Supplementary Information for

# Island biogeography of soil bacteria and fungi: similar patterns, but different mechanisms

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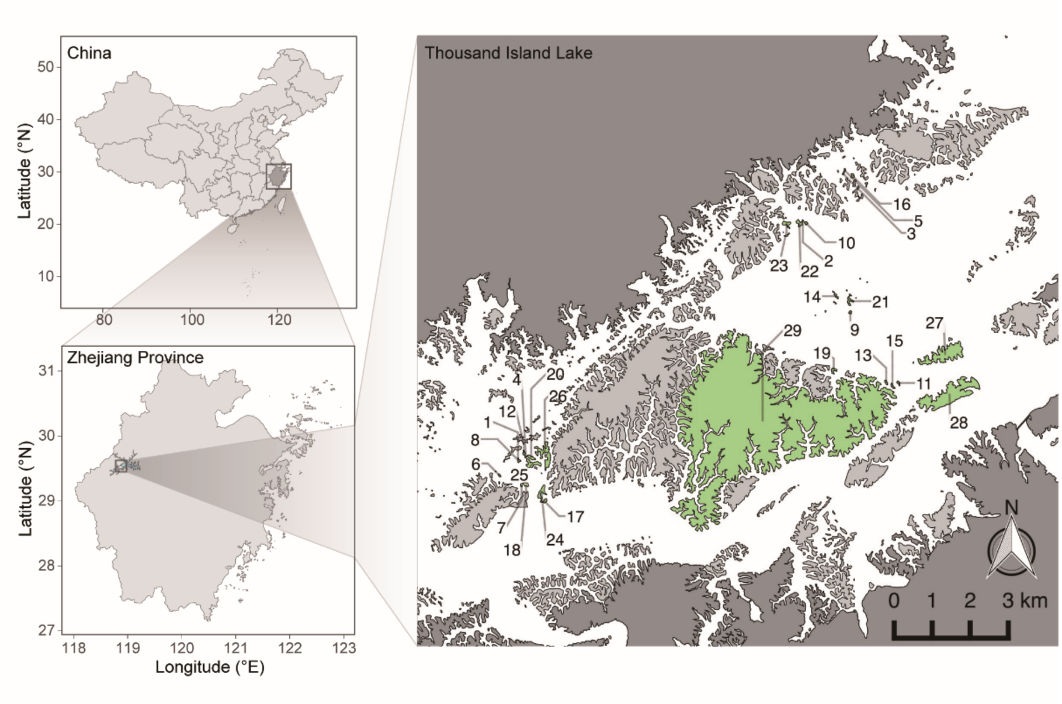

**Figure S1.** The locations of the 29 study islands in the Thousand Island Lake, China. The sampled islands are colored in green and ranked according to their area (from smallest to largest).

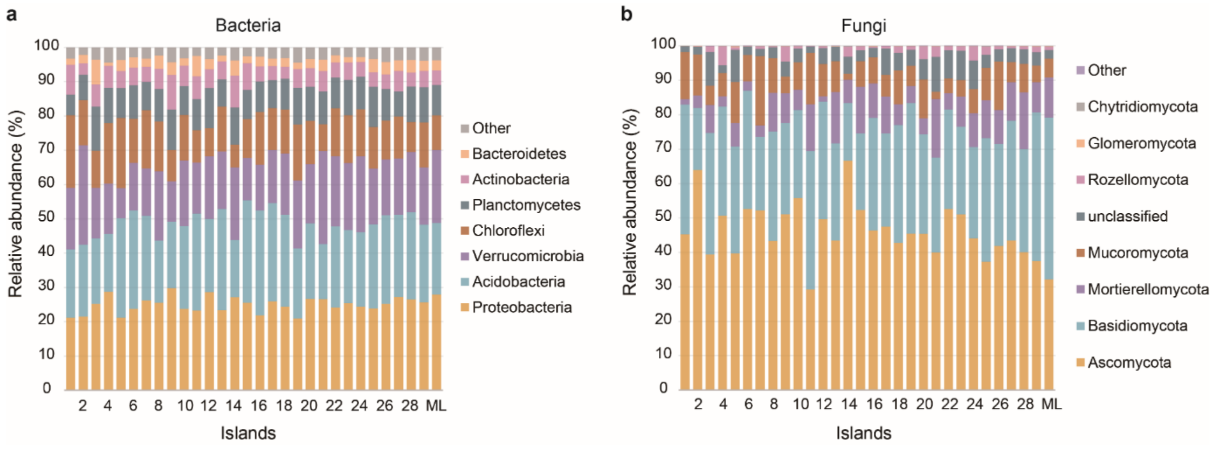

**Figure S2.** The relative abundance of dominant lineages (at the phylum level) on each island and the nearby mainland (ML). The sampled islands are ranked according to their area (from smallest to largest).

