**Additional file 1**



**Fig. S1 Impacts of changing climatic regimes on (a) maize biomass and yield and (b) soil microbial taxonomic and nitrogen functional richness.** Changes of the aboveground biomass and maize yield (seed weight) and belowground taxonomic and functional richness *in situ* (black bars), with climate warming (red bars), and with climate cooling (blue bars).



**Fig. S2 Effects of changing climatic regimes on soil attributes.** Changes in soil geochemical attributes in the three soil systems (Phaeozem, Cambisol and Acrisol) *in situ* and under changing climatic regimes.



**Fig. S3 Effects of changing climatic regimes on nutrient utilization efficiency (NUE).** (a) Climate warming, and (b) climate cooling.



**Fig. S4 Soil microbial composition of rare and abundant communities in the Phaezem, Cambisol and Acrisol soils under changing climatic regimes.**



**Fig. S5 Changes of soil microbial taxonomic diversity of both rare and abundant taxa *in situ* (black bars), with climate warming (red bars), and with climate cooling (blue bars).**



**Fig. S6 The deviation of temporal turnover (exponent of time–decay relationship) of rare and abundant microbial communities under changing climatic regimes from *in situ*.** Red bars represent climate warming, and blue bars represent climate cooling.



**Fig. S7 A priori structural equation model (SEM) including climate and soil attributes as predictors of microbial diversity.** MAT, mean annual temperature; MAP, mean annual precipitation; SOM, soil organic matter; R = rare taxa; A = abundant taxa.

Table S1 Dissimilarity test of microbial community structures in response to changing climatic regimes simulated by soil transplant via ANOSIM analysis. The ANOSIM statistic R is based on the difference of mean ranks between groups.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | |  | *In situ* and Warming | |  | *In situ* and Cooling | |
|  | Phaeozem | Cambisol |  | Cambisol | Acrisol |
| Overall | R |  | 0.282 | 0.176 |  | 0.165 | 0.398 |
| *p* |  | **0.001** | **0.001** |  | **0.002** | **0.001** |
| Rare taxa | R |  | 0.152 | 0.193 |  | 0.171 | 0.348 |
| *p* |  | **0.011** | **0.001** |  | **0.001** | **0.001** |
| Abundant taxa | R |  | 0.274 | 0.135 |  | 0.140 | 0.415 |
| *p* |  | **0.002** | **0.002** |  | **0.001** | **0.001** |

The significant values (*p* < 0.05) are indicated in boldface.Table S2 The effect of climatic factors and soil properties on rare and abundant microbial composition by canonical correspondence analysis (CCA)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Factor | Phaeozem | |  | Cambisol | |  | Acrisol | |
|  | Rare | Abundant |  | Rare | Abundant |  | Rare | Abundant |
| Climatic factors | MAT | **0.001** | **0.001** |  | **0.001** | **0.001** |  | **0.001** | **0.001** |
| MAP | **0.001** | **0.001** |  | **0.001** | **0.001** |  | **0.001** | **0.001** |
| Soil properties | Organic matter | 0.895 | 0.724 |  | **0.007** | **0.02** |  | 0.115 | **0.001** |
| pH | **0.001** | **0.008** |  | **0.026** | 0.081 |  | **0.001** | **0.001** |
| NO- 3-N | **0.001** | **0.001** |  | **0.001** | **0.007** |  | **0.001** | **0.001** |
| NH+ 4-N | 0.113 | 0.612 |  | **0.001** | **0.001** |  | **0.001** | **0.006** |
| Available phosphorus | **0.001** | **0.001** |  | 0.272 | 0.433 |  | **0.046** | **0.017** |
| Available potassium | 0.663 | 0.889 |  | 0.119 | 0.332 |  | **0.001** | **0.002** |

The results of envfit test for rare and abundant microbial composition for Phaezem, Acrisol, and Cambisol soils. Values are *P*-values based on 999 permutations and bolded when < 0.05.

Table S3Nitrogen cycling genes carried by rare and abundant taxa.

|  |  |  |
| --- | --- | --- |
| Gene name | Rare taxa | Abundant taxa |
| *amoA* | ✓ |  |
| *gdh* | ✓ | ✓ |
| *napA* | ✓ |  |
| *narG* | ✓ | ✓ |
| *nasA* | ✓ | ✓ |
| *nifH* | ✓ |  |
| *NiR* | ✓ | ✓ |
| *nirA* | ✓ | ✓ |
| *NirB* | ✓ | ✓ |
| *nirK* | ✓ |  |
| *nirS* | ✓ |  |
| *norB* | ✓ |  |
| *nosZ* | ✓ | ✓ |
| *nrfA* | ✓ |  |

Cells with “✓” indicate that the genes were carried by rare/abundant taxa