# Supporting Information

## Zimmerman and Vitousek 10.1073/pnas.1209872109

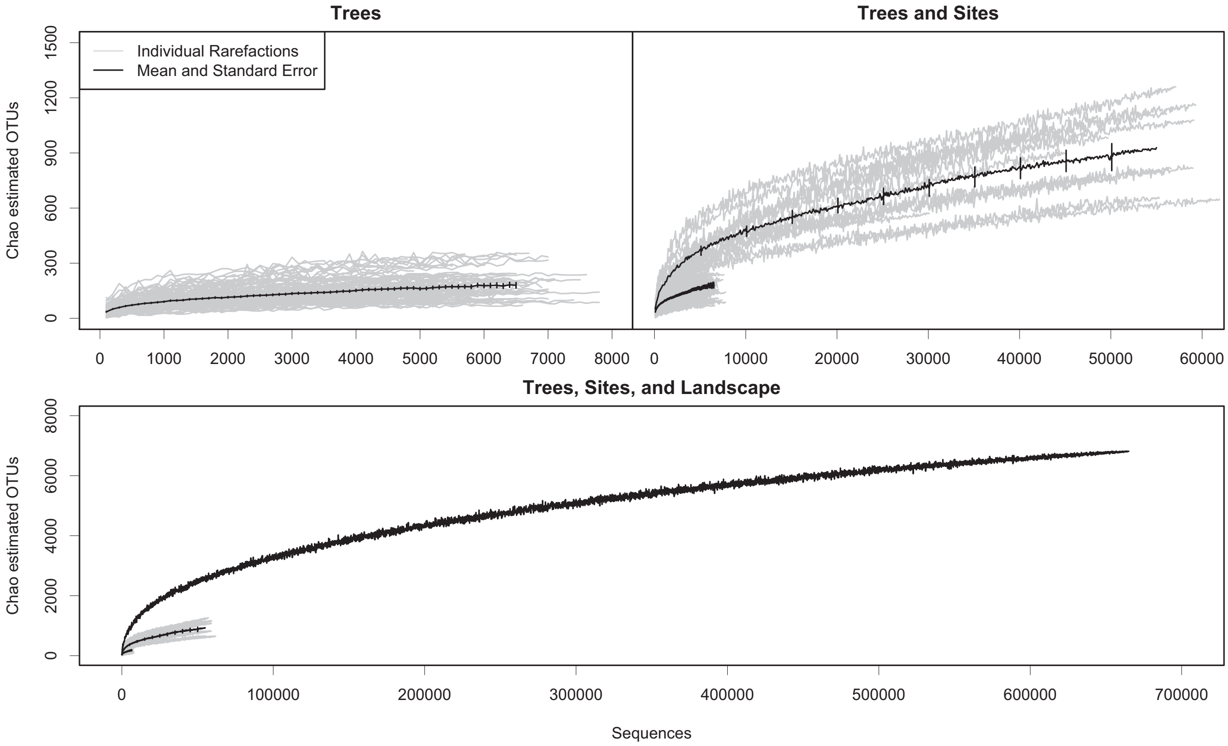

**Fig. S1.** Rarefaction curves of OTU richness using the Chao1 richness estimator. Each gray line represents the mean of five rarefaction runs. OTUs were designated based on 95% similarity of the ITS1 rDNA region.

