



Fig. S1 Mean (\pm SE) AMF richness, diversity, and evenness per root sample based on OTUs designated at 90%, 95%, 97%, and 99% sequence similarity. (a,d) OTU richness by habitat (a) and host species (d); (b,e) Shannon's diversity index by habitat (b) and host species (e); (c,f) OTU evenness by habitat (c) and host species (f). In panels a–c open and solid circles represent samples from the open meadow and willow understory, respectively. In panels d–f symbols represent samples from *T. ceratophorum* (circles), *T. officinale* (squares), and *P. viscosum* (triangles). Asterisks indicate a significant habitat or host effect ($*P \leq 0.05$, $**P \leq 0.01$). The decrease in OTU richness and diversity at 99% similarity was due to an increased number of singletons, which were subsequently removed from the dataset.