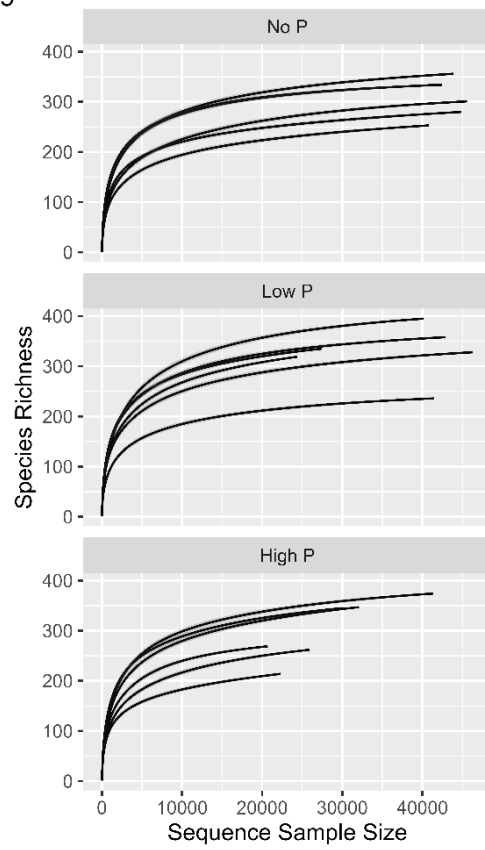


a) 2019



b) 2022

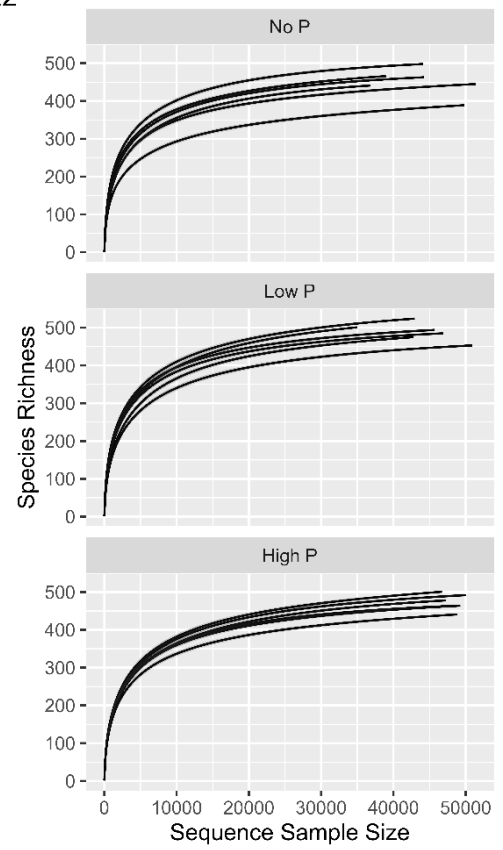


Fig S1. Rarefaction curves for each experimental plot according to long-term P treatment and year.

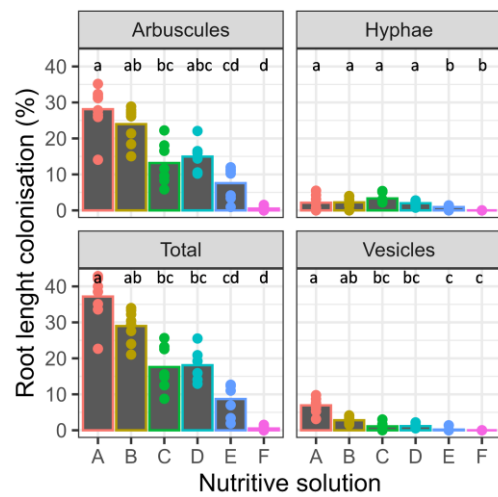


Fig. S2 Limiting N and P enhances wheat root AMF colonisation by *R. irregularis* in artificial soil. Wheat plants were grown under controlled conditions in attapulgite using a range of 6 nutritional treatments with a gradient in N and P concentration. Wheat was grown for 5 weeks after inoculation with 200 spores of *R. irregularis* DAOM197198. AMF root length colonisation measured using the grid intersect method for each AMF structures. Different letters indicate significant differences (p-value < 0.05, detailed in Table S10) assessed by Kruskal-Wallis test followed by post hoc Dunn test with Benjamini-Hochberg correction.

