**Continuous monoculture of annual crops, not plant species, is a strong determinant of microbial community structure in a tropical Oxisol soil**

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**Supplemental tables:**

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| **Microbial OTU richness and diversity between cultivated and fallow soils** | | |
|  | Bacteria and Archaea | Fungi |
| OTU Richness | \*\*P =0.002 | \*\*\*P <0.001 |
| OTU Diversity | \*\*P =0.003 (Shannon) | \*\*P =0.007 (Shannon) |
|  | \*\*\*P <0.001 (Phylogenetic) |  |
| **Microbial community composition between cultivated and fallow soils** | | |
|  | Bacteria and archaea | Fungi |
|  | \*\*\*P =0.001, R2 =0.068 | \*\*\*P =0.001, R2 =0.05 |
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***Table S1:*** *Statistical analysis of microbial richness, diversity, and community composition in fallow and cultivated soil. p value with “\*” mark represents the significant difference between fallow and cultivated soil.*

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| **Microbial OTU richness and diversity among different plant species** | | | | |
|  | **Fallow soil** | | **Cultivated soil** | |
| Bacteria and archaea | Fungi | Bacteria and archaea | Fungi |
| OTU Richness | P =0.3 | P =0.09 | P =0.93 | P =0.82 |
| OTU Diversity | P =0.27(Shannon) | P =0.52(Shannon) | P =0.89(Shannon) | P =0.66(Shannon) |
|  | P =0.07(Phylogenetic) |  | P =0.97(Phylogenetic) |  |

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| **Microbial community composition among different plant species** | |
| **In whole data set** | |
| Bacteria and archaea | Fungi |
| P =0.09, R2 =0.02 | \*P =0.001, R2 =0.05  Lettuce-Maize: P-adj =1, R2 = 0.02  Maize-Mustard cabbage: P-adj =1, R2 = 0.01  Lettuce-Mustard cabbage: P-adj =1, R2 =0.01 |

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| **Microbial community composition in fallow soil** | | **Microbial community composition in cultivated soil** | |
| Bacteria and archaea | Fungi | Bacteria and archaea | Fungi |
| P =0.88, R2 =0.03 | P =0.19, R2 =0.05 | \*P =0.04, R2 =0.07  Lettuce-Maize:  P-adj =0.7, R2 =0.05  Maize-Mustard cabbage:  \*P-adj =0.01, R2 =0.12  Lettuce-Mustard cabbage:  P-adj =1, R2 = 0.03 | \*P =0.001, R2 =0.098  Lettuce-Maize:  P-adj =0.3, R2 =0.06  Maize-Mustard cabbage:  P-adj =0.04, R2 =0.10  Lettuce-Mustard cabbage:  P-adj =0.2, R2 =0.07 |

***Table S2:*** *Statistical analysis of microbial richness, diversity, and community composition in different plant species: Lactuca sativa, Zea mays, and Brassica juncea. P value with “\*” mark represents the significant difference between plant species.*

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| **Microbial OTU richness and diversity among different plant cycles** | | | | |
|  | **Fallow soil** | | **Cultivated soil** | |
| Bacteria and archaea | Fungi | Bacteria and archaea | Fungi |
| OTU Richness | P =0.45 | \*P =0.01  First-second:  P-adj =0.45  Second-third:  \*P-adj =0.01  First-third:  P-adj =0.16 | \*\*\*P =0.001  First-second:  \*P-adj =0.008  Second-third:  P-adj =0.84  First-third:  \*P-adj =0.002 | P =0.1 |
|  | | | | |
| OTU Diversity | P =0.6(Shannon) | \*P =0.001  First-second:  \*P-adj =0.004  Second-third:  \*P-adj =0.0005  First-third:  P-adj =0.7 | \*\*\*P =0.0003 (Shannon)  (First-second: \*  \*P-adj =0.009  Second-third:  P-adj =0.56  First-third:  \*P-adj =0.0005 | P =0.88 |
|  | \*P =0.006(Phylogenetic)  First-second:  P-adj =0.8,  Second-third:  P-adj =0.05  First-third:  \*P-adj =0.01 |  | \*\*\*P =0.0008 (Phylogenetic)  First-second:  \*P-adj =0.01  Second-third:  P-adj =0.6  First-third:  \*P-adj =0.001 |  |

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| **Microbial community composition among different plant cycles** | | | | |
| **In the whole data set** | | | | |
| Bacteria and archaea | | Fungi | | |
| \*\*P =0.001, R2 =0.09  First-second: \*P-adj =0.003, R2 = 0.14  Second-third: \*P-adj =0.006, R2 =0.11  First-third: \*P-adj =0.02, R2 =0.09 | | \*\*\*P =0.001, R2 =0.14  First-second: \*P-adj =0.003, R2 =0.14  Second-third: \*P-adj =0.003, R2 =0.21  First-third: \*P-adj =0.003, R2 =0.30 | | |
| **Fallow soil** | | | **Cultivated soil** | |
| Bacteria and archaea | Fungi | | Bacteria and archaea | Fungi |
| \*\*\*P =0.001, R2 =0.2  First-second:  \*P-adj =0.003, R2 =0.3  Second-third:  \*P-adj =0.003, R2 =0.18  First-second:  \*P-adj =0.003, R2 =0.28 | \*\*\*P =0.001, R2 =0.27  First-second:  \*P-adj =0.003, R2 =0.28  Second-third:  \*P-adj =0.003, R2 =0.44  First-second:  \*P-adj =0.003, R2 =0.55 | | \*\*\*P =0.001, R2 =0.12  First-second:  P-adj =0.2, R2 =0.08  Second-third:  P-adj =0.2, R2 =0.09  First-third:  \*P-adj =0.003, R2 =0.19 | \*P =0.001  R2 = 0.14  First-second:  P-adj =0.03, R2 =0.12  Second-third:  P-adj =0.14, R2 =0.09  First-third:  \*P-adj =0.003, R2 =0.25 |

***Table S3:*** *Statistical analysis of microbial richness, diversity, and community composition in different plant cycle: Plant cycle1, Plant cycle2, and Plant cycle3. p value with “\*” mark represents the significant difference between plant cycles.*

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| **S.N.** | **Content** | **Percentage (%)** |
| 1 | Moisture | 4.83 |
| 2 | Nitrogen | 8.74 |
| 3 | Protein (crude) | 54.6 |
| 4 | .2% Pepsin Digestibility | 93 |
| 5 | Fat (crude) | 22.88 |
| 6 | Ash | 16.91 |
| 7 | Calcium | 5.31 |
| 8 | Phosphorus | 2.80 |
| 9 | Sodium | .58 |
| 10 | P2O5 | 6.41 |
| 11 | Potash | .782 |

***Table S4:*** *Fertilizer (fishmeal) composition applied to the research field.*