**Divergent taxonomic and functional responses of microbial communities to field simulation of aeolian soil erosion and deposition**

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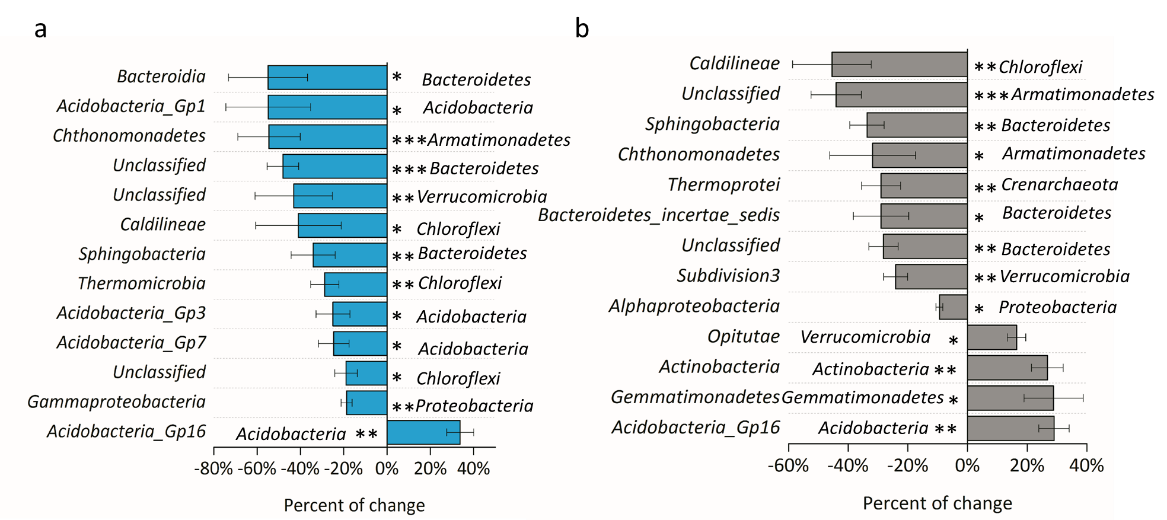
**Supplementary materials**

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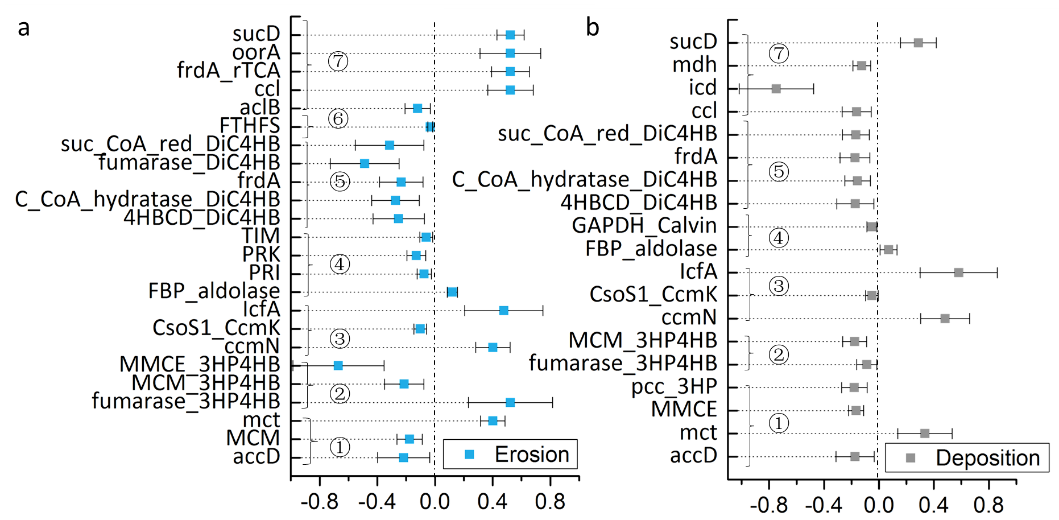
**Figure S1**. Site sketch and pictures of experimental sites. C, control；E, soil erosion; D, soil deposition; G, sheep grazing; EG, soil erosion plus sheep grazing; DG, soil deposition plus sheep grazing.



