**Table 1.** Linear mixed models predicting plant growth response to soil inocula as a function of microbial diversity and community structure. Diversity indices were calculated using the exponential Shannon diversity index, and the “axes” 1 and 2 refer to non-metric multidimensional scaling of microbial communities (Hellinger distance) over two dimensions. Models were run separately for *Koeleria* and *Bromus*, and plot identity was used as a random factor in both models. We also included the *Bromus* invasion status of each plot as a fixed factor (i.e., binary state variable indicating, for each block, whether the plot corresponded to the *Bromus*-invaded patch or the native vegetation patch). For this “*Bromus* invasion status”, a positive *t*-value indicates that the plant species grew better with inocula from *Bromus*-invaded plots. Values in bold indicate significant explanatory variables (*p* < 0.05).

|  |  |  |
| --- | --- | --- |
| **Plant growth response predictor** | ***t*-value** | ***p*-value** |
|  |  |  |
| *Koeleria* |  |  |
| Prokaryotic diversity (Shannon) | 0.96 | 0.34 |
| Prokaryotic richness | -1.10 | 0.27 |
| Fungal diversity (Shannon) | 0.79 | 0.43 |
| Fungal richness | 0.37 | 0.71 |
| Prokaryotes Axis 1 | -0.49 | 0.63 |
| Prokaryotes Axis 2 | -0.27 | 0.79 |
| Fungi Axis 1 | -0.14 | 0.89 |
| Fungi Axis 2 | 0.04 | 0.97 |
| *Bromus* invasion status | **-2.02** | **0.04** |
|  |  |  |
| *Bromus* |  |  |
| Prokaryotic diversity (Shannon) | -1.40 | 0.16 |
| Prokaryotic richness | 0.96 | 0.34 |
| Fungal diversity (Shannon) | -0.39 | 0.70 |
| Fungal richness | -1.59 | 0.11 |
| Prokaryotes Axis 1 | -1.47 | 0.14 |
| Prokaryotes Axis 2 | -1.72 | 0.09 |
| Fungi Axis 1 | -0.85 | 0.40 |
| Fungi Axis 2 | **2.19** | **0.03** |
| *Bromus* invasion status | **2.36** | **0.02** |
|  |  |  |