial taxa and functional genes shift in degraded soil with bacterial wilt

**Running title: Microbial communities respond to soil degradation**

Hongchun Zhang<sup>1a</sup>, Rui Wang<sup>1a</sup>, Shu Chen<sup>1</sup>, Gaofu Qi<sup>1</sup>, Zhili He<sup>1,2</sup>, Xiuyun Zhao<sup>1\*</sup>

<sup>1</sup>College of Life Science and Technology, Huazhong Agricultural University, Wuhan  
430070, China;

<sup>2</sup>Institute for Environmental Genomics and Department of Microbiology and Plant  
Biology, University of Oklahoma, Norman, OK 73019, USA.

<sup>a</sup> Same contribution to this study.

\*Correspondence author, E-mail: xiuyunzh@mail.hzau.edu.cn; Tel:  
+86-15387157410.

**Table S1 Summary for 16S rRNA pyrosequencing data**

<b>Samples</b>	<b>Number of reads</b>	<b>Number of OTUs</b>	<b>Chao 1</b>	<b>Shannon's index</b>
D01	28837	6379	14135	7.54
D02	25414	5948	14530	7.29
D03	25119	5004	10076	7.15
D04	28034	6364	12940	7.71
D05	28034	6881	14886	7.76
H01	44458	10566	53235	8.20
H02	42545	7709	18288	7.96
H03	38881	8233	22691	7.99
H04	25645	9579	37568	8.13
H05	35772	6888	14602	7.82

**Table S2 Summary for 18S rRNA pyrosequencing data**

<b>Sample</b>	<b>Number of reads</b>	<b>Number of OTUs</b>	<b>Chao 1</b>	<b>Shannon's index</b>
H01	24900	1984	7336	4.29
H02	43031	2131	9760	4.39
H03	24976	1458	6643	3.65
H04	25889	2216	10302	4.34
H05	43600	1867	8443	3.99
D01	43685	1524	6140	3.66
D02	45838	1136	6314	3.77
D03	28505	1729	8027	3.79
D04	46567	1348	6633	3.63
D05	38220	1776	8224	3.87

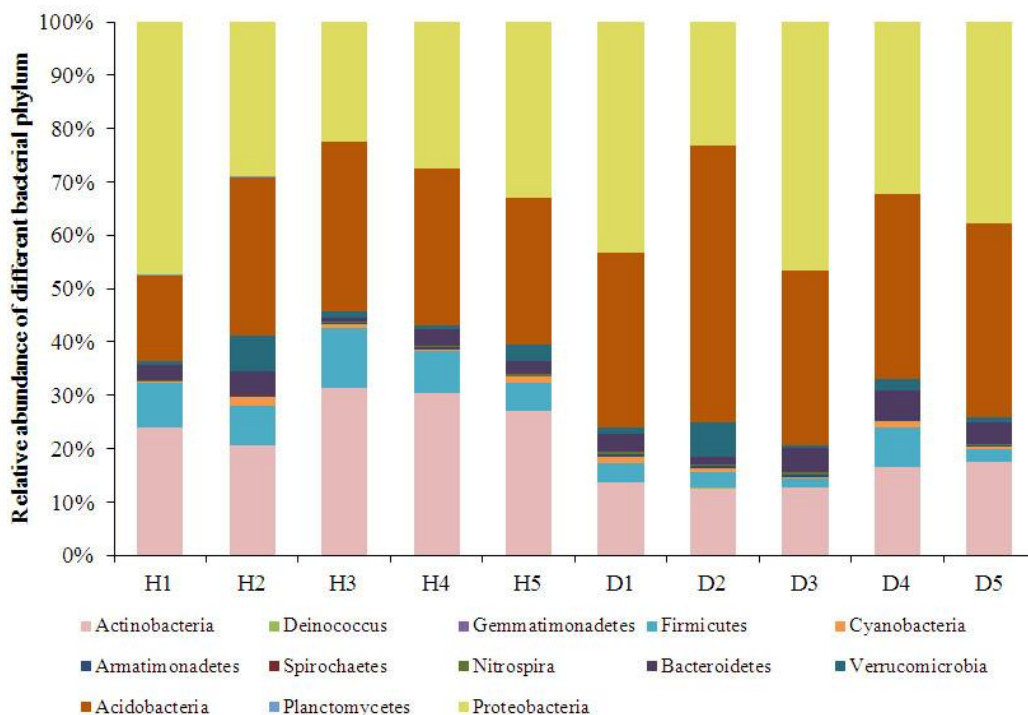
Table S3 Pathogenic *Ralstonia* and *Pseudomonas* OTUs