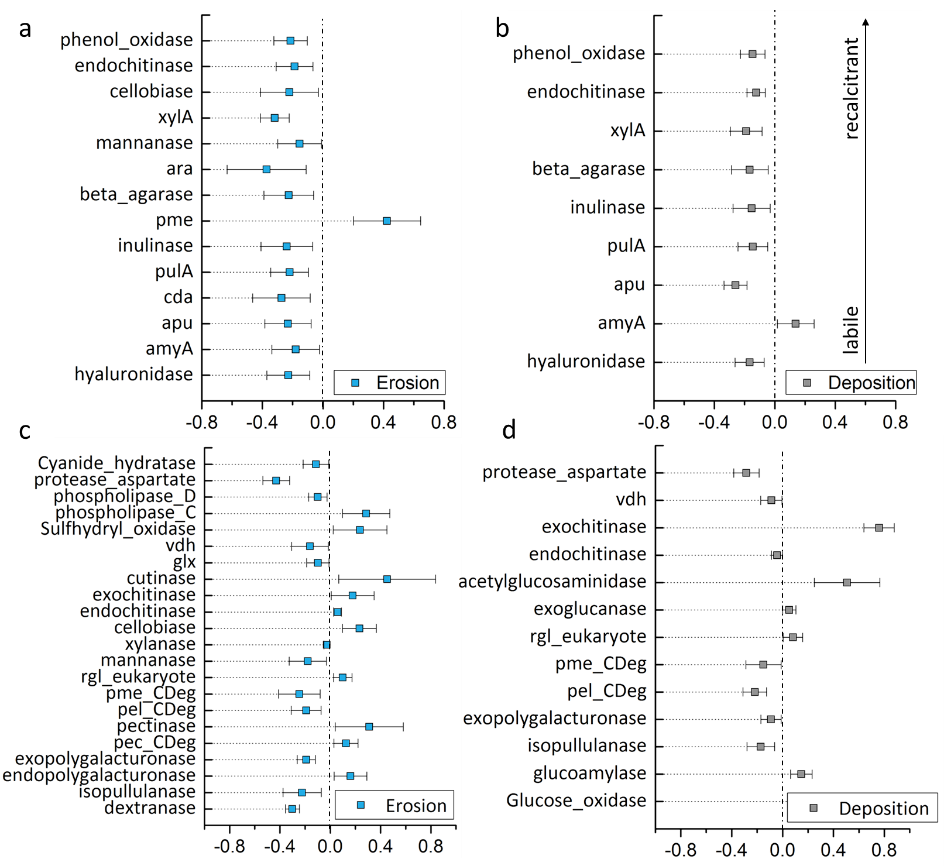
**Figure S2**. Rarefaction curves of control, erosion and deposition samples. E: erosion samples; C; controls; D: deposition samples.

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**Figure S3.** Percentage changes in relative abundances at the class level by (a) soil erosion and (b) soil deposition. Asterisk indicates significant differences. \**P*<0.10; \*\**P*< 0.05; \*\*\**P*<0.01.