### Table S1. Summary of common taxa determined via a BLASTn search of GenBank

| | Sequences | Percentage | OTUs |
|---|---|---|---|
| Fungi | | | |
| Ascomycota | | | |
| *Dothideomycetes* | | | |
| Dothideomycetidae | 239,769 | 36.0 | 428 |
| Pleosporomycetidae | 26,422 | 4.0 | 130 |
| Dothideomycetes incertae sedis | 6,241 | 0.9 | 96 |
| *Sordariomycetes* | | | |
| Xylariomycetidae | 19,199 | 2.9 | 131 |
| Sordariomycetidae | 10,054 | 1.5 | 79 |
| Hypocreomycetidae | 3,785 | 0.6 | 69 |
| Sordariomycetes incertae sedis | 43 | <0.1 | 11 |
| Unknown | 109 | <0.1 | 16 |
| *Leotiomycetes* | 5,347 | 0.8 | 41 |
| *Eurotiomycetidae* | 2,449 | 0.4 | 49 |
| *Chaetothyriomycetidae* | 1,531 | 0.2 | 52 |
| *Mycocaliciomycetidae* | 1,054 | 0.2 | 42 |
| *Lecanoromycetidae* | 88 | <0.1 | 14 |
| Mitosporic *Saccharomycetales* | 203 | <0.1 | 12 |
| *Saccharomycetaceae* | 93 | <0.1 | 4 |
| *Unknown* | 6,662 | 1.0 | 132 |
| Basidiomycota | 2,639 | 0.4 | 187 |
| Chytridiomycetes | 374 | 0.1 | 9 |
| Streptophyta | 2,200 | 0.3 | 16 |
| No hits | 68,546 | 10.3 | 1,221 |
| Not assigned/environmental sample | 268,347 | 40.3 | 1,514 |
| Total | 665,155 | 100 | 4,253 |

Summary includes the number of sequences, the percentage of the total number of sequences that each represented, and the number (based on 95% rDNA ITS1 similarity) of OTUs attributed to each taxon. "Not assigned/environmental sample" refers to those sequences that had a match in GenBank but the best match was to an environmental sample of unidentified taxonomic identity. "No hits" refers to sequences that had no matches to GenBank with an acceptable e-value, either because no similar sequences were found or because sequences were of low complexity or too short to produce good matches. Also note that the majority of Chytridiomycetes identified were in the genus *Rhyzophidium*, members of which have previously been found in canopy debris (1).