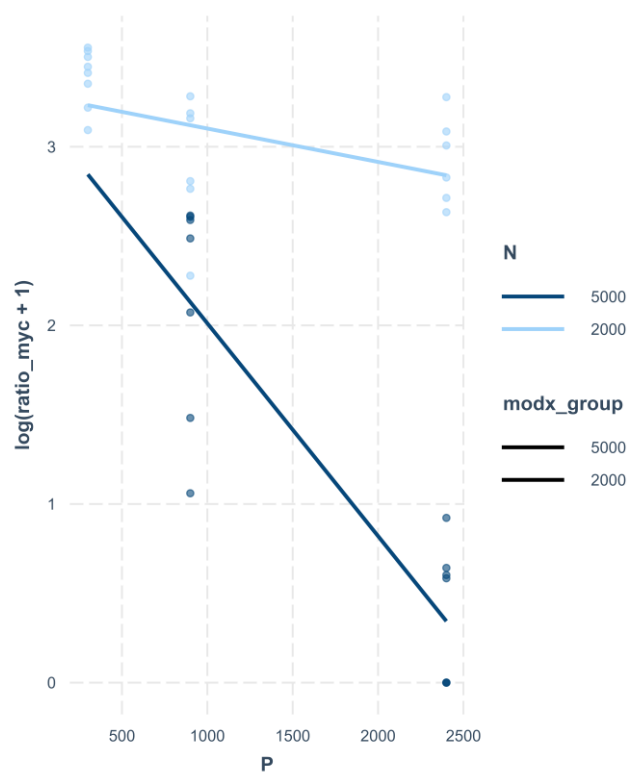


Fig S3. Graph showing the significant interaction between N availability and P availability on mycorrhizal colonisation of wheat (*experiment 3*). In light blue N at a concentration of 2000 μM and in dark blue N at concentration 5000 μM . P range spanning from 500 to 2500 μM . The y axis represents the log transformation of mycorrhizal colonisation.