**Figure S4.** Significantly changed microbial carbon fixation genes by (a) soil erosion and (b) soil deposition. ①3-hydroxypropionate cycle; ②3-hydroxypropionate/4-hydroxybutyrate cycle; ③carboxysome; ④calvin cycle; ⑤dicarboxylate/4-hydroxybutyrate cycle; ⑥reductive acetyl–CoA pathway; and ⑦reductivesuc tricarboxylic acid cycle. The confidence interval is 0.90. Abbreviations of gene names: *accD*, acetyl-CoA carboxylase beta subunit; *MCM*, methylmalonyl-CoA mutase; *ccmN*, carbon dioxide concentrating mechanism protein; *lcfA*, long-chain fatty acid content; *PRI*, plasmid IncL/M family conjugative primase; *TIM*, triosephosphate isomerase; *frdA*, anaerobic fumarate reductase catalytic and NAD/flavoprotein subunit; *FTHFS*, fomate-tetrahydrofolate ligase; *aclB*, ATP-citrate lyase beta subunit; *ccl*, citrulline cluster-linked gene; *oorA*, 2-oxoglutarate-acceptor oxidoreductase subunit OorA; *sucD*, succinyl-CoA synthetase subunit alpha; *icd*, isocitrate dehydrogenase; *mdh*, malate dehydrogenase.



**Figure S5.** The response ratio results showing significantly changed (a) archaeal carbon degradation genes at the eroded site; (b) archaeal carbon degradation genes at the deposited site; (c) fungal carbon degradation genes at the eroded site; and (d) fungal carbon degradation genes at the deposited site. The confidence interval is 0.90. Abbreviations of gene names: *amyA*, alpha-amylase; *apu*, amylopullulanase; *cda*, cytidine deaminase; *pulA*, glycogen debranching enzyme; *pme*, Pectinesterase; *ara*, alpha-N-arabinofuranosidase; *xylA*, xylose isomerase; *glx*, glyoxalase; *vdh*, vanillin dehydrogenase.

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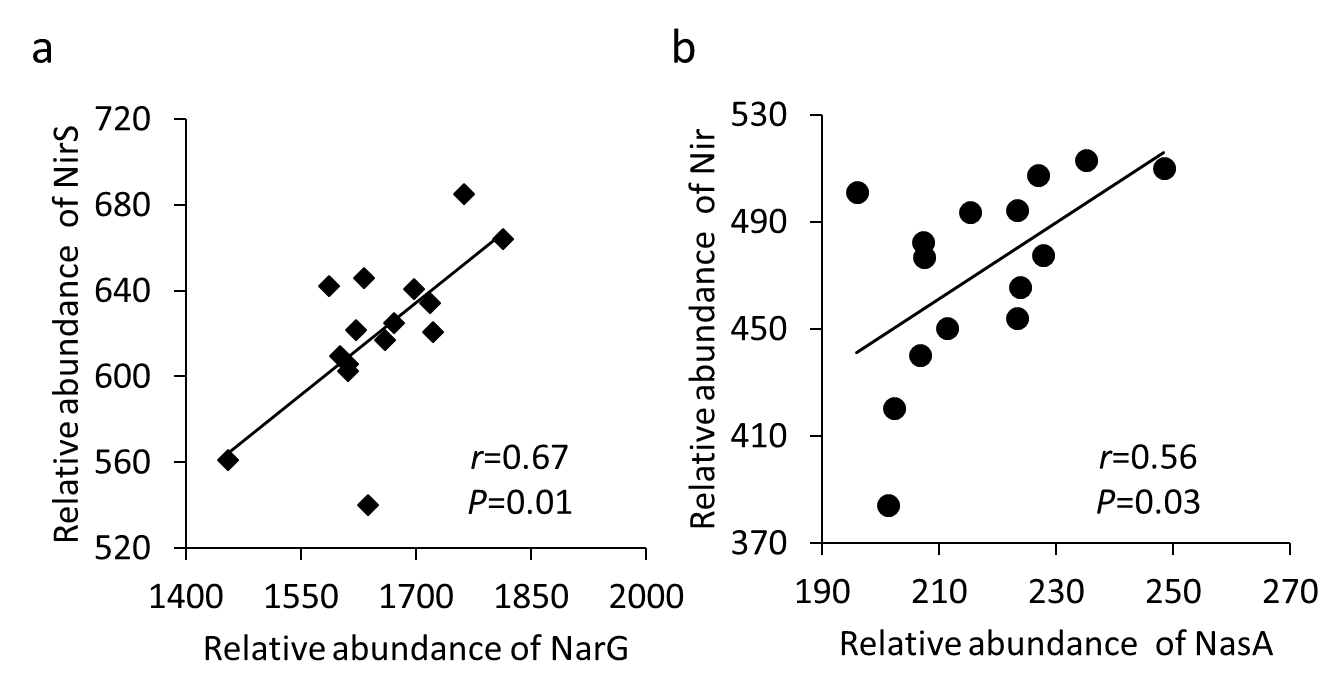
**Figure S6.** Relative abundances of phosphorus cycling genes. Asterisk indicates significant differences analyzed by two-tailed *t*-tests. \*\**P*<0.01. Abbreviations of gene names: *ppk*, polyphosphate kinase; *ppx*, exopolyphosphatase.