1. Longcore JE (2005) Zoosporic fungi from Australian and New Zealand tree-canopy detritus. *Aust J Bot* 53:259–272.

### Table S2. Per-tree diversity summary

| | Samples ($n$) | Sequences | | $S_{obs}$ | | Nonsingles | | Chao1 | | Shannon (H) | | Fisher's α | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Mean (±SD) | Range | Mean (±SD) | Range | Mean (±SD) | Range | Mean (±SD) | Range | Mean (±SD) | Range | Mean (±SD) | Range |
| Total | 130 | 5,117 ± 1,575 | 739–7,897 | 105 ± 42 | 40–257 | 68 ± 30 | 16–190 | 157 ± 68 | 62–359 | 1.87 ± 0.85 | 0.1–3.8 | 19 ± 9 | 6–58 |
| W100Y | 10 | 5,918 ± 957 | 4,388–7,665 | 162 ± 51 | 45–228 | 106 ± 43 | 16–169 | 233 ± 47 | 180–352 | 1.9 ± 1.1 | 0.1–3.6 | 31 ± 11 | 6–47 |
| W100O | 10 | 5,716 ± 1,170 | 3,289–7,092 | 160 ± 73 | 40–257 | 103 ± 57 | 18–190 | 232 ± 87 | 69–329 | 2.1 ± 1.2 | 0.1–3.8 | 32 ± 17 | 6–58 |
| W700Y | 10 | 5,909 ± 1,161 | 4,094–7,897 | 95 ± 28 | 65–154 | 60 ± 27 | 37–116 | 146 ± 32 | 90–199 | 1.3 ± 0.6 | 0.5–2.6 | 16 ± 6 | 10–29 |
| W700O | 10 | 6,196 ± 955 | 4,474–7,805 | 79 ± 23 | 53–113 | 48 ± 20 | 28–78 | 136 ± 44 | 86–215 | 1.1 ± 0.6 | 0.3–1.8 | 13 ± 5 | 8–20 |
| W1100Y | 10 | 2,509 ± 1,312 | 739–5,092 | 93 ± 22 | 55–118 | 80 ± 20 | 44–103 | 103 ± 23 | 62–133 | 3.2 ± 0.4 | 2.2–3.6 | 20 ± 3 | 14–24 |
| W1100O | 10 | 3,019 ± 1,016 | 1,508–4,470 | 86 ± 11 | 67–97 | 70 ± 9 | 54–80 | 98 ± 16 | 73–126 | 2.2 ± 0.8 | 1.2–3.5 | 17 ± 3 | 12–21 |
| W1800Y | 10 | 5,932 ± 1,159 | 3,681–7,536 | 123 ± 22 | 100–157 | 68 ± 8 | 59–88 | 210 ± 79 | 105–347 | 1.8 ± 0.6 | 1.0–3.0 | 22 ± 4 | 18–29 |
| W1800O | 10 | 4,973 ± 1,450 | 2,015–6,553 | 112 ± 15 | 82–131 | 68 ± 9 | 57–89 | 175 ± 42 | 94–245 | 1.8 ± 0.4 | 0.9–2.4 | 21 ± 3 | 15–24 |
| W2400Y | 10 | 5,020 ± 1,254 | 3,319–6,795 | 84 ± 11 | 67–96 | 51 ± 10 | 34–67 | 129 ± 35 | 78–184 | 1.2 ± 0.5 | 0.8–2.3 | 14 ± 2 | 11–16 |
| W2400O | 10 | 4,512 ± 1,393 | 2,208–6,552 | 92 ± 21 | 59–118 | 55 ± 12 | 31–73 | 146 ± 43 | 72–196 | 1.2 ± 0.5 | 0.3–2.0 | 16 ± 4 | 10–22 |
| D700Y | 10 | 5,670 ± 1,102 | 3,853–7,019 | 83 ± 18 | 63–126 | 51 ± 13 | 32–73 | 130 ± 49 | 74–218 | 1.8 ± 0.3 | 1.2–2.1 | 14 ± 4 | 10–23 |
| D700O | 10 | 5,533 ± 1,115 | 3,816–7,499 | 82 ± 23 | 45–110 | 58 ± 22 | 24–84 | 108 ± 19 | 88–150 | 2.0 ± 0.6 | 1.0–2.8 | 14 ± 5 | 6–19 |
| D1700Y | 10 | 5,610 ± 1,144 | 3,698–7,109 | 121 ± 43 | 74–213 | 73 ± 21 | 47–119 | 194 ± 95 | 109–359 | 2.5 ± 0.5 | 1.7–3.1 | 22 ± 9 | 13–42 |

Includes means, SDs, and ranges for the number of sequences, OTUs observed ($S_{obs}$), nonsingleton OTUs, the Chao1 richness estimator, the Shannon diversity index, and Fisher's α index for trees. D, dry; O, old; W, wet; Y, young.

## Table S3. Per-site diversity summary

|  | Samples (*n*) | Sequences | $S_{obs}$ | Nonsingles | Chao1 | Bootstrap | Shannon (H) | Fisher's (α) | β (site/tree) | Inverse β (tree/site) |
|---|---|---|---|---|---|---|---|---|---|---|
| All sites, mean ± SD | 13 | 51,170 ± 11,465 | 551 ± 134 | 341 ± 94 | 872 ± 231 | 692 ± 164 | 2.4 ± 0.8 | 87 ± 24 | 5.35 ± 0.27 | 0.19 ± 0.01 |
| (range) |  | (25,092–61,955) | (401–829) | (255–550) | (570–1,260) | (500–1,032) | (1.4–3.7) | (59–137) | (4.76–5.65) | (0.18–0.21) |
| W100Y | 1 | 59,175 | 771 | 516 | 1,077 | 953 | 2.7 | 125 | 4.76 | 0.21 |
| W100O | 1 | 57,159 | 829 | 550 | 1,260 | 1,032 | 2.9 | 137 | 5.18 | 0.19 |
| W700Y | 1 | 59,090 | 519 | 323 | 818 | 653 | 1.8 | 78 | 5.46 | 0.18 |
| W700O | 1 | 61,955 | 418 | 260 | 648 | 524 | 1.5 | 60 | 5.29 | 0.19 |
| W1100Y | 1 | 25,092 | 463 | 365 | 579 | 580 | 3.7 | 81 | 4.98 | 0.20 |
| W1100O | 1 | 30,191 | 454 | 350 | 570 | 572 | 2.7 | 76 | 5.28 | 0.19 |
| W1800Y | 1 | 59,322 | 652 | 344 | 1,160 | 817 | 2.1 | 102 | 5.30 | 0.19 |
| W1800O | 1 | 49,728 | 586 | 326 | 982 | 739 | 2.3 | 93 | 5.23 | 0.19 |
| W2400Y | 1 | 50,195 | 471 | 267 | 759 | 597 | 1.5 | 72 | 5.61 | 0.18 |
| W2400O | 1 | 45,124 | 510 | 283 | 899 | 646 | 1.4 | 81 | 5.54 | 0.18 |
| D700Y | 1 | 56,696 | 469 | 260 | 814 | 594 | 2.5 | 70 | 5.65 | 0.18 |
| D700O | 1 | 55,326 | 401 | 255 | 653 | 500 | 2.8 | 59 | 4.89 | 0.20 |
| D1700Y | 1 | 56,102 | 621 | 333 | 1,113 | 783 | 3.6 | 98 | 5.13 | 0.19 |

