

**Fig. S1** Priori structural equation models of hypothetical relationships between soil/plant variables and carbon degradation genes (a) and total N cycling genes (b).

**Table S1** Results of structural equation modeling of effect of soil and plant factors on carbon (C) degradation genes and nitrogen (N) cycling genes through all plausible interaction pathways as illustrated in Figure S1. Given are the unstandardized path coefficients (estimates), standard error of regression weight (S.E.), the critical value for the regression weight (C.R.), and the level of significance for the regression weight (P).

|  |  |  |  | Estimate | S.E. | C.R. | *P* |
| --- | --- | --- | --- | --- | --- | --- | --- |
| (a) | Plant\_biomass | <--- | NO3--N | 8.023 | 3.357 | 2.390 | **0.017** |
| DOC | <--- | plant\_biomass | 0.087 | 0.023 | 3.853 | **\*\*\*** |
| DOC | <--- | Moisture | 347.472 | 87.691 | 3.962 | **\*\*\*** |
| TC | <--- | Moisture | 29.556 | 17.723 | 1.668 | 0.095 |
| C degradation genes | <--- | TC | 0.006 | 0.005 | 1.310 | 0.190 |
| C degradation genes | <--- | DOC | 0.002 | 0.001 | 2.456 | **0.014** |
| C degradation genes | <--- | NH4+-N | -0.008 | 0.003 | -2.497 | **0.013** |
| C degradation genes | <--- | Moisture | 0.279 | 0.523 | 0.533 | 0.594 |
| (b) | Plant\_biomass | <--- | NO3--N | 8.023 | 3.357 | 2.390 | **0.017** |
| DOC | <--- | Moisture | 347.472 | 87.691 | 3.962 | **\*\*\*** |
| DOC | <--- | plant\_biomass | 0.087 | 0.023 | 3.853 | **\*\*\*** |
| TN | <--- | Moisture | 2.961 | 1.658 | 1.786 | 0.074 |
| N cycling genes | <--- | NH4+-N | -0.018 | 0.006 | -2.851 | **0.004** |
| N cycling genes | <--- | DOC | 0.003 | 0.002 | 1.696 | 0.090 |
| N cycling genes | <--- | TN | 0.222 | 0.099 | 2.238 | **0.025** |
| N cycling genes | <--- | Moisture | 0.968 | 1.046 | 0.925 | 0.355 |

\*\*\* indicates *P* < 0.001. Boldface indicates significant level for the regression weight.

**Table S2** The detected gene probes number involving in C, N, S, and P cycling (mean ± SE, *n*=7).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene category | No. of total gene probes detected | No. of gene probes detected in different treatment | | | |  | *P* value of two-way ANOVA | | |
| CK | N | W | WN |  | *W* | *N* | *W×N* |
| **Carbon cycling** | **8931** | **7834 ± 57** | **7864 ± 48** | **8041 ± 41** | **8113 ± 32** |  | **<0.001** | 0.329 | 0.687 |
| Carbon fixation | 2378 | 2081 ± 16 | 2083 ± 12 | 2144 ± 12 | 2161 ± 12 |  | **<0.001** | 0.491 | 0.591 |
| Carbon degradation | 6409 | 5631 ± 41 | 5655 ± 36 | 5772 ± 29 | 5822 ± 20 |  | **<0.001** | 0.331 | 0.726 |
| **Nitrogen cycling** | **2763** | **2406 ± 17** | **2418 ± 19** | **2485 ± 14** | **2499 ± 12** |  | **<0.001** | 0.444 | 0.936 |
| Nitrogen fixation | 405 | 337 ± 3 | 342 ± 5 | 353 ± 3 | 358 ± 2 |  | **<0.001** | 0.248 | 0.986 |
| Ammonification | 426 | 369 ± 2 | 371 ± 4 | 379 ± 3 | 383 ± 2 |  | **0.001** | 0.315 | 0.780 |
| Nitrification | 39 | 30 ± 0.6 | 32 ± 0.9 | 33 ± 0.7 | 33 ± 0.4 |  | **0.008** | 0.174 | 0.452 |
| Denitrification | 1464 | 1291 ± 8 | 1289 ± 8 | 1331 ± 8 | 1332 ± 6 |  | **<0.001** | 0.962 | 0.855 |
| Assimilatory N reduction | 210 | 193 ± 2 | 194 ± 1 | 199 ± 1 | 198 ± 1 |  | **0.001** | 0.876 | 0.440 |
| Dissimilatory N reduction | 148 | 125 ± 1 | 128 ± 2 | 127 ± 1 | 131 ± 2 |  | **0.050** | 0.057 | 0.692 |
| **Phosphorus cycling** | **897** | **792 ± 6** | **797 ± 5** | **821 ± 4** | **818 ± 4** |  | **<0.001** | 0.824 | 0.427 |
| **Sulfur cycling** | **1768** | **1501 ± 13** | **1509 ± 12** | **1553 ± 11** | **1576 ± 7** |  | **<0.001** | 0.204 | 0.508 |