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**Figure S7.** Relative abundances of potassium cycling genes. Asterisk indicates significant differences analyzed by two-tailed *t*-tests. \*\**P*<0.01; \**P*<0.05. Abbreviations of gene names: *kdpA*, potassium-transporting ATPase subunit A; *kefBC*, glutathione-regulated potassium-efflux system protein (K(+)/H(+) antiporter); *ktrBD*, ktr system potassium uptake protein B; *kup*, potassium transporter; *trkA*, potassium transporter membrane protein; *trkGH*, potassium uptake transporter.



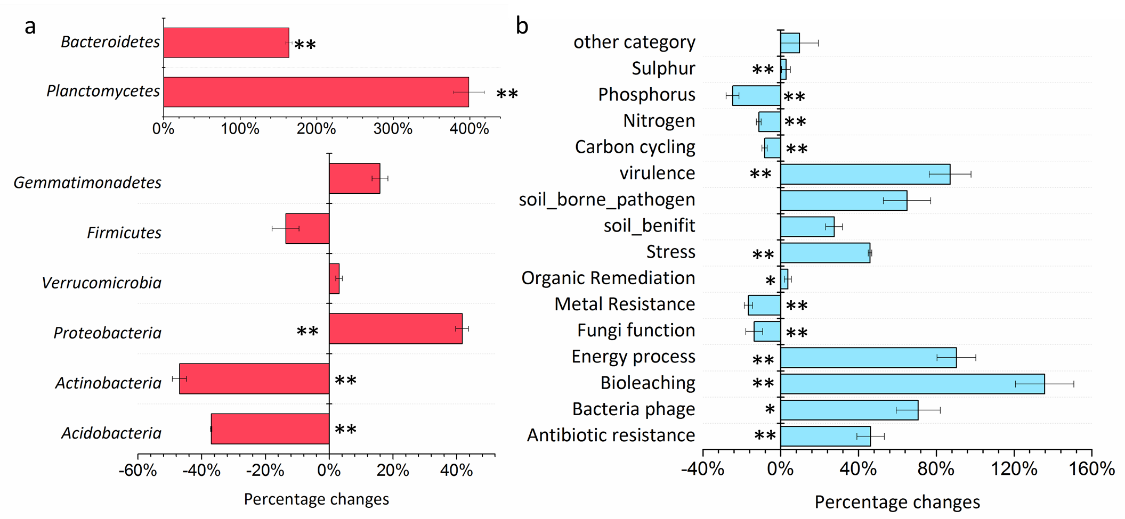
**Figure S8.** The Pearson correlation between soil pH and microbial taxonomic α-diversity measured by the Simpson index.

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**Figure S9.** Pearson correlations between (a) relative abundance of *narG* and *nirS*; and (b) relative abundance of *nasA* and *nir*.



**Figure S10** Percent change of significantly changed stress genes (a) at eroded sites (b) at deposited sites. Asterisk indicates significant differences analyzed by T-test. \*\*\**P*<0.01; \*\**P*<0.05; \**P*<0.10.