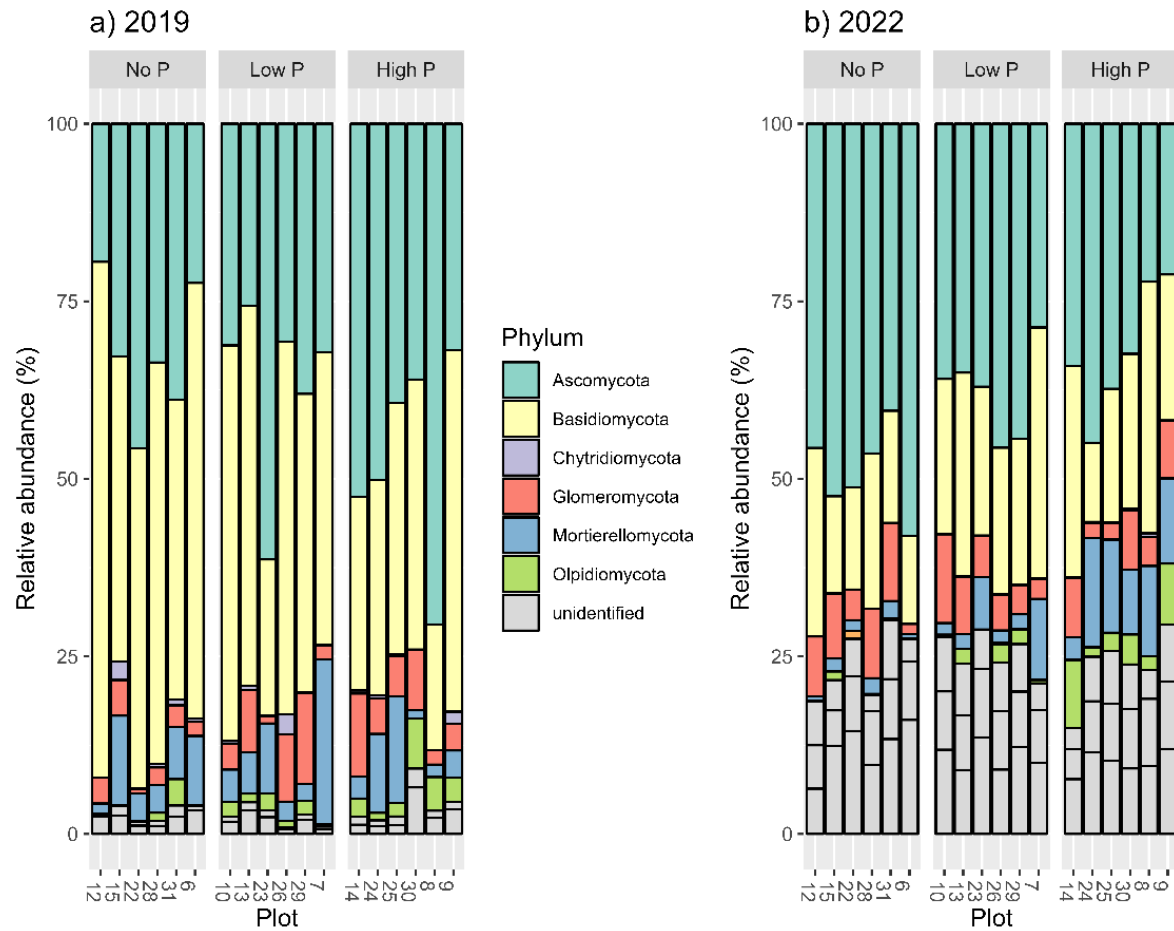


Fig S4. Relative abundance of fungal phylum in wheat roots in plots from a long-term phosphorus fertilisation field trial. Phosphorus fertilisation treatments: No P (no P addition), Low P (replacement P addition, P Olsen equivalent to 2x No P), and High P (P Olsen equivalent to 10 x No P). Wheat was sampled in (a) 2019 and (b) 2022.