Includes means, SDs, and ranges for the total number of sequences, OTUs observed ($S_{obs}$), nonsingleton OTUs, the Chao1 richness estimator, the bootstrap richness estimator, the Shannon diversity index, and Fisher's α index for sites. β-diversity using the given site or location as a base is also included as Whittaker's multiplicative β, as well as the inverse of that value. The inverse value represents the proportion of γ (total) richness captured by the mean value of α (local) richness. D, dry; O, old; W, wet; Y, young.

## Table S4. Per-location diversity summary

|  | Samples (*n*) | Sequences | $S_{obs}$ | Nonsingles | Chao1 | Bootstrap | Shannon (H) | Fisher's α | β (location/site) | Inverse β (site/location) |
|---|---|---|---|---|---|---|---|---|---|---|
| All locations, mean ± SD | 7 | 95,020 ± 28,021 | 848 ± 205 | 519 ± 155 | 1,340 ± 295 | 1,066 ± 249 | 2.7 ± 0.8 | 129 ± 33 | 1.63 ± 0.05 | 0.61 ± 0.02 |
| (range) |  | (56,102–121,045) | (708–1,229) | (417–817) | (999–1,793) | (783–1,521) | (1.5–3.6) | (98–192) | (1.54–1.68) | (0.6–0.65) |
| W100 | 1 | 116,334 | 1,229 | 817 | 1,793 | 1,521 | 2.9 | 192 | 1.54 | 0.65 |
| W700 | 1 | 121,045 | 782 | 480 | 1,246 | 989 | 1.8 | 112 | 1.67 | 0.60 |
| W1100 | 1 | 55,283 | 769 | 584 | 999 | 971 | 3.6 | 126 | 1.68 | 0.60 |
| W1800 | 1 | 109,050 | 1,005 | 547 | 1,655 | 1,262 | 2.3 | 153 | 1.62 | 0.62 |
| W2400 | 1 | 95,319 | 822 | 453 | 1,418 | 1,044 | 1.5 | 124 | 1.68 | 0.60 |
| D700 | 1 | 112,022 | 708 | 417 | 1,157 | 891 | 2.8 | 101 | 1.63 | 0.61 |
| D1700 | 1 | 56,102 | 621 | 333 | 1,113 | 783 | 3.6 | 98 | NA | NA |

Includes means, SDs, and ranges for the total number of sequences, OTUs observed ($S_{obs}$), nonsingleton OTUs, the Chao1 richness estimator, the bootstrap richness estimator, the Shannon diversity index, and Fisher's α index for locations. β-diversity using the given location or site as a base is also included as Whittaker's multiplicative β, as well as the inverse of that value. The inverse value represents the proportion of γ (total) richness captured by the mean value of α (local) richness. D, dry; O, old; W, wet; Y, young.

