**Tables**

**Table 1.** Results of separate linear regression between different metrics (ɑ-Diversity Metric) of the rhizosphere microbiome (Simpson diversity, species richness and species evenness) and four root traits (root topology, root architecture, root size and root morphology) examined in *I*. *purpurea*. ɑ-Diversity metrics were treated as response variables for each root trait, and block and competition treatment (Treatment) were included in the final modelǂ as fixed main effects. Linear regression coefficient slopes (𝛣) are reported with ± 1 standard error. P < 0.05 \*; P <0.01 \*\*; P <0.001\*\*\*; P =0.09 ^

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **α-Diversity metric** | **Root topology (PC1)** | **Root architecture (PC2)** | **Root size (PC3)** | **Root morphology (PC4)** |
| *Sp.* richness | 3.379 +/- 4.65 | **-5.734 +/- 2.223\*** | 1.998 +/- 2.81 | 3.503 +/- 3.518 |
| *Sp.* evenness | -6.197e^6 +/- 66.198e^6 | **7.252e^5 +/- 3.19e^58\*** | 0.284e^5 +/- 3.999e^5 | 2.615e^5 +/- 5.018e^5 |
| Simpson Diversity | 1.447e^3 +/- 1.258e^3 | -9.071e^4 +/- 6.315e^4 | 9.578e^4 +/- 7.577e^4 | 8.7e^4 +/- 9.766e^4 |

Note**:** The modelǂ included community composition as a response variable, with Root trait, Treatment, and Block as fixed effects.

ǂModel: ɑ-Diversity = *B*0(Root trait) + *B*1(Block) +*B*2(Treatment)