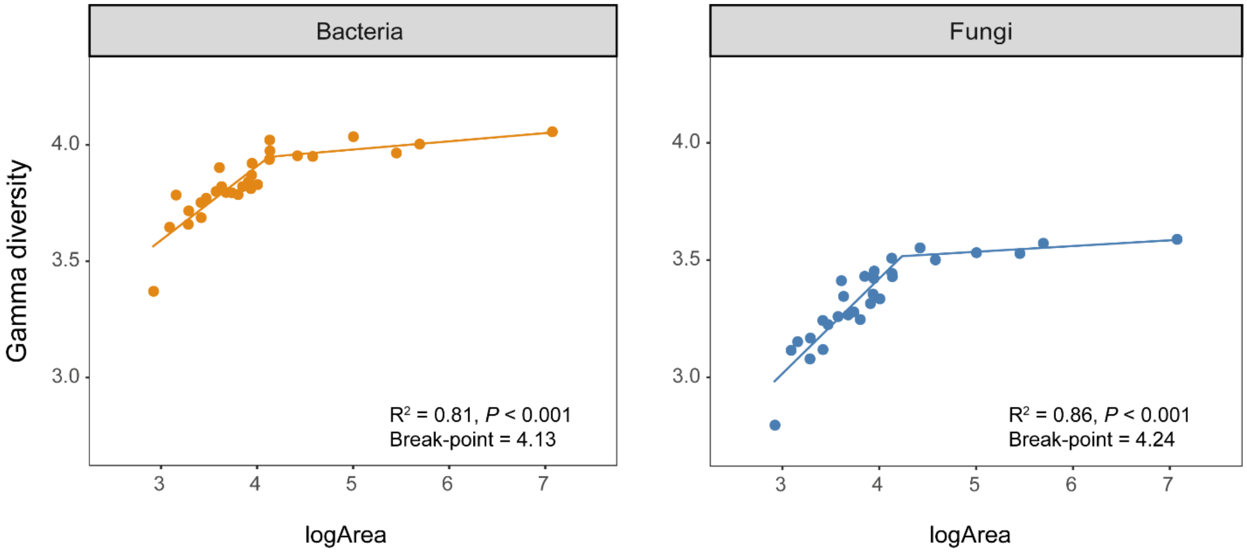

**Figure. S3.** Segmented regressions showing the breaking points for the effects of island area on the gamma diversity of bacteria and fungi. Gamma diversity-area relationships can be better modeled by segmented regressions than simple linear regression according to the Akaike information criterion (AIC) values, indicating the existence of island threshold size (~2 ha) below which diversity precipitously declined.

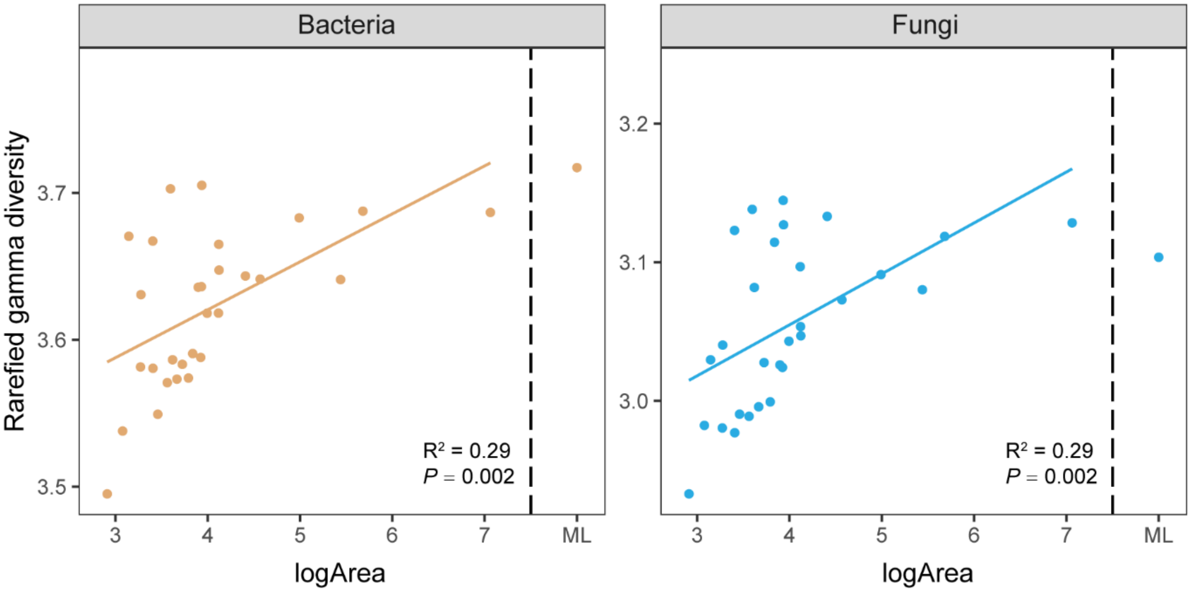

**Figure S4.** The effect of island area on the rarefied gamma diversity of soil bacteria and fungi. Gamma diversity was rarefied to the same number of reads (16,762 and 5,580 sequences for bacteria and fungi, respectively) for each island. Rarefied gamma diversity still showed significant positive relationships with island area for both bacteria and fungi, indicating that the sampling effect is not the sole mechanism responsible for the observed island species-area relationships. The rarefication was run 999 times. ML indicates mainland.