**Figure S11.** Percentage changes in relative abundance between universal section (ECD overlap) and representative section (CD-E) (a) at the phylum level and (b) at the gene category level. E: erosion; C: control; D: deposition. Asterisk indicates significant differences analyzed by ANOVA. \*\**P*<0.01; \**P*<0.05.

**Table S1.** Summary of environmental variable measurements

|  |  |  |  |
| --- | --- | --- | --- |
|  | Eroded sites | Control | Deposited sites |
| Soil Ta (oC) | 19.74±0.21b\* | 18.94±0.39 | 18.38±0.20 |
| Water content(% w/w) | 5.00±0.00 | 5.00±0.00 | 5.00±0.00 |
| pH | 7.13±0.05 | 7.10±0.10 | 7.10±0.08 |
| TOC (%) | 1.41±0.03\* | 1.58±0.09 | 1.52±0.08 |
| DOC (mg/kg) | 65.48±6.41 | 74.13±3.43 | 123.46±20.59\*\* |
| NO3- (mg/kg) | 4.34±0.16 | 4.13±0.63 | 5.90±1.04 |
| TN (%) | 0.16±0.00 | 0.17±0.01 | 0.17±0.01 |
| NH4+ (mg/kg) | 5.39±0.68 | 6.00±0.73 | 7.89±1.20 |
| Dv | 2.67±0.01 | 2.68±0.01 | 2.67±0.02 |
| Sand(%) | 72.48±1.10 | 71.18±1.50 | 71.98±2.82 |
| Silt(%) | 15.18±0.60 | 16.02±0.76 | 15.52±1.42 |
| Clay(%) | 12.34±0.53 | 12.80±0.75 | 12.50±1.41 |
| MBC (mg/kg) | 288.80±49.70 | 226.84±45.36 | 263.45±51.48 |
| MBN (mg/kg) | 35.87±8.14 | 24.27±6.80 | 28.80±9.23 |
| Plant species richness | 177.20±19.19 | 159.80±37.13 | 129.40±14.60 |
| Plant coverage (%) | 36.38±2.95\* | 53.29±8.27 | 57.54±8.05 |
| Soil respiration (μmol/m2/s) | 1.06±0.06\* | 1.15±0.06 | 1.30±0.05\*\* |

aAbbreviations: T – temperature; TOC – total organic carbon; DOC – dissolved organic carbon; TN – total nitrogen; Dv – volume fractal dimension of soil particles; MBC – microbial biomass carbon; MBN – microbial biomass nitrogen.

bAll data are presented as mean ± s.e. calculated from five replicates. The significantly changed mean values as compared to the control sites were indicated by asterisks. \*\**P*<0.05; \**P*<0.10.

**Table S2.** Three nonparametric dissimilarity tests to compare treatments with their controls

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Taxonomic composition | | | | | Functional gene composition | | | | |
| Level |  | MRPP | Anosim | Adonis | Level |  | MRPP | Anosim | Adonis |
| Phylum | Ea vs C | 0.211 | 0.277 | 0.158 | Category | E vs C | 0.0733 | **0.048**b | 0.068 |
| D vs C | 0.062 | 0.061 | 0.**038** | D vs C | **0.027** | **0.019** | **0.023** |
| Class | E vs C | 0.173 | 0.163 | 0.101 | Sub1 | E vs C | 0.055 | 0.089 | 0.060 |
| D vs C | **0.045** | 0.056 | 0.**045** | D vs C | **0.011** | **0.018** | **0.013** |
| Order | E vs C | 0.141 | 0.257 | 0.104 | Sub2 | E vs C | 0.054 | **0.035** | **0.044** |
| D vs C | 0.056 | 0.097 | **0.042** | D vs C | **0.008** | **0.007** | **0.001** |
| Family | E vs C | 0.140 | 0.249 | 0.140 | Family | E vs C | **0.018** | **0.022** | **0.021** |
| D vs C | 0.061 | 0.074 | **0.044** | D vs C | **0.009** | **0.007** | **0.001** |
| Genus | E vs C | 0.146 | 0.188 | 0.106 | Probe | E vs C | **0.027** | **0.039** | **0.016** |
| D vs C | 0.062 | 0.077 | **0.038** | D vs C | **0.013** | **0.036** | **0.016** |
| Specie | E vs C | **0.007** | **0.009** | **0.001** |  | | | | |
| D vs C | **0.009** | **0.003** | **0.001** |

aE: the eroded site; C: the control site; and D: the deposited site.

bValues of significance at *P*<0.05 are shown in bold.

