# Supplementary Materials for

**Specific bacterial consortium isolated from intercropping system enhances P uptake in rice**

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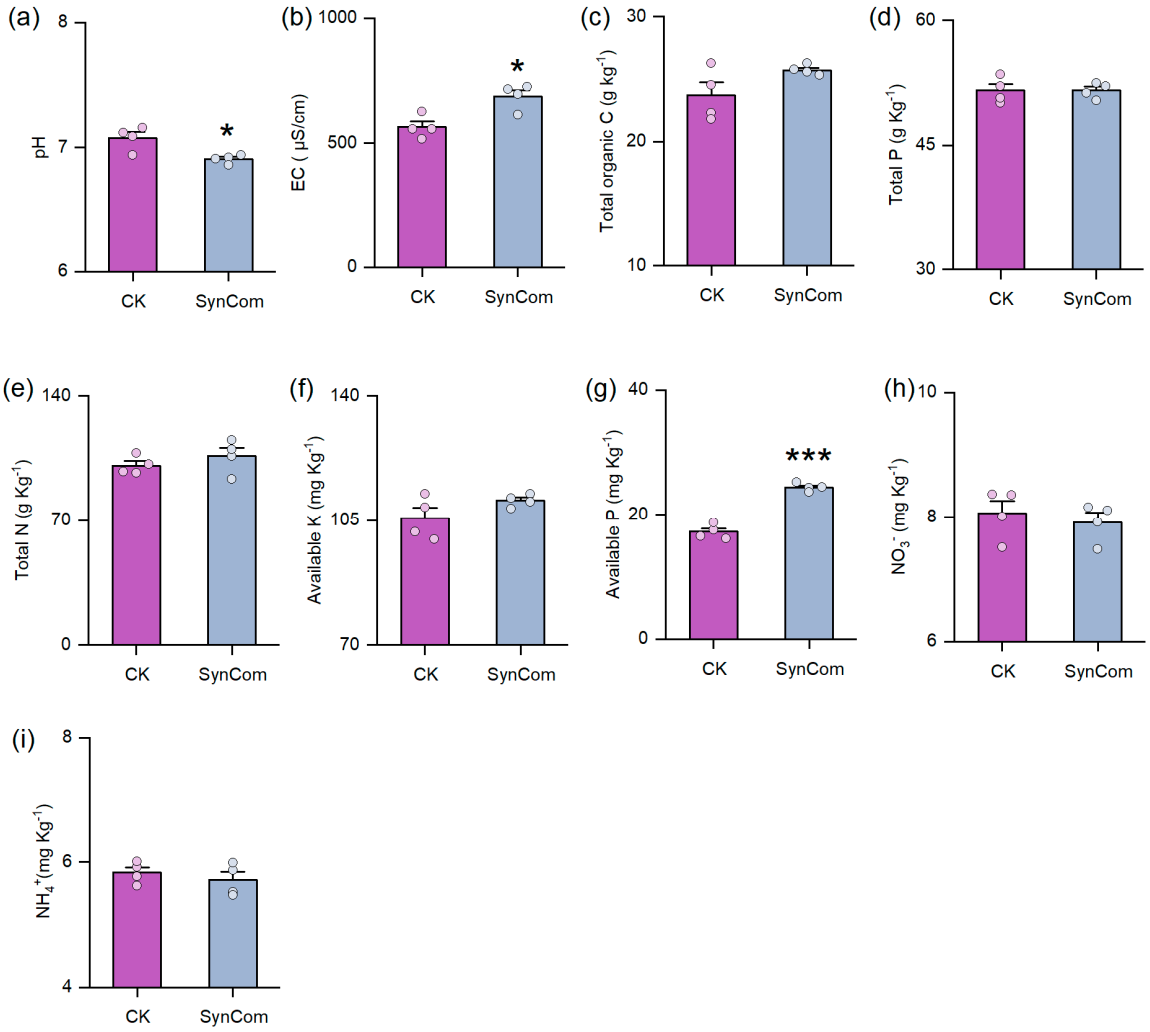



**Figure S1. Nutrient contents in rhizosphere soils inoculated with SynCom and with sterilized water**. The soil pH (**a**), EC (**b**), total organic carbon (**c**), total P (**d**), total N (**e**), available K (**f**), available P (**g**), $NO_3^-$(**h**) and $NH_4^+$(**i**) in rhizosphere soil of rice plants after inoculated bacterial synthetic community (SynCom) and sterilized water (CK). n = 4 biological replicates were measured for all the treatment. Data are average ± s.e.m. Data points represent individual replicate samples. Asterisks indicate significant differences between treatments (ANOVA, FDR-corrected LSMeans, $*P < 0.05$; $**P < 0.01$; $***P < 0.001$).