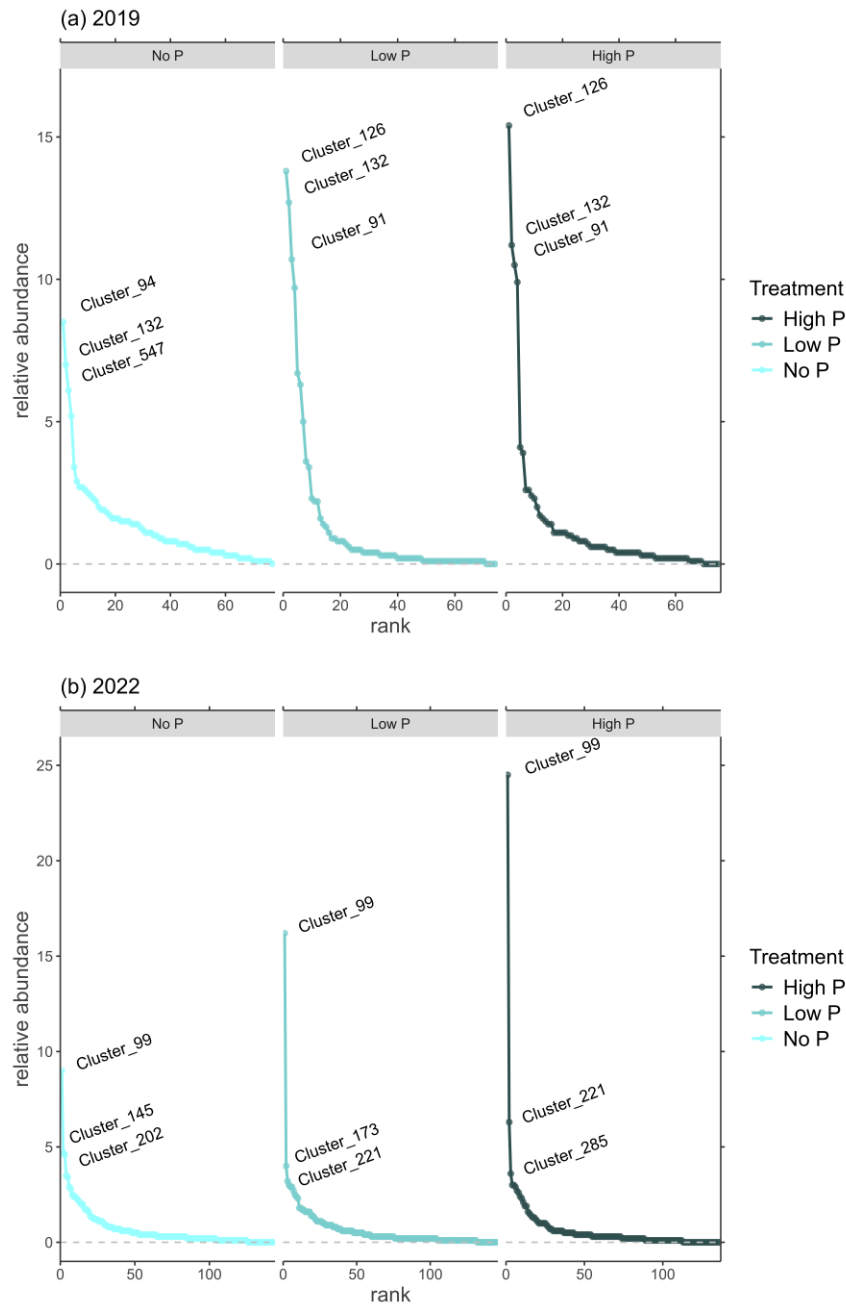


Fig S5. Rank abundance curves of AMF zOTU cluster distribution per year and P treatment. The x-axis represents the ranked zOTUs from high to low. The y-axis shows the average relative abundance for a given zOTU. The three most abundant zOTUs per treatment and year are annotated. Note that cluster definition is independent for 2019 and 2022.

