

Supplementary Materials

Potential Role of Sugars in the Hyphosphere of Arbuscular Mycorrhizal Fungi to Enhance Organic Phosphorus Mobilization

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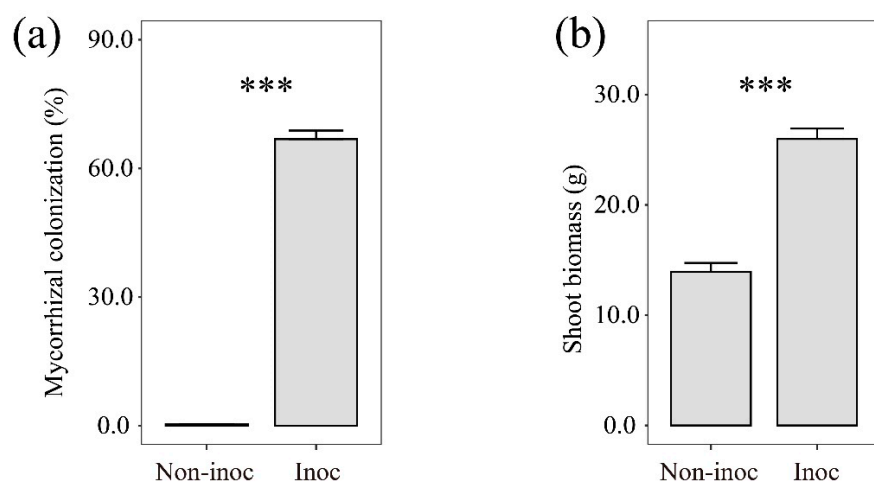


Figure S1 (a) Mycorrhizal colonization of the soil in hyphal compartments in AM fungus-inoculated pots. (b) Shoot biomass of maize plants in AM fungus-inoculated or non-inoculated pots. The asterisks indicate significant differences between the two treatments (t -test, $p < 0.001$). Non-inoc, non-inoculated pots. Inoc, AM fungus-inoculated pots.



Figure S2 Venn plot showing the number of ASVs enriched in the hyphal compartments upon the three sugars' addition with two concentrations compared to non-sugar addition in non-inoculated pots. Green represents the number of ASVs enriched at 0.2 mmol C kg⁻¹ soil compared to 0 mmol C kg⁻¹ soil. Red represents the number of ASVs enriched at 2 mmol C kg⁻¹ soil compared to 0 mmol C kg⁻¹ soil. Orange represents the number of the same ASVs enriched at both 0.2 mmol C kg⁻¹ soil and 2 mmol C kg⁻¹ soil.

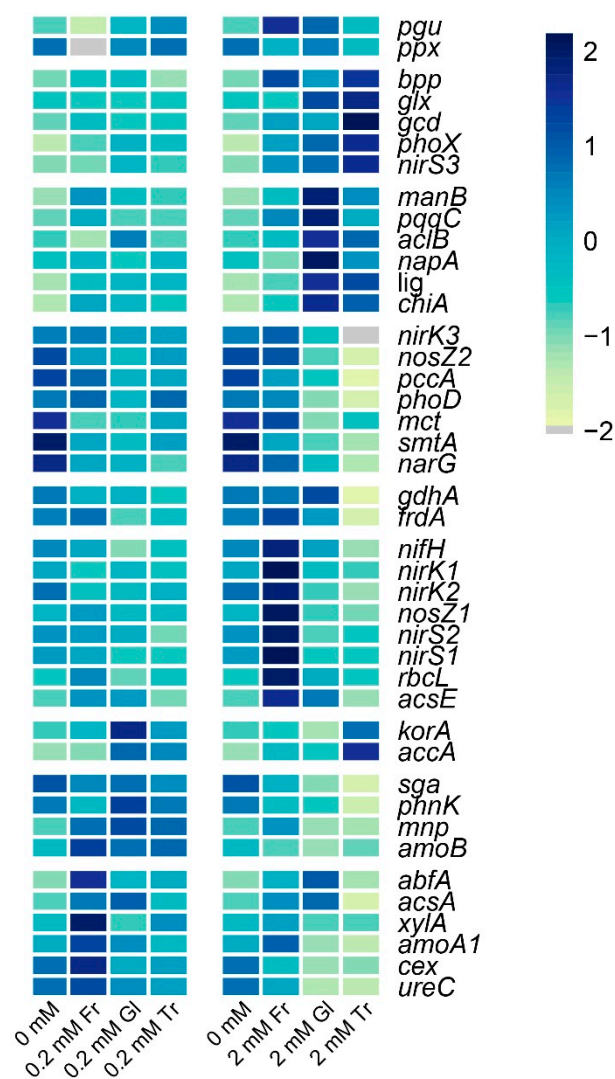


Figure S3 Heatmap of SmartChip profile, relative abundance of carbon (C), nitrogen (N) and phosphorus (P) turnover functional genes in the hyphal compartments upon three forms of sugar addition with three added concentrations (0, 0.2, 2 mmol C kg⁻¹ soil) in non-inoculated pots. The values shown represent the mean relative abundance ($n=4$) of genes in the respective sugar addition. Fr: fructose, Gl: glucose, Tr: trehalose.

Table S1 The topological properties of co-occurrence networks in hyphal compartments after the addition of three forms of sugars

	Fructose	Glucose	Trehalose
Total nodes	1485	1231	1254
Total edges	3396	2415	2768
Average Connectivity	4.574	3.924	4.41
Average clustering coefficient	0.577	0.585	0.650
Relative Modularity	0.784	0.875	0.777
Average path length	11.019	13.164	9.826
Graph diameter	25.345	38.026	24.140

Table S2 Classification of functional genes

Gene name	Gene function
<i>chiA, Lig, Glx, xylA, abfA, manB, mnp, cex,</i> <i>sga, pgu</i>	carbon degradation
<i>aclB, accA, rbcL, acsA, mct, smtA, korA,</i> <i>pccA, frdA, acsE</i>	carbon sequestration
<i>ppx, bpp, phoX, phnK, phoD, pqqC, gcd, gdhA</i>	phosphorus cycle
<i>amoA1, napA, nirS3, nirK1, nirK2, amoB,</i> <i>nirS2, ureC, narG, nosZ2, nirK3, nosZ1,</i> <i>nirS1, nifH</i>	nitrogen cycle