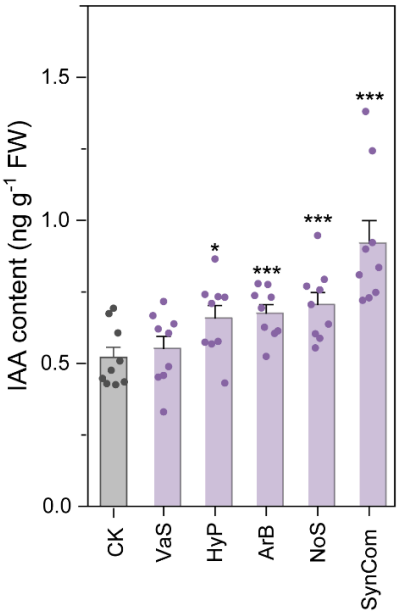



**Figure S2. Special enriched bacterial strains and SynCom affect IAA content in rice root.** CK, Sterilized water; VaS, *Variovorax_paradoxus*; HyP, *Hydrogenophaga_pseudoflava*; ArB, *Acidovorax_sp.*; NoS, *Novosphingobium_subterraneum*; SynCom, bacterial synthetic community (SynCom). Data are average ± s.e.m. Data points represent individual replicate samples. n = 9 biological replicates were measured for all the treatment. Asterisks indicate significant differences between treatments (ANOVA, FDR-corrected LSMeans, **P* < 0.05; ****P* < 0.001).