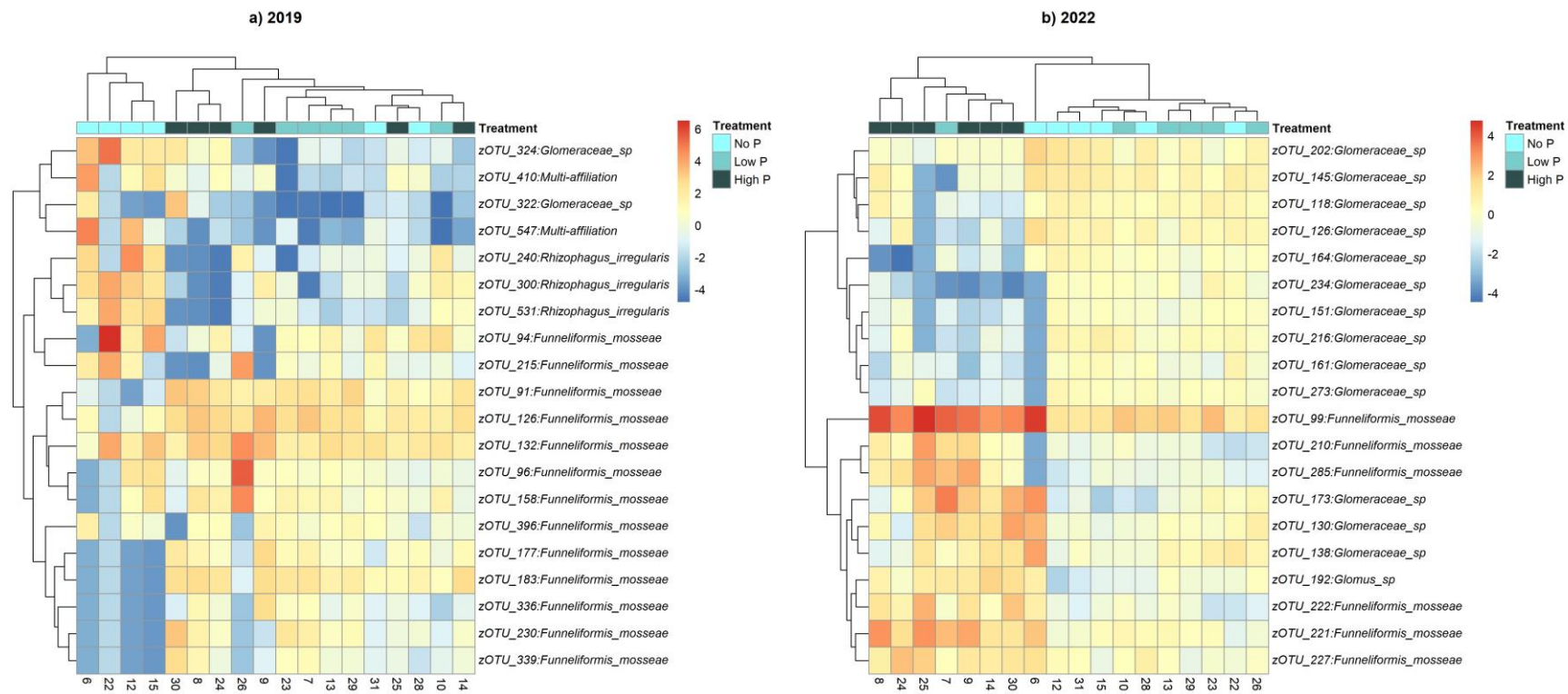


Fig S6. Heatmap showing the root-associated AMF community composition in each plot based on an analysis of the 20 most abundant zOTU clusters. zOTU counts were CLR transformed, scaled and centered before representation. Taxonomic information associated to each zOTU can be found in Supplementary tables S7 & S8. Note that zOTU definition is independent for 2019 and 2022.