**Table S3** Adonis analysis of the effects of nitrogen deposition and precipitation increment on the functional gene composition based on the signal intensity of all detected genes and genes involved in C, N, S and P cycling (permutation=999).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gene category** | **W** | | **N** | | **W×N** | |
| *F* | *P* | *F* | *P* | *F* | *P* |
| **All genes** | 4.485 | 0.001 | 4.356 | 0.001 | 2.221 | 0.006 |
| **Carbon cycling** | 4.481 | 0.001 | 4.394 | 0.001 | 2.215 | 0.005 |
| Carbon fixation | 4.743 | 0.001 | 4.524 | 0.001 | 2.435 | 0.003 |
| Carbon degradation | 4.396 | 0.001 | 4.291 | 0.001 | 2.132 | 0.006 |
| **Nitrogen cycling** | 4.983 | 0.001 | 4.556 | 0.001 | 2.239 | 0.007 |
| Nitrogen fixation | 4.669 | 0.001 | 4.575 | 0.001 | 2.202 | 0.013 |
| Ammonification | 5.231 | 0.001 | 5.179 | 0.001 | 2.181 | 0.008 |
| Nitrification | 7.618 | 0.001 | 4.395 | 0.002 | 4.516 | 0.001 |
| Denitrification | 5.136 | 0.001 | 4.655 | 0.001 | 2.135 | 0.010 |
| Assimilatory N reduction | 3.358 | 0.001 | 3.325 | 0.001 | 1.858 | 0.041 |
| Dissimilatory N reduction | 4.060 | 0.001 | 4.173 | 0.001 | 2.597 | 0.008 |
| **Phosphorus cycling** | 4.548 | 0.001 | 4.971 | 0.001 | 2.437 | 0.001 |
| **Sulfur cycling** | 4.514 | 0.001 | 4.387 | 0.001 | 2.366 | 0.004 |

Abbreviation: W: precipitation increment; N: nitrogen addition.

**Table S4** Variables responsible for the changes in the abundance of genes involved in the N cycling processes.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genes | Model | *R2* | *F* | *P* |
| **Nitrogen fixation** |  |  |  |  |
| *nifH* | y = 251.641+0.347(DOC) | 0.197 | 6.387 | 0.018 |
| **Nitrification** |  |  |  |  |
| *amoA* | y = 10.750+2.073(TN) | 0.164 | 5.110 | 0.032 |
| *hao* | - |  |  |  |
| **Denitrification** |  |  |  |  |
| *narG* | y = 501.429+204.113(moisture) | 0.182 | 5.792 | 0.024 |
| *nirK* | y = 186.237+11.552(TN) | 0.174 | 5.463 | 0.027 |
| *nirS* | y = 162.416+0.225(DOC) | 0.201 | 6.552 | 0.017 |
| *norB* | y = 46.887+5.240(BR)+0.018(TP) | 0.361 | 7.075 | 0.004 |
| *nosZ* | y = 295.336+142.658(moisture)-1.025(NH4+) | 0.359 | 7.009 | 0.004 |
| **Ammonification** |  |  |  |  |
| *ureC* | - |  |  |  |
| *gdh* | y = 86.440+0.025(GG biomass)+0.052(TP) | 0.427 | 9.312 | 0.001 |
| **Assimilatory N reduction** |  |  |  |  |
| *nasA* | y = 59.554+3.579(TN) | 0.195 | 6.300 | 0.019 |
| *narB* | - |  |  |  |
| *nirA* | y =36.097+3.926(TN) | 0.192 | 6.174 | 0.020 |
| *nirB* | - |  |  |  |
| **Dissimilatory N reduction** |  |  |  |  |
| *napA* | y = 75.935+0.021(plant biomass)-0.427(NH4+) | 0.373 | 7.437 | 0.003 |
| *nrfA* | - |  |  |  |