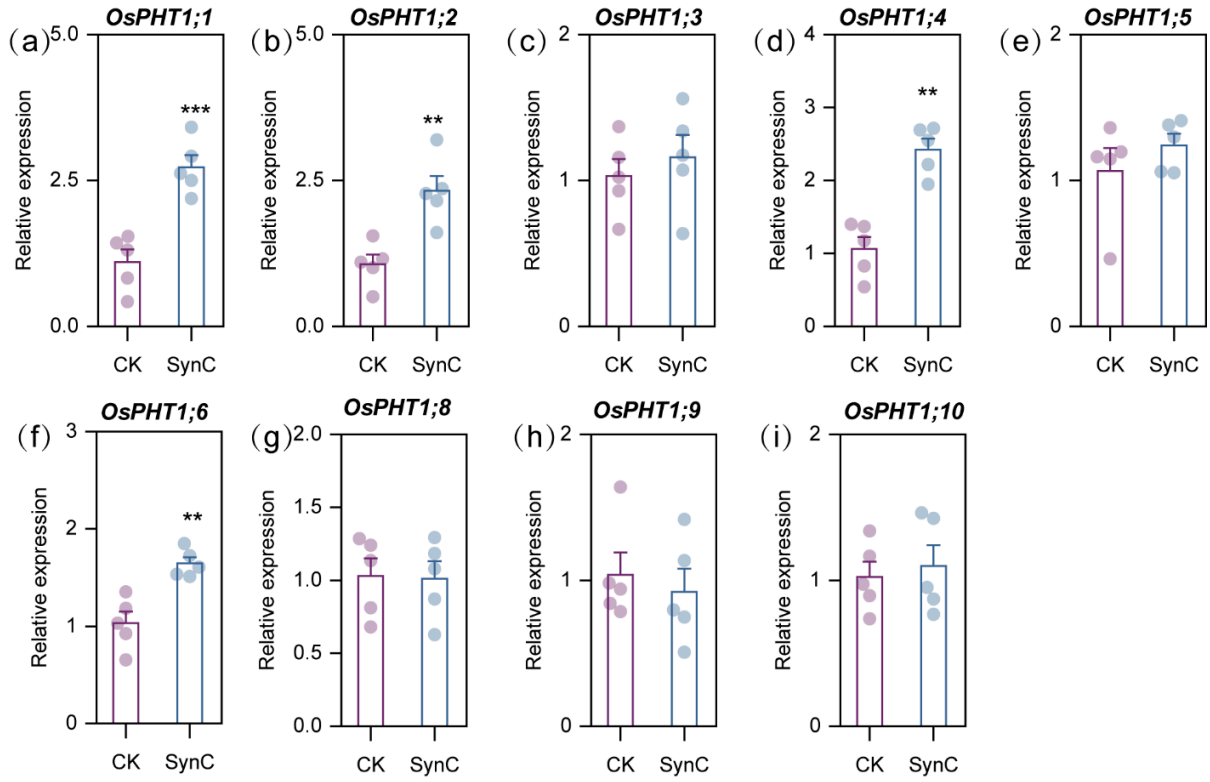



**Figure S3. SynCom regulates the expression of Pi transporter genes.** The expression levels of *OsPHT1;1* (**a**), *OsPHT1;2* (**b**), *OsPHT1;3* (**c**), *OsPHT1;4* (**d**), *OsPHT1;5* (**e**), *OsPHT1;6* (**f**), *OsPHT1;7* (**g**), *OsPHT1;8* (**h**), *OsPHT1;9* (**i**), *OsPHT1;10* (**j**) in rice plants inoculated sterilized water (CK) or bacterial synthetic community (SynC). n = 10 biological replicates were measured for all the treatment. Data are average ± s.e.m. Data points represent individual replicate samples. Asterisks indicate significant differences between treatments (ANOVA, FDR-corrected LSMeans, $^{**}P < 0.01$; $^{***}P < 0.001$).

**Supplemental Table S1**. Topological features of co-occurrence networks. Bacterial co-occurrence networks of rice plants in bulk and rhizosphere after rice monoculture and rice/soybean intercropping.

| Properties | Bacteria | | | |
|---|---|---|---|---|
| | Bulk | | Rhizosphere | |
| | RM | IRS | RM | IRS |
| **Average degree** | 19 | 18.317 | 15.426 | 14.074 |
| **Average path length** | 2.306 | 2.32 | 2.662 | 2.582 |
| **Average Weighted Degree** | 7.417 | **9.495** | 9.32 | 4.732 |
| **Density Plot** | 0.184 | 0.183 | 0.154 | 0.134 |
| **Clustering coefficient** | 0.564 | 0.566 | 0.605 | 0.536 |
| **Network diameter** | 7 | 5 | 6 | 6 |
| **Modularity** | 0.669 | 0.464 | 0.38 | **0.833** |
| **Number of edges** | 988 | 925 | 779 | 760 |
| **Nodes** | 104 | 101 | 101 | **108** |

**Supplemental Table S2** Gene ID and primer sequences of genes for RT-qPCR.

| Gene name | Gene ID | Forward primer (5'-…-3') | Reverse primer (5'-…-3') |
|---|---|---|---|
| *OsPHT1;1* | Os03g0150600 | CGCTTCCGTACGAGTGGTAGT | GGTTCTTTCAAATCCAGGGAAA |
| *OsPHT1;2* | Os03g0150800 | GACGAGACCGCCCAAGAAG | TTTTCAGTCACTCACGTCGAGAC |
| *OsPHT1;3* | Os10g0444600 | TGCGACTGCTGTATTCAGTACGT | ACAAATGCCATCAAATATGAACAGA |
| *OsPHT1;4* | Os04g0186400 | TATTGCGGCTTAGATTGCATTAG | TCCAAATCAAATGGGCACTAAG |
| *OsPHT1;5* | Os04g0185600 | TGCTACTGCCCATGACTAGGATT | CCATAGAAGAGATCCAGAGAAGCTGTA |
| *OsPHT1;6* | Os08g0564000 | CCGCCCCTGCAAACTGTA | GAACTGGCGGTTTCTTCGAT |
| *OsPHT1;7* | Os03g0136400 | GCAAGTCGCTCGAGGAGATG | TGGAATTAACGGGTGGATCAC |
| *OsPHT1;8* | Os10g0444700 | AGAAGGCAAAAGAAATGTGTGTTAAAT | AAAATGTATTCGTGCCAAATTGCT |
| *OsPHT1;9* | Os06g0324800 | AGAAAAACATAGGCTTGTCATCCTTT | AAAACCTAAGAAGCACTGTAAATAAATCC |
| *OsPHT1;10* | Os06g0325200 | ATGTCGCCCATCCTTCCA | TCGCTTTCCGACGATGATC |
| *OsPHT1;11* | Os01g0657100 | GAGAAGTTCCCTGCTTCAAGCA | TGCATATCCCAGATGAGCGTATC |
| *OsPHT1;12* | Os03g0150500 | AACGAGATGACGAACACTTGCA | TCCTGTACCTAAAAAGCAAGTACTAACATAGT |
| *OsPHT1;13* | Os04g0186800 | TTAGCATAATTCTTTTAGTAGTTAAATAGGAGATG | TGATTTAAGATAAGGATTGAATGCACAT |
| *OsACTIN* | Os03g50885 | TGGACAGGTTATCACCATTGGT | CCGCAGCTTCCATTCCTATG |