OTU designation	Nearest strain (% identity) <sup>a</sup>	Abundance in Healthy soils <sup>b</sup>	Abundance in Degraded soils <sup>b</sup>
890	<i>Ralstonia solanacearum</i> strain in4ss52 (99%)	6.6 ± 1.52 B	15.6 ± 2.66 A
10283	<i>Ralstonia solanacearum</i> strain in4ss52 (98%)	0.2 ± 0.45 b	1.6 ± 0.89 a
12313	<i>Ralstonia solanacearum</i> strain 08BF31TG (99%)	0.4 ± 0.54 B	2.2 ± 0.84 A
1075	<i>Pseudomonas corrugate</i> strain BS3649 (99%)	2.4 ± 0.54 B	4.4 ± 0.89 A
1197	<i>Pseudomonas mediterranea</i> strain DSM 16733 (99%)	2.2 ± 1.09 b	4.2 ± 1.64 a
4678	<i>Pseudomonas aeruginosa</i> strain BOAKS 44E (99%)	0.8 ± 0.44 b	2.4 ± 1.51 a
11417	<i>Pseudomonas corrugata</i> strain BS3649 (99%)	0.2 ± 0.44 B	1.8 ± 0.83 A
13587	<i>Pseudomonas corrugata</i> strain BS3649 (98%)	0.2 ± 0.44 B	1.2 ± 0.44 A
14466	<i>Pseudomonas corrugata</i> strain BS3649 (98%)	0 B	1.4 ± 0.54 A
23851	<i>Pseudomonas syringae</i> isolate 21 (97%)	0 B	1.8 ± 0.83 A

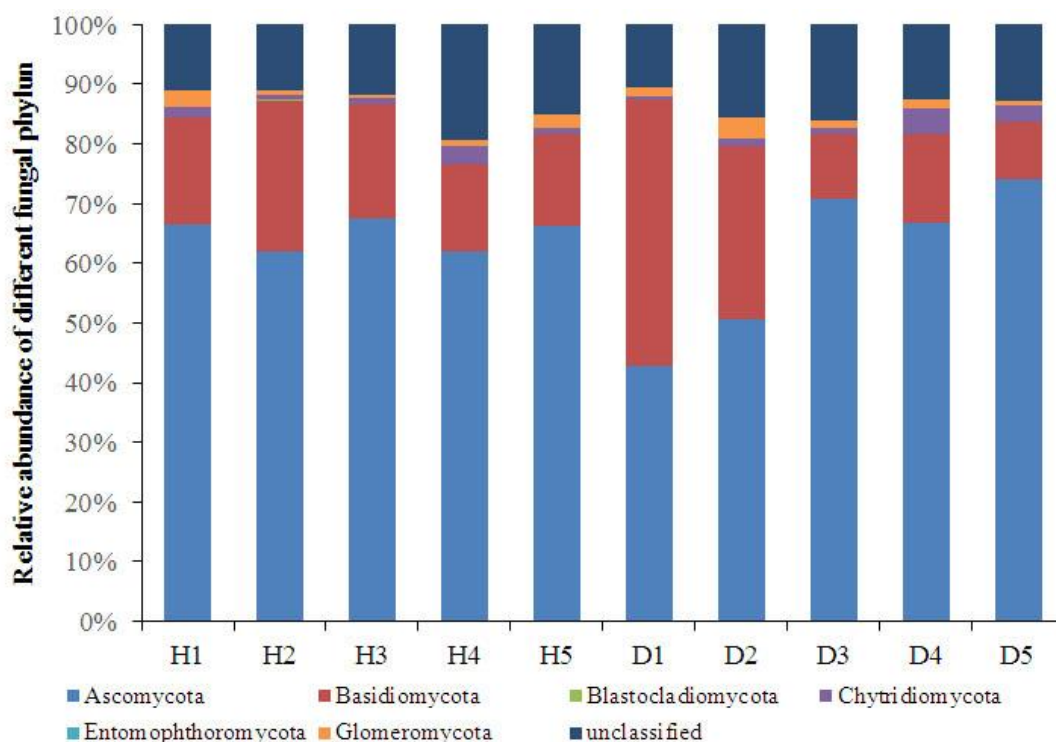
<sup>a</sup> % identity values are from analyses using BLAST (NCBI) where coverage was at least 97%.