## Table S5. Landscape diversity summary

|  | Samples (n) | Sequences | $S_{obs}$ | Nonsingles | Chao1 | Bootstrap | Shannon (H) | Fisher's α | β (landscape/location) | Inverse β (location/landscape) |
|---|---|---|---|---|---|---|---|---|---|---|
| Landscape | 1 | 665,155 | 4,253 | 2,552 | 6,812 | 5,320 | 3.6 | 608 | 5.01 | 0.20 |

Includes sequences, OTUs observed ($S_{obs}$), nonsingleton OTUs, the Chao1 richness estimator, the bootstrap richness estimator, the Shannon diversity index, and Fisher's α index for the entire landscape. β-diversity using the given landscape or location as a base is also included as Whittaker's multiplicative β, as well as the inverse of that value. The inverse value represents the proportion of γ (total) richness captured by the mean value of α (local) richness.

**Table S6. Sensitivity of analyses to community distance metrics: PERMANOVA**

| | PERMANOVA using distance matrices | |
|---|---|---|
| Community | $R^2$ | *P* |
| Chao | | |
| Rainfall | 0.35986 | 0.001 |
| Elevation | 0.17612 | 0.001 |
| Flow Age | 0.02318 | 0.001 |
| Residuals | 0.44084 | |
| Total | 1 | |
| Jaccard | | |
| Rainfall | 0.13896 | 0.001 |
| Elevation | 0.1202 | 0.001 |
| Flow Age | 0.01456 | 0.008 |
| Residuals | 0.72628 | |
| Total | 1 | |
| Horn | | |
| Rainfall | 0.23329 | 0.001 |
| Elevation | 0.20399 | 0.001 |
| Flow Age | 0.02169 | 0.002 |
| Residuals | 0.54102 | |
| Total | 1 | |
| Bray | | |
| Rainfall | 0.19121 | 0.001 |
| Elevation | 0.16265 | 0.001 |
| Flow Age | 0.01724 | 0.01 |
| Residuals | 0.6289 | |
| Total | 1 | |

This table includes the variance and *P* values for the PERMANOVA analyses.

**Table S7. Sensitivity of analyses to community distance metrics: ANOSIM**

| | ANOSIM | |
|---|---|---|
| Distance metric | R | *P* |
| Chao | 0.659 | 0.001 |
| Jaccard | 0.738 | 0.001 |
| Horn | 0.678 | 0.001 |
| Bray | 0.738 | 0.001 |
| Rarefied Bray | 0.733 | 0.001 |
| Raup–Crick | 0.873 | 0.001 |

This table includes the sample statistic (R) and *P* values for the ANOSIM test.

**Table S8. Sensitivity of analyses to community distance metrics: dbRDA**

| | dbRDA constrained with PCNM (*P*) | | |
|---|---|---|---|
| Distance metric | Rainfall | Elevation | Flow age |
| Chao | 0.01 | 0.01 | 0.01 |
| Jaccard | 0.01 | 0.01 | 0.02 |
| Horn | 0.01 | 0.01 | 0.01 |
| Bray | 0.01 | 0.01 | 0.02 |
| Rarefied Bray | 0.01 | 0.01 | 0.02 |

This table includes the *P* values for the dbRDA analyses conditioned using principal components of neighbor matrices (PCNM).

**Table S9. Sensitivity of analyses to community distance metrics: partial Mantel**

| | Rainfall | Elevation | Flow age |
|---|---|---|---|
| Mantel R | 0.174 | 0.379 | NA |
| *P* | 0.001 | 0.001 | NA |

**Table S10. Comparison of the OTU richness found in this study to other research, when rarefied to the same number of sequences**

| Paper | Amend et al. (1) | Jumpponen and Jones (2) | Redford et al. (3) |
|---|---|---|---|
| Organisms of interest | Indoor fungi | Phyllosphere fungi | Phyllosphere bacteria |
| Scope | Global | Two locations (one host) | Local (many hosts) + global (one host) |
| No. of sequences | 97,557 | 18,020 | 115,394 |
| 97% 16S OTUs | | | 5,476 |
| ITS1 95% OTUs | 3,500* | 689 | |
| Rarefied richness from this study | 1,895 | 846 | 2,042 |