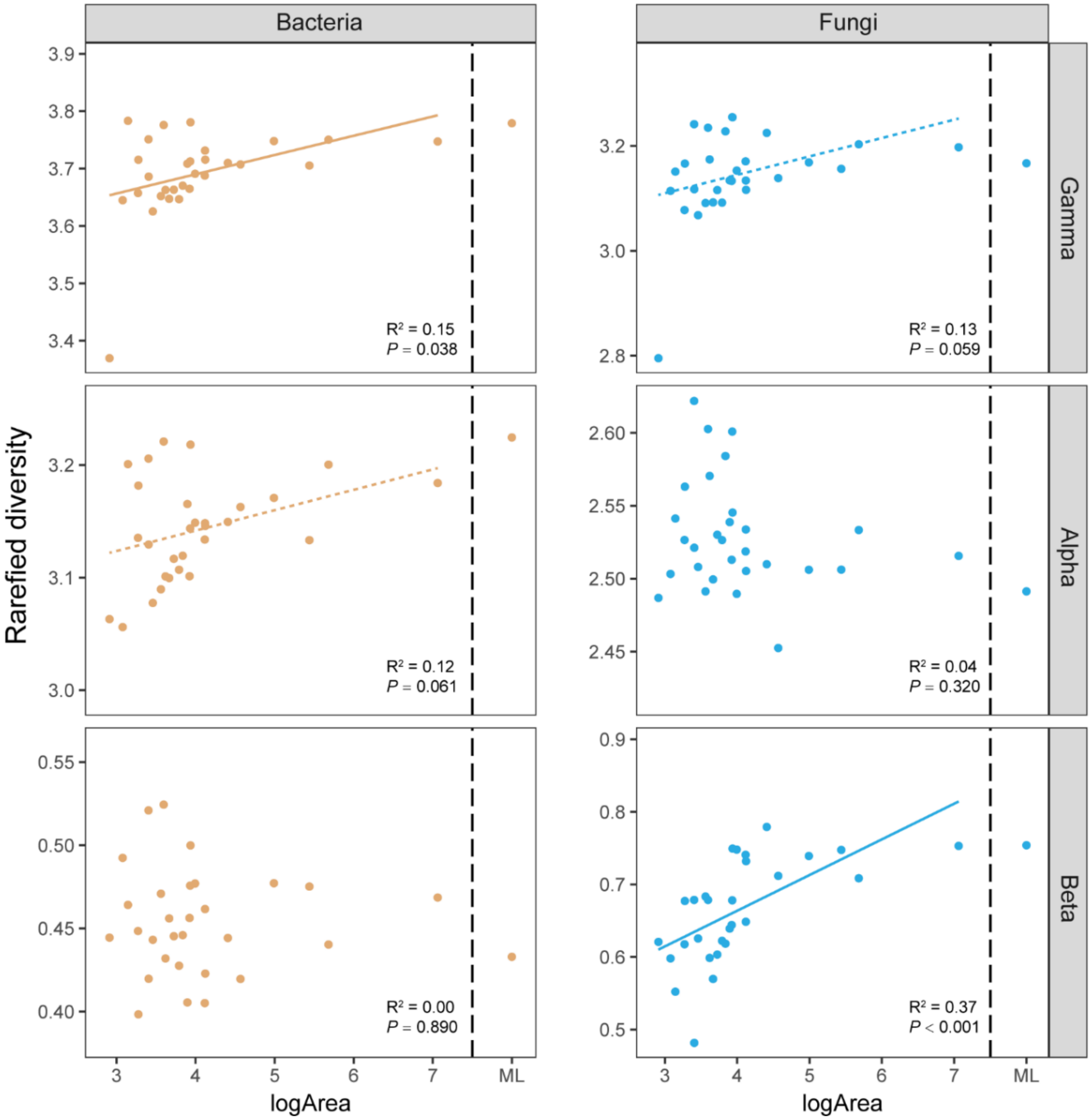

**Figure S5.** The effect of island area on the rarefied gamma, alpha and beta diversity, when all islands were rarefied to equal sample size. We calculated the three diversity components by rarifying down to four samples per island (besides the smallest island with two samples). The solid lines represent significant linear regressions ($P < 0.05$), and the dashed lines represent marginally significant regressions ($P < 0.10$). ML indicates mainland.

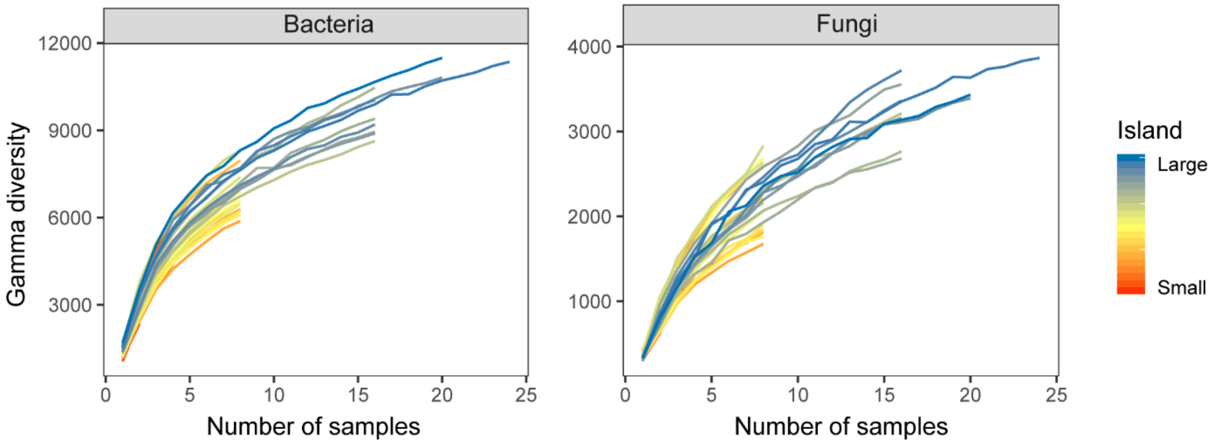

**Figure S6.** The relationship between the estimated gamma diversity and the number of soil samples on the 29 islands. All islands shared similar rarefaction curves, and gamma diversity were generally higher on larger islands at equal sample size. The sampled islands are colored according to their area.