<sup>b</sup> The different lower-case letters and capital letters in same row indicated significant difference between healthy and degraded soils at  $P < 0.05$  and  $P < 0.01$ , respectively.

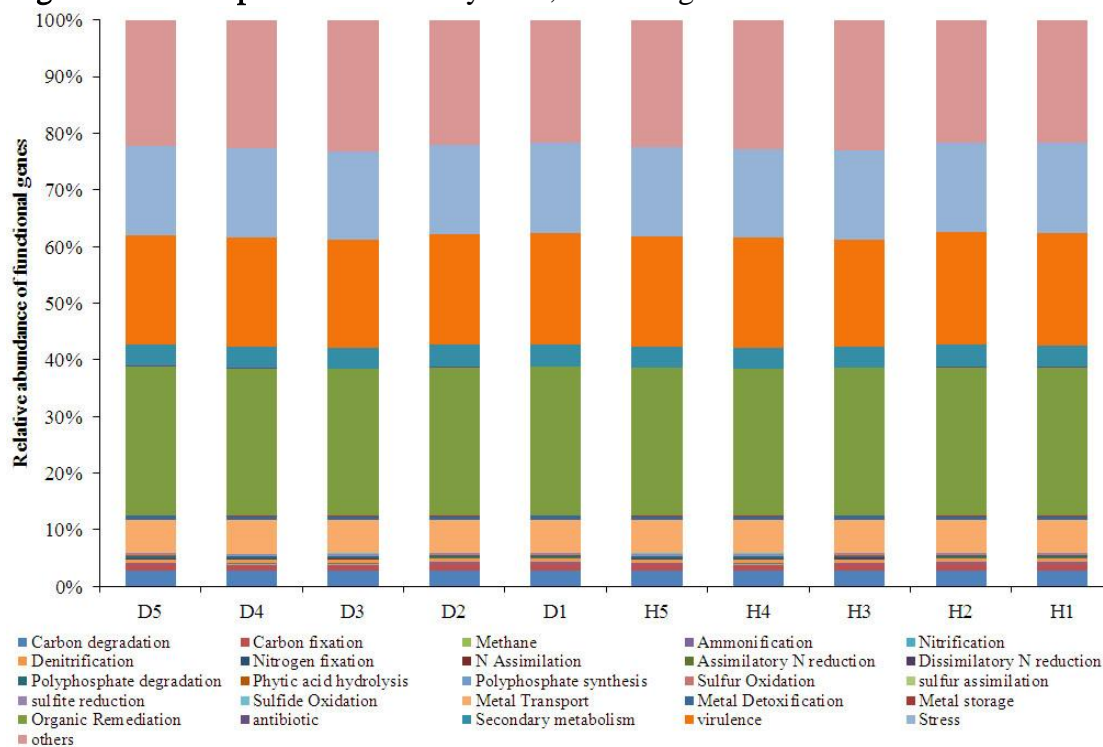
**Figure S1** Relative abundances of the dominant bacterial taxa in healthy and degraded soil samples at the phylum level. H1-5: healthy soils; D1-5: degraded soils.



