

**Table 3.** Multiple stepwise regression model results for bacterial and fungal taxa that significantly correlated with tissue type or environmental factors.

Taxon	Explanatory variable	T	<i>p</i> -value
<b>Whole plant bacterial community (Genus)</b>			
<i>Cupriavidus</i>	P	34.12666	< 0.001
<i>Brevibacterium</i>	OM	5.984721	< 0.001
<b>Whole plant fungal community (Species)</b>			
<i>Saitozyma podzolica</i>	tissue (root)	326.7589	< 0.001
Sporormiaceae_F_OTU_583	tissue (root)	65.27728	< 0.001
<i>Aporospora</i> _F_OTU_199	tissue (root)	-5.26803	< 0.001
<b>Whole plant fungal community (Genus)</b>			
<i>Saitozyma</i>	tissue (root)	326.7589	< 0.001
<i>Neocamarosporium</i>	tissue (root)	-5.98923	< 0.001
<b>Whole plant fungal community (Class)</b>			
Dothideomycetes	tissue (root)	-6.271	< 0.001
<b>Aerial tissue fungal community (Species)</b>			
<i>Acremonium chrysogenum</i>	RadM	-40.1085	< 0.001