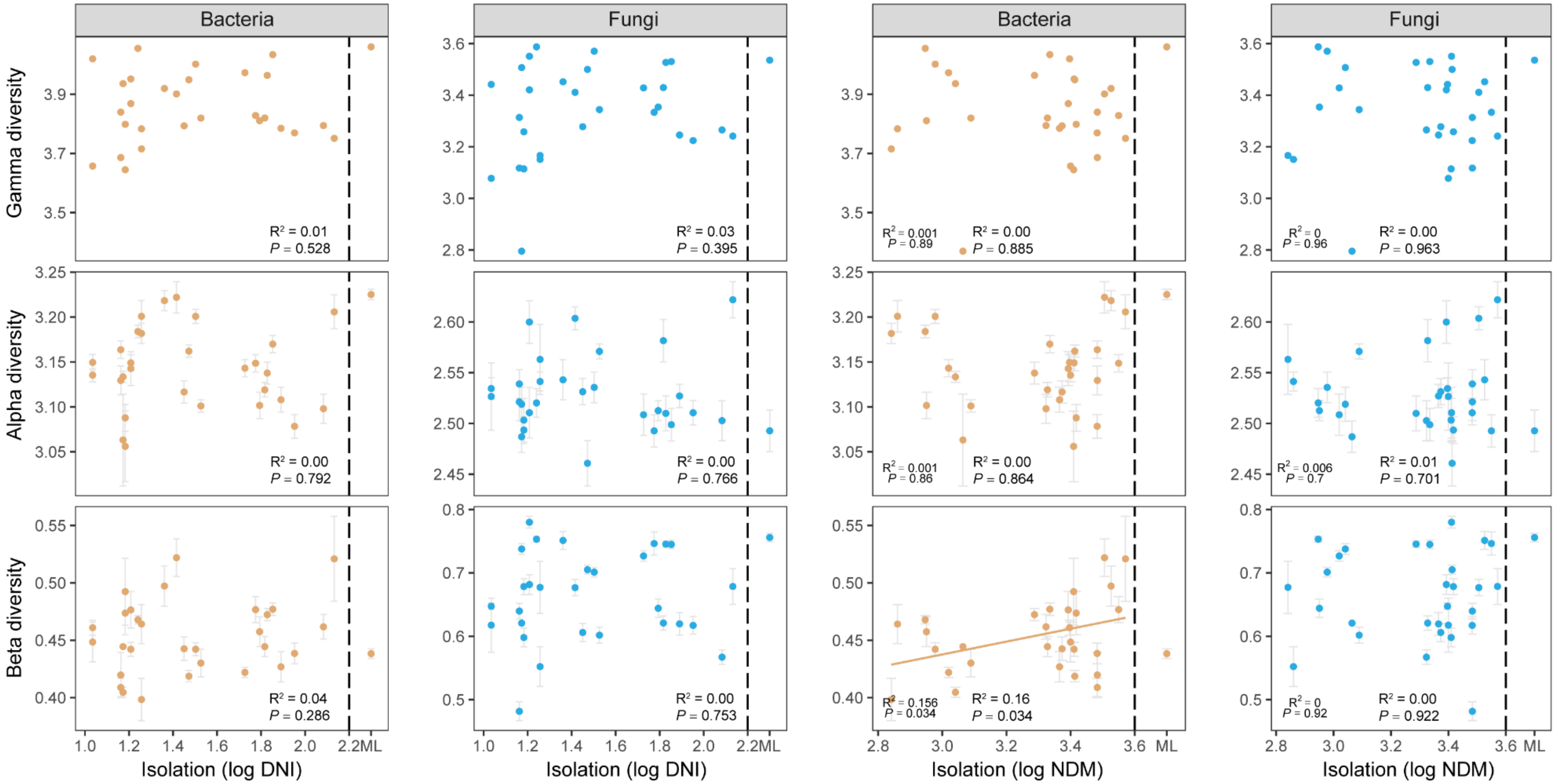

**Figure S7.** The effect of island isolation on the alpha, beta and gamma diversity of soil bacteria and fungi. Gamma diversity was measured as the estimated total OTU richness (based on Chao2 estimator) per island. Alpha diversity was measured as the average OTU richness per sample within each island. Beta diversity was measured as average pairwise Bray-Curtis dissimilarities among samples within each island. Error bars represent standard error. Island isolation was measured as distance to the nearest island (DNI) and the nearest distance to the mainland (NDM). ML indicates mainland.

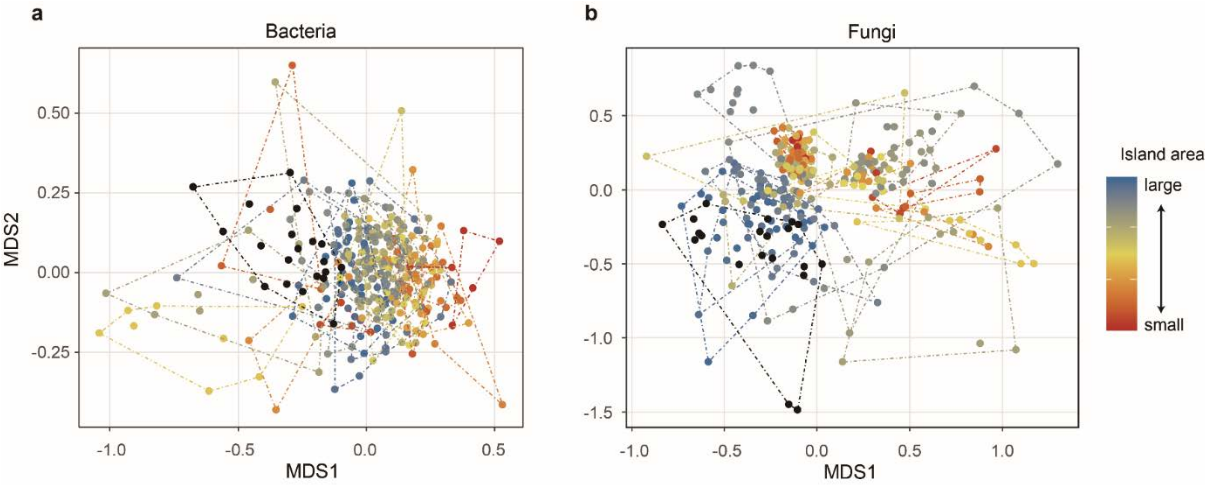

**Figure S8.** Ordination of the 306 samples by two-dimensional nonmetric multidimensional scaling (NMDS). NMDS was based on pairwise Bray–Curtis dissimilarity values. Samples are colored according to island size, with black dots representing the samples from the mainland.

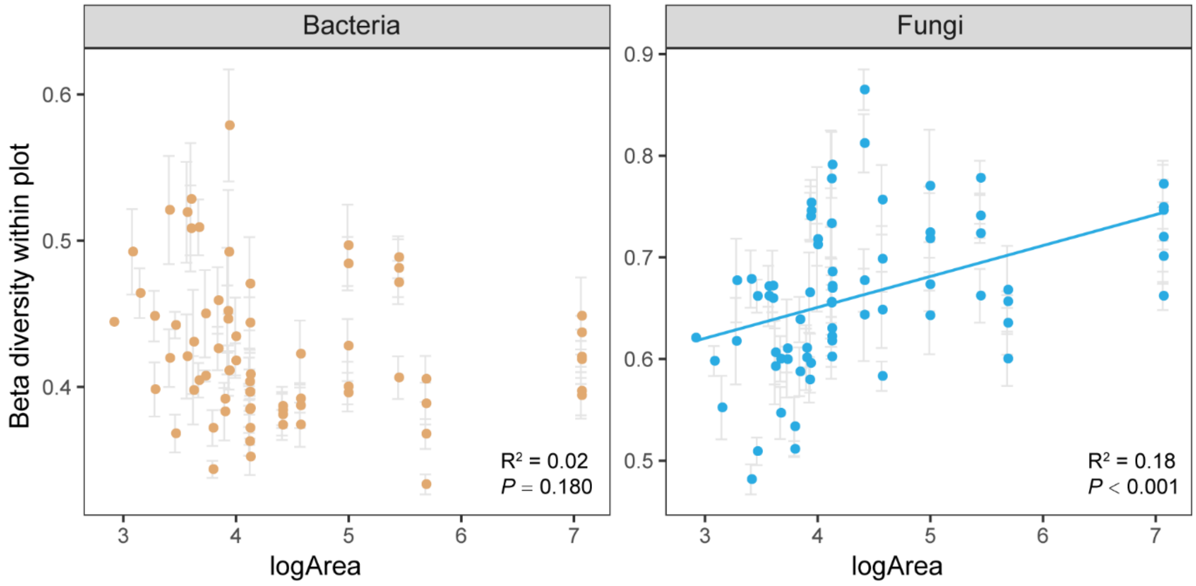

**Figure S9**. The effect of island area on the beta diversity within plot for soil bacteria and fungi. Beta diversity was measured as average pairwise Bray-Curtis dissimilarities among four samples within the same plot (20 m × 20 m) on each island. Error bars represent standard error.