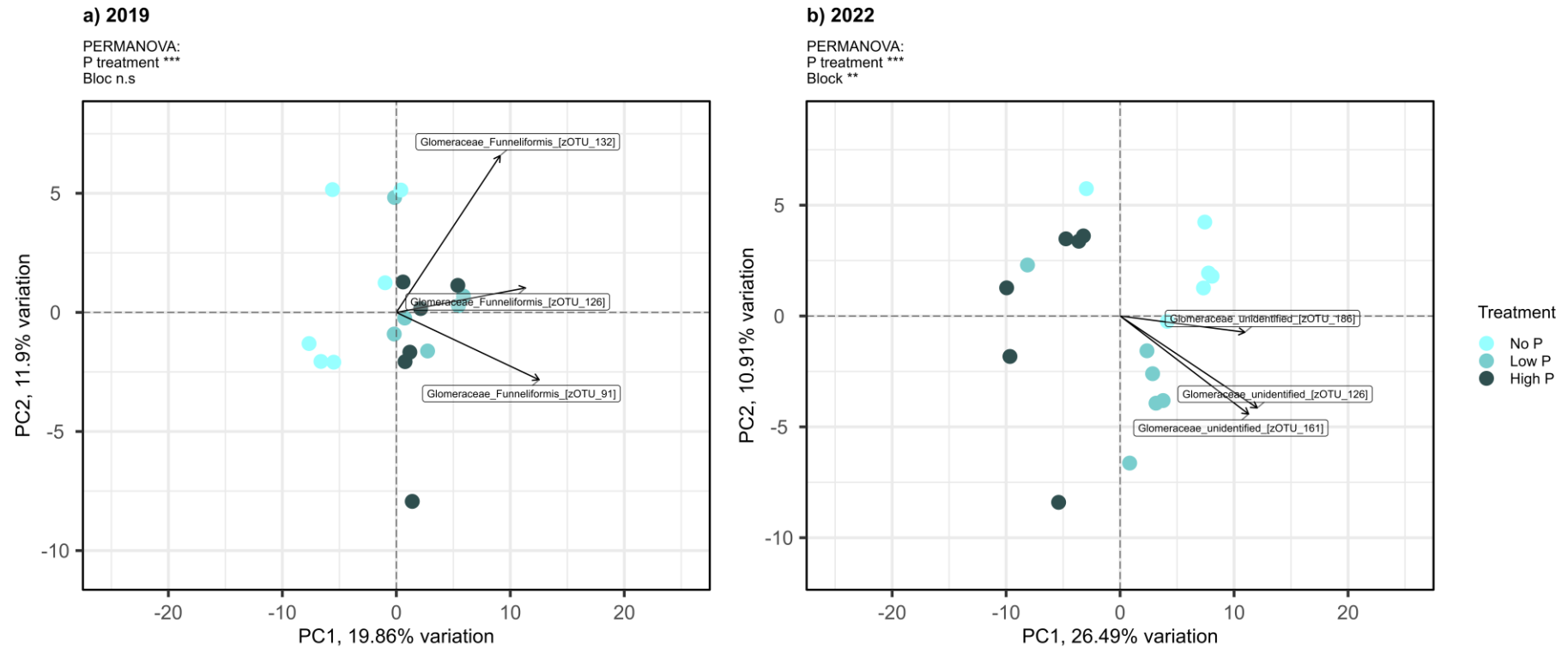


Fig S7. PCAs based on Aitchison distances with CLR transformed AMF zOTU clusters grouped by P treatment. Plots are represented by coloured circles and arrows represent the zOTUs with the greatest loadings in the PCA. Taxonomic information associated to each zOTU can be found in Supplementary tables S7 & S8. Percentages of total variance explained by each principal component (PC1 and PC2) are displayed in the axis titles. Analysis by PERMANOVA detected a significant separation in AMF composition among different P treatments for both years (a) 2019 and (b) 2022. Community differences in centroid location test results: PERMANOVA₂₀₁₉: *P treatment* $R^2 = 0.27$ $F_{2,13} = 2.84$ $p < 0.01$ *block* $R^2 = 0.12$ $F_{2,13} = 1.27$ $p = 0.17$; PERMANOVA₂₀₂₂: *P treatment* $R^2 = 0.27$ $F_{2,13} = 3.28$ $p < 0.001$ *block* $R^2 = 0.19$ $F_{2,13} = 2.31$ $p < 0.01$. Community differences in multivariate dispersion test results: PERMDISP₂₀₁₉ $F_{2,15} = 7.15$ $p < 0.01$; PERMDISP₂₀₂₂ $F_{2,15} = 0.23$, $p = 0.83$. Pairwise PERMANOVA results among treatments can be found in Table S17.

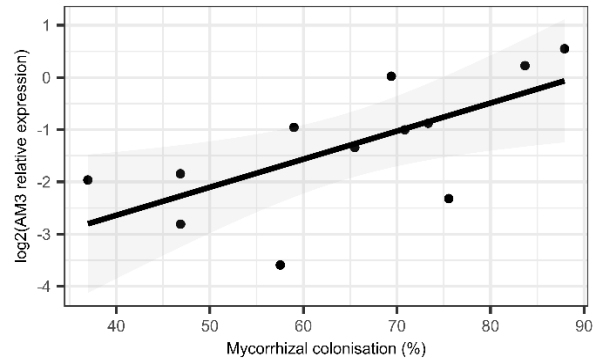


Fig S8. Correlation between the relative expression of the AM3 marker gene and the AMF colonisation level quantified by microscopy using the grid line intersect method. Wheat roots were collected in field during the campaign 2022. $R^2=0.48$. Note that the level of AMF root colonisation may be overestimated when wheat is grown in field soil, due to the potential misidentification of intracellular structures formed by endophytic fungi.