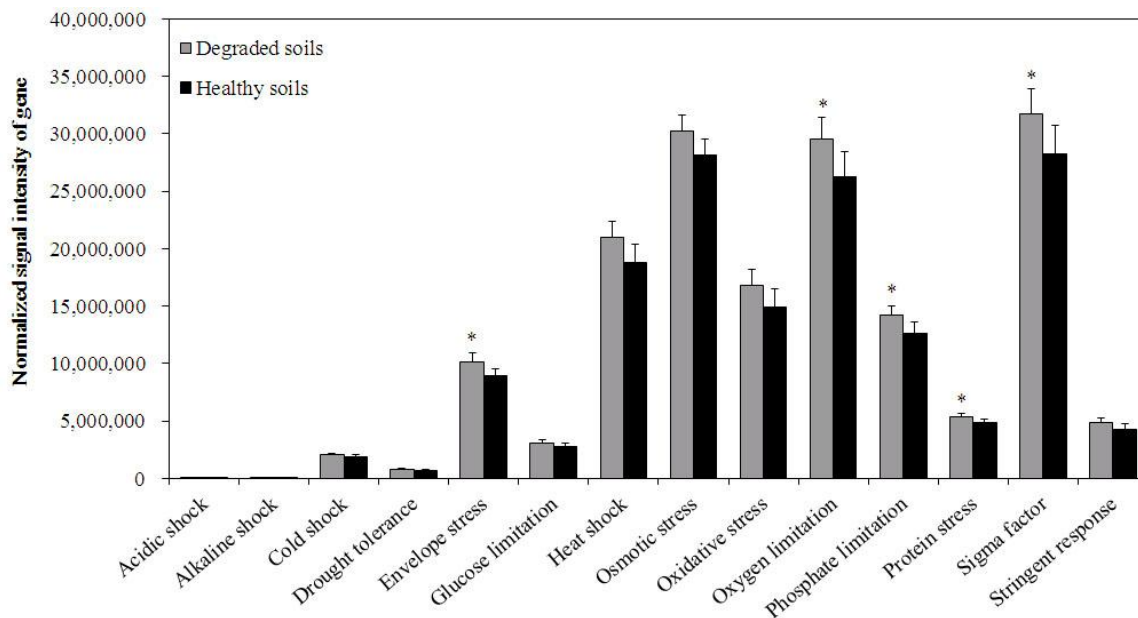
**Figure S2** Relative abundances of the dominant fungal taxa in healthy and degraded soil samples at the phylum level. H1-5: healthy soils; D1-5: degraded soils.



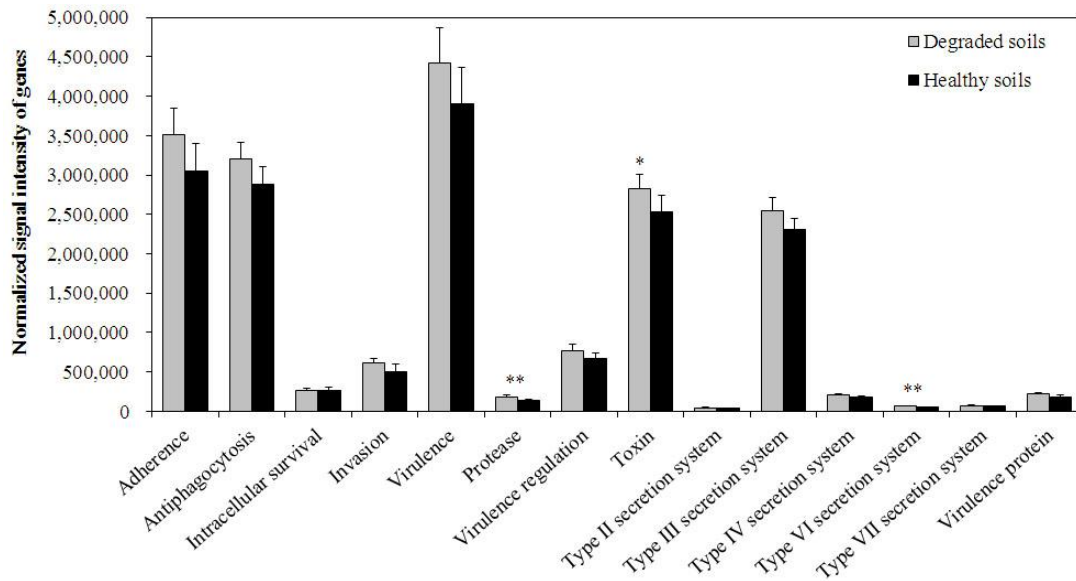
**Figure S3 Relative abundance of various functional groups detected in healthy and degraded soil samples. H1-5: healthy soils; D1-5: degraded soils.**



**Figure S4 Stress related genes.** The normalized signal intensity of functional genes involved in stress was compared between healthy and degraded soils. All data are presented as the mean  $\pm$  SE. \*  $P < 0.05$ .



**Figure S5 Virulence related genes.** The normalized signal intensity of genes involved in virulence was compared between healthy and degraded soils. All data are presented as the mean  $\pm$  SE. \*\*  $P < 0.01$ , \*  $P < 0.05$ .



**Figure S6 Metal related genes.** The normalized signal intensity of metal resistance genes was compared between healthy and degraded soils. All data are presented as the mean  $\pm$  SE. \*\*  $P < 0.01$ , \*  $P < 0.05$ .