**Table S1.** Soil properties of the 29 study islands and the nearby mainland sites (ML) in the Thousand Island Lake region, China. Each mean in table has an associated SE.

| Island | Soil moisture (%) | Available Ca (mg/kg) | Available Mg (mg/kg) | Available Al (mg/g) | Available P (mg/kg) | TOC (%) | Total N (mg/g) | Total P (mg/g) | pH |
|---|---|---|---|---|---|---|---|---|---|
| 1 | 13.36±0.47 | 58.4±15.9 | 25.3±8.8 | 1.14±0.13 | 3.21±0.19 | 18.41±0.24 | 1.37±0.10 | 0.28±0.00 | 4.36±0.07 |
| 2 | 9.34±1.23 | 60.2±12.8 | 13.6±1.8 | 1.45±0.20 | 1.82±0.22 | 13.88±0.71 | 0.88±0.05 | 0.16±0.01 | 4.09±0.06 |
| 3 | 13.99±1.04 | 282.9±43.9 | 39.6±6.1 | 1.27±0.07 | 3.19±0.64 | 15.83±2.58 | 1.28±0.20 | 0.30±0.05 | 4.30±0.05 |
| 4 | 11.14±1.85 | 60.9±6.3 | 23.5±2.1 | 1.34±0.15 | 2.95±0.19 | 22.21±1.89 | 1.37±0.07 | 0.21±0.02 | 4.24±0.02 |
| 5 | 14.66±1.15 | 223.7±51.8 | 31.9±4.7 | 1.20±0.16 | 5.05±0.37 | 26.86±1.35 | 1.86±0.08 | 0.28±0.02 | 4.15±0.07 |
| 6 | 14.09±1.55 | 286.5±66.2 | 40.8±7.3 | 1.21±0.08 | 7.27±1.31 | 27.35±3.80 | 1.90±0.28 | 0.19±0.03 | 4.03±0.05 |
| 7 | 12.20±0.67 | 43.3±7.3 | 24.3±3.4 | 0.93±0.15 | 2.60±0.17 | 15.84±3.13 | 1.10±0.12 | 0.19±0.01 | 4.37±0.04 |
| 8 | 10.46±0.95 | 54.9±9.7 | 12.7±1.4 | 1.08±0.13 | 2.65±0.17 | 26.51±2.30 | 1.44±0.10 | 0.15±0.02 | 4.12±0.03 |
| 9 | 9.66±0.55 | 59.6±11.0 | 20.5±3.5 | 0.95±0.13 | 2.76±0.19 | 12.13±1.20 | 1.00±0.05 | 0.28±0.01 | 4.35±0.04 |
| 10 | 18.28±0.53 | 1153.0±196.5 | 158.4±20.2 | 1.13±0.09 | 6.88±0.39 | 22.04±2.31 | 1.44±0.15 | 0.13±0.01 | 4.43±0.08 |
| 11 | 14.02±0.64 | 79.8±9.1 | 28.0±3.8 | 1.13±0.08 | 3.38±0.21 | 23.10±2.27 | 1.42±0.11 | 0.27±0.01 | 4.17±0.06 |
| 12 | 13.75±0.88 | 108.2±23.1 | 18.7±2.0 | 0.76±0.08 | 5.16±1.39 | 29.09±2.58 | 1.50±0.17 | 0.32±0.01 | 4.16±0.05 |
| 13 | 9.42±0.26 | 50.1±6.1 | 14.0±1.0 | 0.96±0.05 | 3.13±0.10 | 18.74±2.14 | 1.14±0.08 | 0.20±0.02 | 4.21±0.02 |
| 14 | 16.33±1.37 | 63.5±10.9 | 16.9±2.2 | 0.81±0.08 | 3.11±0.23 | 18.18±1.76 | 1.26±0.08 | 0.30±0.02 | 4.14±0.08 |
| 15 | 16.14±0.85 | 118.5±16.3 | 19.5±1.4 | 1.31±0.05 | 3.69±0.27 | 22.76±2.59 | 1.41±0.11 | 0.25±0.01 | 4.09±0.03 |
| 16 | 14.50±1.07 | 62.2±12.3 | 23.6±4.7 | 0.83±0.11 | 3.51±0.31 | 19.05±1.81 | 1.30±0.11 | 0.22±0.02 | 4.30±0.04 |
| 17 | 16.19±0.55 | 56.2±12.6 | 20.9±3.1 | 1.31±0.12 | 2.79±0.17 | 21.87±1.56 | 1.40±0.07 | 0.24±0.03 | 4.17±0.04 |
| 18 | 18.80±1.04 | 90.0±19.0 | 22.4±3.3 | 1.12±0.12 | 3.23±0.18 | 32.52±2.86 | 1.83±0.07 | 0.26±0.02 | 4.13±0.03 |
| 19 | 16.13±0.56 | 831.5±114.0 | 82.9±7.3 | 1.19±0.12 | 5.57±0.72 | 17.48±0.89 | 1.07±0.05 | 0.10±0.00 | 4.48±0.07 |
| 20 | 12.29±1.03 | 87.6±13.3 | 24.8±4.3 | 1.01±0.03 | 3.14±0.16 | 28.30±1.27 | 1.75±0.05 | 0.29±0.02 | 4.03±0.10 |
| 21 | 13.13±0.56 | 71.1±8.7 | 34.7±5.2 | 1.08±0.05 | 3.95±0.19 | 18.25±1.01 | 1.31±0.04 | 0.35±0.02 | 4.30±0.04 |
| 22 | 13.71±0.81 | 72.6±13.8 | 60.9±17.1 | 1.08±0.08 | 2.88±0.11 | 20.11±2.00 | 1.33±0.08 | 0.18±0.02 | 4.39±0.06 |
| 23 | 13.67±0.45 | 64.3±7.8 | 24.0±2.5 | 1.02±0.05 | 2.90±0.10 | 22.82±1.25 | 1.40±0.06 | 0.26±0.01 | 4.34±0.04 |
| 24 | 14.34±0.56 | 73.1±8.8 | 31.5±3.2 | 1.12±0.08 | 3.26±0.17 | 31.17±2.48 | 1.88±0.13 | 0.29±0.03 | 4.26±0.04 |
| 25 | 15.70±0.49 | 41.2±4.5 | 19.3±1.5 | 1.01±0.08 | 2.88±0.10 | 17.94±1.61 | 1.20±0.06 | 0.15±0.01 | 4.20±0.03 |
| 26 | 14.67±0.71 | 67.6±12.9 | 33.5±6.1 | 0.97±0.04 | 2.90±0.27 | 20.42±1.60 | 1.41±0.10 | 0.21±0.02 | 4.29±0.04 |
| 27 | 14.61±0.74 | 68.5±14.9 | 18.6±2.6 | 0.84±0.06 | 2.66±0.18 | 23.96±2.74 | 1.41±0.13 | 0.25±0.01 | 4.18±0.03 |
| 28 | 17.42±0.70 | 64.7±7.9 | 22.4±2.5 | 0.98±0.08 | 3.18±0.18 | 27.73±1.24 | 1.68±0.07 | 0.24±0.01 | 4.10±0.04 |
| 29 | 16.76±0.94 | 71.9±7.5 | 27.9±4.2 | 1.13±0.06 | 3.21±0.12 | 27.30±1.95 | 1.60±0.10 | 0.22±0.02 | 4.20±0.04 |
| ML | 15.98±0.43 | 136.4±11.2 | 59.8±5.1 | 1.00±0.04 | 2.88±0.12 | 29.10±1.49 | 1.73±0.07 | 0.21±0.01 | 4.37±0.02 |