**Table S3.** Diversity indices of sequencing and GeoChip data

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Phylogenetic diversity | Microbial species richness | Sequencing -  the Shannon index | Sequencing -  the inverse Simpson index | GeoChip -  the Shannon index | GeoChip -  The inverse Simpson index |
| Erosion | 193±4ba | 5515±200a | 7.316±0.069a | 650±97a | 9.956±0.157a | 21261±3223a |
| Control | 200±4a | 5686±195a | 7.352±0.091a | 657±148a | 9.713±0.103b | 16569±1631b |
| Deposition | 195±5ab | 5509±141a | 7.351±0.032a | 683±69a | 9.882±0.090a | 19611±1746ab |

aAll data are presented as mean ± s.e. calculated from five replicates. Significant (*P*<0.05) differences among samples are indicated by alphabetic letters.

**Table S4.** Weighted and unweighted net relatedness indices (NRI) values calculated based on phylogenetic distance matrices.

|  |  |  |  |
| --- | --- | --- | --- |
|  | Erosion | Control | Deposition |
| Weight | 3.57±0.91a\* | 1.65±0.47 | 4.34±0.50\*\*\* |
| Unweighted | 4.06±0.96\*\*\* | 0.31±0.45 | 3.95±0.46\*\*\* |

aAll data are presented as mean ± s.e. calculated from five replicates. Asterisk indicates significant differences. \**P*<0.10; \*\**P*< 0.05; \*\*\**P*<0.01.

**Table S5.** Percentage changes of nitrogen cycling genes in bacteria, archaea and fungi

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene category | Name | Bacteria | | Archaea | | Fungi | |
|  |  | aE vs C | D vs C | E vs C | D vs C | E vs C | D vs C |
| Ammonification | gdh | -0.04% | -6.30% | -15.11% | -0.12% | -- | -- |
|  | ureC | -4.62% | **b-4.47%** | **-16.43%** | **-19.62%** | **-27.93%** | -10.24% |
| Anammox | hzo | 36.30% | 22.61% | -- | -- | -- | -- |
| Assimilatory N reduction | nasA | -1.18% | **-11.60%** | 23.83% | 31.08% | -- | -- |
|  | nir | -5.09% | -8.78% | 5.88% | 11.22% | -- | -- |
| Denitrification | narG | 1.28% | 4.20% | **-20.14%** | -8.47% | -- | -- |
|  | nirK | 4.28% | -2.76% | -11.55% | -6.86% | -- | -- |
|  | nirS | -1.44% | -1.42% | -- | -- | -- | -- |
|  | norB | -1.36% | -4.94% | 17.44% | **-16.56%** | -- | -- |
|  | nosZ | 2.73% | -3.41% | 2.82% | -5.69% | -- | -- |
| Dissimilatory N reduction | napA | -11.37% | -1.82% | **-20.50%** | **-16.44%** | **--** | -- |
|  | nrfA | 2.93% | -0.85% | -- | -- | -- | -- |
| Nitrification | amoA | **-7.56%** | -2.39% | **-12.76%** | 0.10% | -- | -- |
|  | hao | **-14.53%** | **-29.61%** | -- | -- | -- | -- |
| Nitrogen fixation | nifH | -8.04% | 0.62% | -14.14% | -3.44% | -- | -- |

aE: the eroded site; C: the control site; and D: the deposited site.

bThe significant (*P*<0.05) percentages of changes are shown in bold.