Amend et al. (1) describe the diversity of indoor fungi from a set of global samples, Jumpponen and Jones (2) describe the phyllosphere fungal communities of *Quercus macrocarpa* in urban and rural sites, and Redford et al. (3) describe phyllosphere bacteria communities from a large number of different plants hosts at one site and then for one host at many sites around the world.
*Approximate from figure.

1. Amend AS, Seifert KA, Samson R, Bruns TD (2010) Indoor fungal composition is geographically patterned and more diverse in temperate zones than in the tropics. *Proc Natl Acad Sci USA* 107:13748–13753.
2. Jumpponen A, Jones KL (2009) Massively parallel 454 sequencing indicates hyperdiverse fungal communities in temperate *Quercus macrocarpa* phyllosphere. *New Phytol* 184:438–448.
3. Redford AJ, Bowers RM, Knight R, Linhart Y, Fierer N (2010) The ecology of the phyllosphere: Geographic and phylogenetic variability in the distribution of bacteria on tree leaves. *Environ Microbiol* 12:2885–2893.

**Table S11. Comparison of surface-sterilized and non–surface-sterilized leaves**

| | Surface-sterilized | | | Not surface-sterilized | | |
|---|---|---|---|---|---|---|
| | $S_{obs}$ | Rarefied | Chao1 | $S_{obs}$ | Rarefied | Chao1 |
| W100O: tree 6 | 186 | 180 | 212 | 223 | 199 | 333 |
| W100Y: tree 8 | 162 | 156 | 209 | 258 | 258 | 548 |

The “Rarefied” column represents richness rarefied to 5,333 sequences, the lowest number in any of the four samples in the table. O, old; W, wet; Y, young.

**Table S12. Site characteristics**

| Site code | Mean annual temperature (°C) | Mean rainfall (mm/y) | Flow age (y bp) | Elevation (m) | Easting (m) | Northing (m) |
|---|---|---|---|---|---|---|
| W100Y | 22.2 | 3,900 | Young | 90 | 280,609 | 2,179,988 |
| W100O | 22.2 | 3,900 | Old | 97 | 280,589 | 2,179,777 |
| W700Y | 18.9 | 5,500 | Young | 728 | 269,321 | 2,179,147 |
| W700O | 18.9 | 5,500 | Old | 726 | 269,440 | 2,178,343 |
| W1100Y | 17.2 | 4,000 | Young | 1,142 | 262,292 | 2,178,451 |
| W1100O | 17.2 | 4,000 | Old | 1,144 | 262,049 | 2,179,796 |
| W1800Y | 13.9 | 2,200 | Young | 1,767 | 251,003 | 2,174,911 |
| W1800O | 13.9 | 2,200 | Old | 1,788 | 250,406 | 2,175,256 |
| W2400Y | 10.6 | 1,000 | Young | 2,440 | 243,061 | 2,168,284 |
| W2400O | 10.6 | 1,000 | Old | 2,485 | 243,429 | 2,167,539 |
| D700Y | 18.9 | 500 | Young | 691 | 204,302 | 2,194,604 |
| D700O | 18.9 | 500 | Old | 707 | 205,136 | 2,194,867 |
| D1700Y | 14.4 | 550 | Young | 1,697 | 214,927 | 2,174,342 |

Site codes represent the rainfall (D, dry ; W, wet), elevation (in meters), and substrate age (O, old; Y, young) of each location. For flow age, “Young” refers to substrate derived from flows that occurred between 100 and 150 y before present, and “Old” refers to substrate from flows that occurred ca. 3,000 y before present. Global positioning system coordinates are presented in meters with Easting and Northing values from the Universal Transverse Mercator projection (NAD 1983 Zone 5).