**Table S2.** Characteristics and microbial diversity of the 29 study islands and the nearby mainland sites (ML) in the Thousand Island Lake region, China. Refer to Fig. S1 for survey sites.

| Island | Latitude (N) | Longitude (E) | Area ($m^2$) | NDM (m) | DNI (m) | Bacteria Gamma | Fungi Gamma | Bacteria Alpha | Fungi Alpha | Bacteria Beta | Fungi Beta |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 29°34'9" | 118°53'56" | 815 | 1160 | 15 | 2342 | 624 | 1165±137 | 307±11 | 0.44 | 0.62 |
| 2 | 29°30'52" | 118°49'14" | 1197 | 2567 | 15 | 4414 | 1301 | 1152±106 | 320±15 | 0.49±0.03 | 0.60±0.01 |
| 3 | 29°34'50" | 118°54'38" | 1396 | 725 | 18 | 6070 | 1416 | 1592±64 | 348±7 | 0.46±0.02 | 0.55±0.03 |
| 4 | 29°30'53" | 118°49'22" | 1870 | 2511 | 11 | 4543 | 1196 | 1366±23 | 339±24 | 0.45±0.02 | 0.62±0.04 |
| 5 | 29°34'48" | 118°54'37" | 1890 | 694 | 18 | 5192 | 1466 | 1521±39 | 369±27 | 0.40±0.02 | 0.68±0.04 |
| 6 | 29°32'50" | 118°54'41" | 2538 | 3725 | 136 | 5636 | 1743 | 1611±69 | 420±18 | 0.52±0.04 | 0.68±0.03 |
| 7 | 29°30'29" | 118°49'17" | 2550 | 3044 | 15 | 4853 | 1310 | 1350±51 | 333±15 | 0.42±0.02 | 0.48±0.01 |
| 8 | 29°30'38" | 118°48'56" | 2878 | 3040 | 90 | 5881 | 1675 | 1202±37 | 325±9 | 0.44±0.01 | 0.62±0.01 |
| 9 | 29°30'49" | 118°49'15" | 3645 | 2615 | 15 | 6286 | 1812 | 1229±42 | 313±9 | 0.47±0.02 | 0.68±0.01 |
| 10 | 29°33'4" | 118°54'28" | 3949 | 3205 | 26 | 7965 | 2576 | 1677±67 | 402±11 | 0.52±0.02 | 0.68±0.01 |
| 11 | 29°34'7" | 118°53'60" | 4160 | 1228 | 34 | 6599 | 2209 | 1263±20 | 373±6 | 0.43±0.01 | 0.60±0.01 |
| 12 | 29°31'50" | 118°55'27" | 4638 | 2106 | 121 | 6225 | 1842 | 1259±46 | 321±14 | 0.46±0.01 | 0.57±0.01 |
| 13 | 29°30'56" | 118°49'20" | 5307 | 2363 | 28 | 6213 | 1896 | 1312±38 | 341±10 | 0.44±0.01 | 0.61±0.01 |
| 14 | 29°31'51" | 118°55'15" | 6181 | 2321 | 78 | 6094 | 1760 | 1287±40 | 337±9 | 0.43±0.01 | 0.62±0.02 |
| 15 | 29°31'47" | 118°55'21" | 6876 | 2128 | 66 | 6604 | 2688 | 1317±25 | 385±18 | 0.44±0.01 | 0.62±0.01 |
| 16 | 29°30'29" | 118°49'22" | 7880 | 3043 | 15 | 6913 | 2059 | 1460±32 | 347±11 | 0.41±0.01 | 0.64±0.01 |
| 17 | 29°34'46" | 118°54'46" | 8388 | 893 | 62 | 6467 | 2258 | 1269±41 | 326±7 | 0.46±0.01 | 0.64±0.01 |
| 18 | 29°30'16" | 118°49'41" | 8542 | 2471 | 16 | 7389 | 2635 | 1398±57 | 401±20 | 0.48±0.02 | 0.68±0.02 |
| 19 | 29°33'0" | 118°54'40" | 8625 | 3359 | 23 | 8310 | 2831 | 1657±42 | 352±16 | 0.50±0.02 | 0.75±0.01 |
| 20 | 29°32'1" | 118°54'23" | 9856 | 3547 | 60 | 6732 | 2156 | 1410±32 | 312±11 | 0.48±0.01 | 0.75±0.02 |
| 21 | 29°34'6" | 118°53'54" | 13071 | 1099 | 15 | 8629 | 3213 | 1362±19 | 334±12 | 0.40±0.00 | 0.74±0.01 |
| 22 | 29°30'52" | 118°49'26" | 13172 | 2494 | 11 | 10464 | 2765 | 1415±29 | 344±8 | 0.46±0.01 | 0.65±0.00 |
| 23 | 29°34'6" | 118°53'39" | 13264 | 1046 | 53 | 9397 | 2681 | 1395±31 | 328±14 | 0.42±0.00 | 0.73±0.01 |
| 24 | 29°30'22" | 118°49'37" | 25619 | 2576 | 16 | 8950 | 3555 | 1414±29 | 332±19 | 0.44±0.01 | 0.78±0.01 |
| 25 | 29°30'46" | 118°49'30" | 36958 | 2588 | 30 | 8894 | 3161 | 1455±23 | 295±14 | 0.42±0.00 | 0.71±0.01 |
| 26 | 29°30'59" | 118°49'39" | 97930 | 2164 | 71 | 10813 | 3390 | 1486±34 | 319±11 | 0.48±0.01 | 0.74±0.01 |
| 27 | 29°32'10" | 118°55'56" | 274942 | 1939 | 67 | 9200 | 3364 | 1381±38 | 327±13 | 0.47±0.01 | 0.75±0.01 |
| 28 | 29°31'30" | 118°55'52" | 479759 | 950 | 32 | 10043 | 3719 | 1592±29 | 346±12 | 0.44±0.01 | 0.70±0.01 |
| 29 | 29°31'55" | 118°53'22" | 11538756 | 884 | 17 | 11354 | 3866 | 1532±26 | 335±11 | 0.47±0.00 | 0.75±0.00 |
| ML | 29°39'10" | 119°0'27" |  |  |  | 11489 | 3434 | 1682±23 | 318±15 | 0.44±0.00 | 0.76±0.01 |