**Table S6.** Correlations between carbon degradation genes and *amoA* & *ureC*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| C degradation genes | *amoA* | *ureC* | C degradation genes |  | *amoA* | *ureC* |
| Glucose\_oxidase\_fungi | -0.28 | -0.24 | xylanase |  | -0.14 | 0.04 |
| dextranase\_fungi | 0.96 | 0.81 | CDH\_2\_carveol\_dehydrogenase |  | -0.44 | 0.05 |
| invertase\_fungi | 0.02 | 0.18 | cellobiase |  | 0.02 | 0.47 |
| lactase\_fungi | -0.15 | -0.08 | endoglucanase |  | 0.50 | -0.09 |
| hyaluronidase | a**0.70** | 0.33 | exoglucanase |  | -0.19 | -0.48 |
| *amyA* | 0.21 | -0.17 | *camDCBA* |  | 0.30 | **0.51** |
| *amyX* | 0.02 | -0.47 | acetylglucosaminidase |  | 0.21 | 0.43 |
| *apu* | 0.13 | 0.48 | chitin\_deacetylase\_fungi |  | -0.12 | 0.14 |
| *cda* | **0.69** | 0.39 | chitinase |  | 0.10 | 0.25 |
| glucoamylase | 0.25 | **0.64** | endochitinase |  | 0.11 | 0.25 |
| isopullulanase | 0.09 | **0.60** | exochitinase |  | -0.05 | 0.31 |
| *nplT* | 0.41 | 0.37 | cutinase |  | 0.16 | 0.19 |
| *pulA* | **0.67** | 0.26 | *glx* |  | 0.43 | 0.07 |
| inulinase | **0.89** | 0.43 | Ligninase |  | -0.28 | -0.08 |
| endopolygalacturonase\_fungi | -0.21 | -0.27 | *mnp* |  | 0.09 | 0.03 |
| exopolygalacturonase\_fungi | **0.80** | 0.33 | phenol\_oxidase |  | -0.12 | 0.03 |
| *pec\_CDeg* | -0.46 | -0.20 | *vanA* |  | 0.11 | 0.06 |
| pectate\_lyase | **0.61** | 0.25 | *vdh* |  | 0.12 | 0.45 |
| pectin\_lyase\_Oomycetes | 0.17 | 0.34 | *CDH* |  | -0.28 | -0.31 |
| pectinase | -0.41 | -0.30 | *limEH* |  | -0.06 | -0.15 |
| *pel\_CDeg* | 0.30 | **0.80** | *LMO* |  | -0.39 | -0.31 |
| *Pg\_Oomycetes* | -0.50 | -0.39 | alpha\_galactosidase\_fungi |  | -0.02 | -0.14 |
| *pme* | **0.51** | 0.49 | Sulfhydryl\_oxidase |  | -0.45 | -0.16 |
| *pme\_CDeg* | **0.62** | **0.57** | phospholipase\_A2\_fungi |  | 0.07 | -0.47 |
| *rgaE* | 0.33 | 0.48 | phospholipase\_C\_fungi |  | **-0.64** | -0.42 |
| *rgh* | **0.55** | 0.12 | phospholipase\_D\_fungi |  | **0.51** | -0.15 |
| *rgl* | **0.54** | **0.56** | metalloprotease\_fungi |  | 0.21 | 0.16 |
| alginase | -0.17 | 0.28 | protease\_aspartate\_fungi |  | **0.76** | 0.45 |
| beta\_agarase | 0.35 | 0.12 | protease\_cysteine\_fungi |  | **0.93** | 0.45 |
| *ara* | 0.15 | -0.12 | protease\_serine\_fungi |  | 0.11 | 0.17 |
| mannanase | **0.74** | **0.57** | Cyanide\_hydratase\_Fungi |  | **0.51** | **0.51** |
| *xylA* | -0.30 | **-0.55** |  |  |  |  |

aThe significant (*P*<0.05) Pearson correlations are shown in bold.