**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 individual environmental predictors within variable groups presented in Figure 4. Values calculated using a distance-based redundancy analysis after accounting for spatial arrangement of study plots. X2 and p values are reported only for a predictor 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 | Vert SD | - | - | - | Χ2: 12.2  p<0.001 | - | - | - | Χ2: 33.2  p<0.001 |
| VAI | - | - | - | Χ2: 27.4  p<0.001 | - | - | - | Χ2: 37.6  p<0.001 |
| VCI | - | Χ2: 11.2  p<0.001 | - | - | - | - | - | - |
| Tree diversity | Tree richness | - | - | - | Χ2: 49.4  p<0.001 | - | - | - | Χ2: 56.6  p<0.001 |
| AM dominance | Χ2: 12.1  p<0.001 | Χ2: 15.5  p<0.001 | - | Χ2: 29.5  p<0.001 | Χ2: 17.2  p<0.001 | Χ2: 14.7  p<0.001 | Χ2: 22.7  p<0.001 | - |
| Stand properties | BAI | - | - | - | - | - | - | - | Χ2: 89.5  p<0.001 |
| Stand age | - | - | - | Χ2: 13.5  p<0.001 | - | - | Χ2: 12.9  p<0.001 | Χ2: 24.6  p<0.001 |
| Soil properties | C:N | Χ2:7.81  p=0.005 | Χ2: 52.0  p<0.001 | Χ2: 14.6  p<0.001 | Χ2: 333  p<0.001 | Χ2: 38.9  p<0.001 | Χ2: 84.2  p<0.001 | Χ2: 76.3  p<0.001 | Χ2: 188  p<0.001 |
| pH | Χ2: 143  p<0.001 | Χ2: 9.27  p=0.002 | Χ2: 166  p<0.001 | Χ2: 214  p<0.001 | Χ2: 132  p<0.001 | Χ2: 61.3  p<0.001 | Χ2: 309  p<0.001 | Χ2: 81.6  p<0.001 |
| % Fe | - | Χ2: 9.01  p=0.028 | - | Χ2: 53.8  p<0.001 | - | Χ2: 27.2  p<0.001 | - | Χ2: 155  p<0.001 |
| Nplots | | 36 | 37 | 38 | 36 | 34 | 36 | 36 | 36 |