* The sampled islands are ranked according to their area (from smallest to largest). Island isolation was measured as the nearest distance to the mainland (NDM) and distance to the nearest island (DNI). Gamma diversity was measured as the estimated total OTU richness (based on Chao2 estimator) per island. Alpha diversity was measured as the average OTU richness per sample within each island. Beta diversity was measured as average pairwise Bray-Curtis dissimilarities among samples within each island. Each mean in table has an associated SE.

**Table. S3** The effect of island area and isolation on the alpha, beta and gamma diversity of soil bacteria and fungi.

| Independent Variable | Dependent variable | | Bacteria | | | Fungi | | |
|---|---|---|---|---|---|---|---|---|
| | | | Slope | $R^2$ | *P* | Slope | $R^2$ | *P* |
| Island area | Gamma diversity | Chao1 | **0.108** | **0.60** | **0.000** | **0.131** | **0.61** | **0.000** |
| | | Chao2 | **0.124** | **0.56** | **0.000** | **0.159** | **0.59** | **0.000** |
| | | Jack1 | **0.129** | **0.61** | **0.000** | **0.151** | **0.62** | **0.000** |
| | | Jack2 | **0.133** | **0.58** | **0.000** | **0.162** | **0.60** | **0.000** |
| | | ACE | **0.106** | **0.61** | **0.000** | **0.134** | **0.63** | **0.000** |
| | | ICE | **0.123** | **0.54** | **0.000** | **0.165** | **0.58** | **0.000** |
| | Alpha diversity | OTU richness (q = 0) | 0.018 | 0.13 | 0.058 | -0.008 | 0.03 | 0.352 |
| | | Exponential of Shannon entropy (q = 1) | 0.042 | 0.10 | 0.097 | **-0.042** | **0.14** | **0.047** |
| | | Inverse Simpson (q =2) | 0.049 | 0.09 | 0.119 | **-0.051** | **0.16** | **0.035** |
| | Beta diversity | Jaccard | 0.004 | 0.09 | 0.108 | **0.022** | **0.22** | **0.010** |
| | | Bray-Curtis | 0.001 | 0.00 | 0.903 | **0.049** | **0.36** | **0.001** |
| | | $\mathrm{RC}_{\mathrm{bray}}$ | 0.157 | 0.10 | 0.101 | 0.105 | 0.13 | 0.054 |
| | | 1-CqN (q = 0) | 0.005 | 0.09 | 0.110 | **0.027** | **0.22** | **0.011** |
| | | 1-CqN (q = 1) | 0.003 | 0.01 | 0.649 | **0.058** | **0.35** | **0.001** |
| | | 1-CqN (q = 2) | -0.016 | 0.04 | 0.274 | **0.069** | **0.24** | **0.006** |
| Island isolation (DNI) | Gamma diversity | Chao1 | 0.046 | 0.02 | 0.517 | 0.075 | 0.03 | 0.376 |
| | | Chao2 | 0.053 | 0.01 | 0.528 | 0.089 | 0.03 | 0.395 |
| | | Jack1 | 0.053 | 0.01 | 0.532 | 0.074 | 0.02 | 0.452 |
| | | Jack2 | 0.062 | 0.02 | 0.489 | 0.086 | 0.02 | 0.415 |
| | | ACE | 0.046 | 0.02 | 0.502 | 0.065 | 0.02 | 0.443 |
| | | ICE | 0.060 | 0.02 | 0.481 | 0.094 | 0.03 | 0.391 |
| | Alpha diversity | OTU richness (q = 0) | -0.007 | 0.00 | 0.792 | 0.006 | 0.00 | 0.766 |
| | | Exponential of Shannon entropy (q = 1) | 0.035 | 0.01 | 0.600 | -0.028 | 0.01 | 0.627 |
| | | Inverse Simpson (q =2) | 0.101 | 0.05 | 0.227 | -0.025 | 0.01 | 0.704 |
| | Beta diversity | Jaccard | -0.002 | 0.00 | 0.776 | 0.000 | 0.00 | 0.989 |
| | | Bray-Curtis | 0.020 | 0.04 | 0.286 | 0.013 | 0.00 | 0.753 |
| | | $\mathrm{RC}_{\mathrm{bray}}$ | 0.154 | 0.01 | 0.550 | 0.048 | 0.00 | 0.748 |
| | | 1-CqN (q = 0) | -0.002 | 0.00 | 0.764 | -0.002 | 0.00 | 0.957 |
| | | 1-CqN (q = 1) | 0.014 | 0.02 | 0.427 | 0.001 | 0.00 | 0.977 |
| | | 1-CqN (q = 2) | 0.055 | 0.08 | 0.143 | 0.016 | 0.00 | 0.828 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Island isolation (NDM) | Gamma diversity | Chao1 | -0.035 | 0.00 | 0.741 | -0.036 | 0.00 | 0.778 |
| | | Chao2 | -0.018 | 0.00 | 0.885 | -0.007 | 0.00 | 0.963 |
| | | Jack1 | -0.022 | 0.00 | 0.861 | -0.024 | 0.00 | 0.867 |
| | | Jack2 | -0.011 | 0.00 | 0.937 | -0.013 | 0.00 | 0.937 |
| | | ACE | -0.028 | 0.00 | 0.786 | -0.029 | 0.00 | 0.820 |
| | | ICE | -0.005 | 0.00 | 0.970 | 0.000 | 0.00 | 0.998 |
| | Alpha diversity | OTU richness (q = 0) | -0.007 | 0.00 | 0.864 | 0.012 | 0.01 | 0.701 |
| | | Exponential of Shannon entropy (q = 1) | 0.002 | 0.00 | 0.987 | 0.129 | 0.08 | 0.126 |
| | | Inverse Simpson (q =2) | 0.003 | 0.00 | 0.978 | 0.120 | 0.06 | 0.214 |
| | Beta diversity | Jaccard | 0.001 | 0.00 | 0.882 | -0.015 | 0.01 | 0.685 |
| | | Bray-Curtis | **0.056** | **0.16** | **0.034** | -0.006 | 0.00 | 0.922 |
| | | $RC_{bray}$ | 0.299 | 0.02 | 0.431 | -0.081 | 0.00 | 0.711 |
| | | 1-CqN (q = 0) | 0.002 | 0.00 | 0.857 | -0.015 | 0.00 | 0.737 |
| | | 1-CqN (q = 1) | 0.051 | 0.13 | 0.050 | -0.015 | 0.00 | 0.842 |
| | | 1-CqN (q = 2) | **0.157** | **0.29** | **0.002** | 0.046 | 0.01 | 0.666 |

