## *New Phytologist* Supporting Information

# Article title: **Forest structural diversity is linked to soil microbial diversity**

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The following Supporting Information is available for this article:

**Fig. S1** Correlations among forest structural diversity, productivity, and environmental predictors.

**Fig. S2** Relationships between the richness of a) AM tree species and AM fungal taxa, and b) EM tree species and EM fungal taxa from soil samples collected at 0-5 cm depth and 5-10 cm depth in plots within the Indiana CFI network.

**Fig. S3**  Effects of soil pH on the alpha diversity of a) soil bacteria, b) total fungi, and c) AM and d) EM fungi, calculated with the inverse Simpson’s index.

**Table S1** Drivers of microbial alpha diversity with the random effect of sampling location (Indiana county) to account for potential spatial patterns.

**Table S2** Relative variation in microbial community composition (beta diversity) explained by structural diversity and environmental predictor categories in a distance-based redundancy analysis after accounting for spatial arrangement of study plots.

**Fig. S1** Correlations among forest structural diversity, productivity, and environmental predictors. Parameters with correlation coefficients greater than 0.7 were not included together in linear models to avoid conflicts in explaining variance.

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**Fig. S2** Relationships between the richness of a) AM tree species and AM fungal taxa, and b) EM tree species and EM fungal taxa from soil samples collected at 0-5 cm depth and 5-10 cm depth in plots within the Indiana CFI network.

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**Fig. S3**  Effects of soil pH on the alpha diversity of a) soil bacteria, b) total fungi, and c) AM and d) EM fungi, calculated with the inverse Simpson’s index. Points represent measured values of microbial richness and soil pH at 0-5 cm and 5-10 cm depth in forest soils collected across Indiana; lines represent the marginal effects of soil pH independent of the effects of other soil and vegetation factors, and are plotted only where significant. Significance determined at α=0.05.

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**Table S1** Drivers of microbial alpha diversity with the random effect of sampling location (Indiana county) to account for potential spatial patterns. Test statistics and p values reported only for  parameters with significant influence on one of the four microbial groups tested either in the 0-5 cm soil depth or 5-10 cm soil depth. Marginal R2 indicates the model fit including  fixed effects only; conditional R2 additionally includes the random effect of county. ICC=Intraclass correlation coefficient.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **0-5 cm** | | | | **5-10 cm** | | | |
| **AM Fungi** | **EM Fungi** | **Bacteria** | **Total Fungi** | **AM Fungi** | **EM Fungi** | **Bacteria** | **Total Fungi** |
| Total tree richness | - | - | - | - | - | - | - | β= -0.23  p= 0.042 |
| AM dominance | - | - | - | - | - | - | - | - |
| Stand age | - | β= 0.57  p= 0.027 | - | - | - | - | - | - |
| Basal Area Increment | - | - | - | - | - | - | - | β= 0.37  p= 0.014 |
| VertSD | - | - | - | - | - | - | - | - |
| VAI | - | β= 0.43  p= 0.025 | - | - | - | - | - | - |
| VCI | - | - | - | - | - | - | - | - |
| C:N | - | - | - | - | - | - | - | - |
| pH | β= 0.43  p= 0.04 | - | β= 0.59  p= 0.002 | - | - | - | β= 0.63  p= 0.013 | - |
| FeOx (percent) | - | - | - | - | - | - | - | - |
| **Random Effects** |  | | | | | | | |
| ICC | 0.00 | 0.03 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 | 0.00 |
| Marginal R2 | 0.447 | 0.434 | 0.589 | 0.333 | 0.277 | 0.203 | 0.427 | 0.764 |
| Conditional R2 | 0.447 | 0.452 | 0.589 | 0.333 | 0.294 | 0.203 | 0.427 | 0.764 |

**Table S2** Relative variation in microbial community composition (beta diversity) explained by structural diversity and environmental predictor categories in a distance-based redundancy analysis after accounting for spatial arrangement of study plots. X2 and p values are reported only for a predictor category that explains significant variation in the community composition at α= 0.05.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Group** | **Variable** | **0-5 cm** | | | | **5-10 cm** | | | |
| **Bacteria** | **Total Fungi** | **AMF** | **EMF** | **Bacteria** | **Total Fungi** | **AMF** | **EMF** |
| Structural diversity | VertSD | Χ2:8.84  p=0.031 | Χ2:11.7  p=0.008 | - | Χ2:39.8  p<0.001 | Χ2:8.42  p=0.038 | - | - | Χ2:71.6  p<0.001 |
| VAI |
| VCI |
| Tree diversity | Tree richness | Χ2:9.92  p=0.007 | Χ2:14.8  p<0.001 | - | Χ2:67.5  p<0.001 | Χ2:13.1  p=0.001 | Χ2:15.7  p<0.001 | Χ2:26.0  p<0.001 | Χ2:50.7  p<0.001 |
| AM domi-nance |
| Productivity and age | BAI | - | - | - | Χ2:18.8  p<0.001 | - | - | Χ2:15.9  p<0.001 | Χ2:84.5  p<0.001 |
| Stand age |
| Soil properties | C:N | Χ2:106  p<0.001 | Χ2:59.1  p<0.001 | Χ2:194  p<0.001 | Χ2:547  p<0.001 | Χ2:87  p<0.001 | Χ2:129  p<0.001 | Χ2:275  p<0.001 | Χ2:280  p<0.001 |
| pH |
| % Fe |
| Nplots | | 36 | 37 | 38 | 36 | 34 | 36 | 36 | 36 |