*Supporting Information for*

**Mechanisms of soil bacterial and fungal community assembly differ among and within islands**

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*Supporting Information includes six supplementary figures:*

**Figure S1.** The locations of the 29 surveyed islands in the Thousand Island Lake, Zhejiang Province, China and the nearby mainland site (indicated with the red dot). Islands are ordered according to their area (from the smallest to largest).

**Figure S2**. The relationship between island area (m2; log10-transformed) and each soil property (mean ± sd). Soil properties were standardized to have mean 0 and variance 1. **AP**: available P; **TP**: total P; **TN**: total N; **TOC**: total organic carbon; **AAl**: available Al; **ACa**: available Ca; **AMg**; available Mg. “ML” is short for mainland.

**Figure S3**. The relationship between island area (m2; log10-transformed) and heterogeneity of each soil property. Heterogeneity was calculated as the mean Euclidean distance of each soil property within islands. **AP**: available P; **TP**: total P; **TN**: total N; **TOC**: total organic carbon; **AAl**: available Al; **ACa**: available Ca; **AMg**; available Mg.

**Figure S4**. Mantel correlograms between the pairwise Euclidean distances of OTUs’ optimal environmental conditions (calculated using abundance-weighted means) and phylogenetic distances (panel a: bacteria; panel b: fungi). Closed squares indicate significant phylogenetic signals at the significance level of α = 0.05 after Bonferroni correction for multiple testing.

**Figure S5. The distribution of bacterial standardized phylogenetic turnover (βNTI: panel a) and taxonomic turnover (RCbray: panel b), and the percentages of the five structuring processes (panel c), and their variation along the island area (m2; log10-transformed) gradient (panel d), after subsampling each island to four samples. HS**: homogeneous selection; **VS**: variable selection; **HD**: homogenizing dispersal; **DL**: dispersal limitation. Islands are sorted based on their area and labeled from 1 to 29 (from smallest to largest). ML is short for mainland. No analyses were conducted for the smallest island (island No. 1), which had too few samples (two) to give reliable results. The vertical dash lines mark the positions of -2 and 2 in panel a, and -0.95 and 0.95 in panel b. Each line in panel d was fitted using local polynomial regression with 95% confidence interval.

**Figure S6. The distribution of fungal standardized phylogenetic turnover (βNTI: panel a) and taxonomic turnover (RCbray: panel b), and the percentages of the five structuring processes (panel c), and their variation along the island area (m2; log10-transformed) gradient (panel d), after subsampling each island to four samples. HS**: homogeneous selection; **VS**: variable selection; **HD**: homogenizing dispersal; **DL**: dispersal limitation. Islands are sorted based on their area and labeled from 1 to 29 (from smallest to largest). ML is short for mainland. No analyses were conducted for the smallest island (island No. 1), which had too few samples (two) to give reliable results. The vertical dash lines mark the positions of -2 and 2 in panel a, and -0.95 and 0.95 in panel b. Each line in panel d was fitted using local polynomial regression with 95% confidence interval.



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