* Gamma diversity was calculated as the total OTU richness per island based on Chao1, Chao2, Jack1, Jack2, ACE, and ICE estimators. Alpha diversity was measured as average OTU richness, the exponent of Shannon entropy, and the inverse Simpson index per sample, which are equal to the effective number of species based on Hill numbers (q = 0, 1, 2, respectively). Beta diversity was measured as average Jaccard, Bray-Curtis dissimilarity, and the Bray–Curtis based Raup–Crick ($RC_{bray}$) values among samples within each island, as well as the unifying similarity and differentiation measures through Hill numbers (1-CqN, q = 0, 1, 2). $RC_{bray}$ was generated by a statistical null modeling approach following the procedure described by Stegen et al. (2015). Diversity measures through Hill numbers were calculated following Chao et al. (2014). Island isolation was measured as distance to the nearest island (DNI) and nearest distance to the mainland (NDM). Significant values are highlighted in bold ($P < 0.05$).

Chao, A., Chiu, C-H., Jost, L. Unifying species diversity, phylogenetic diversity, functional diversity, and related similarity and differentiation measures through Hill numbers. *Annu. Rev. Ecol. Syst*. **45**, 297-324 (2014).

Stegen, J.C., Lin, X.J., Fredrickson, J.K., Konopka, A.E. Estimating and mapping ecological processes influencing microbial community assembly. *Front. Microbiol*. **6**, 370 (2015).

**Table S4.** The influences of island area and isolation on soil properties and habitat heterogeneity at the island level. Significant values are highlighted in bold ($P < 0.05$). Soil properties were standardized to have a mean value of 0 and variance of 1.

| Independent Variable | Dependent Variable | Slope | $R^2$ | *P* |
|---|---|---|---|---|
| Island area | **Soil moisture** | **0.361** | **0.18** | **0.020** |
| | Available Ca | -0.242 | 0.05 | 0.244 |
| | Available Mg | -0.075 | 0.01 | 0.647 |
| | Available Al | -0.183 | 0.08 | 0.143 |
| | Available P | -0.132 | 0.02 | 0.522 |
| | TOC | 0.237 | 0.11 | 0.083 |
| | Total N | 0.182 | 0.06 | 0.202 |
| | Total P | -0.016 | 0.00 | 0.924 |
| | pH | -0.062 | 0.01 | 0.662 |
| | **Habitat heterogeneity** | **0.045** | **0.24** | **0.007** |
| Island isolation (DNI) | Soil moisture | 0.276 | 0.02 | 0.518 |
| | Available Ca | 0.112 | 0.00 | 0.839 |
| | Available Mg | -0.432 | 0.04 | 0.313 |
| | Available Al | -0.469 | 0.07 | 0.153 |
| | Available P | 0.542 | 0.04 | 0.313 |
| | TOC | 0.645 | 0.11 | 0.073 |
| | Total N | 0.505 | 0.07 | 0.178 |
| | Total P | 0.136 | 0.00 | 0.760 |
| | **pH** | **-0.977** | **0.26** | **0.005** |
| | Habitat heterogeneity | 0.058 | 0.06 | 0.214 |
| Island isolation (NDM) | Soil moisture | -0.693 | 0.05 | 0.269 |
| | Available Ca | 0.322 | 0.01 | 0.693 |
| | Available Mg | 0.209 | 0.00 | 0.743 |
| | Available Al | -0.509 | 0.04 | 0.299 |
| | Available P | 0.394 | 0.01 | 0.622 |
| | TOC | -0.142 | 0.00 | 0.795 |
| | Total N | -0.468 | 0.03 | 0.403 |
| | **Total P** | **-1.704** | **0.25** | **0.006** |
| | pH | 0.078 | 0.00 | 0.888 |
| | Habitat heterogeneity | 0.011 | 0.00 | 0.879 |