*Supplementary material*

# Corn-domesticated bacteria synergy removes pyrene and enhances crop biomass: A sustainable farmland remediation strategy

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**Table S1.** Sources and descriptions of samples used for degradation analysis.

| No. | Origin |
|---|---|
| WNB | Activity sludge No.1 |
| WNC | Activity sludge No.2 |
| WB1 | Polluted farmland soil No.1 |
| WB2 | Polluted farmland soil No.2 |
| WF2 | Mixture of supernatant of sludge No.1 and No.2 (1:1) |
| WH2 | Mixture of supernatant of soil No.1 and No.2 (1:1) |
| ETN19 | Pure bacterial strain preserved in the laboratory |

**Table S2. Physicochemical properties of the non-polluted farmland soil.**

| pH | SOM (g/kg） | Available K （mg/kg） | Available P (mg/kg) | Hydrolyzable N （mg/kg) | Total N （%) | Total K (mg/kg) | Total P (mg/kg) |
|---|---|---|---|---|---|---|---|
| 5.9 | 16.5 | 110 | 68.3 | 94.5 | 0.128 | 15325 | 735 |

**Table S3.** Corn biomass characteristics under different treatments (mean±SD, n = 3).

| Treatment | | Straw DW (g/plant) | Root DW (g/plant) | Treatment | | Straw DW (g/plant) | Root DW (g/plant) |
|---|---|---|---|---|---|---|---|
| Control | B | 0.93±0.19 cd | 0.13±0.01 e | Control+corn | C | 0.85±0.19 d | 0.11±0.04 e |
| ASS* | WNB | 1.80±0.25 ab | 0.44±0.09 ab | ASS+corn | CWNB | 1.50±0.63 abcd | 0.17±0.10 de |
| | WNC | 1.57±0.37 abc | 0.37±0.16 abcd | | CWNC | 1.84±0.31 ab | 0.26±0.07 bcde |
| | WH2 | 2.04±0.40 a | 0.43±0.21 abc | | CWH2 | 1.78±0.18 ab | 0.22±0.05 cde |
| PFS | WB1 | 1.58±0.27 abc | 0.37±0.12 abcd | PFS+corn | CWB1 | 1.93±0.40 ab | 0.25±0.05 bcde |
| | WB2 | 1.86±0.47 ab | 0.30±0.10 bcde | | CWB2 | 1.29±0.31 bcd | 0.14±0.06 e |
| | WF2 | 1.38±0.11 abcd | 0.28±0.42 bcde | | CWF2 | 1.88±0.87 ab | 0.24±0.19 bcde |
| DS | ETN19 | 1.86±0.20 ab | 0.50±0.18 a | DS+corn | CETN19 | 1.04±0.23 cd | 0.11±0.06 e |

**Note:** Straw DW and Root DW are expressed as dry weight per individual plant (g/plant). Values represent mean ± standard deviation (n = 3).

**Table S4**. FEAST analysis of soil bacteria source across different treatments and combined with corn after 30 days.

| | ASS | | | PFS | | |
|---|---|---|---|---|---|---|
| | WH2 | WNB | WNC | WB1 | WB2 | WF2 |
| DBC | 0.16±0.00 | 0.10±12.74 | 0.14±3.04 | 5.62±1.77 | 0.43±0.75 | 0.42±0.72 |
| RSS | 18.57±4.32 | 18.39±7.37 | 19.43±8.73 | 23.07±4.17 | 25.12±2.22 | 21.74±5.03 |
| PCS | 0.81±0.19 | 0.49±0.35 | 1.20±0.58 | 0.00±0.00 | 0.12±0.21 | 0.71±0.94 |
| Others | 41.69±12.42 | 43.25±9.93 | 37.99±26.81 | 25.17±13.10 | 23.84±6.23 | 32.23±12.66 |

**Table S5.** Co-occurrence network analysis of microorganisms of corn root surrounding soils in different combined bioremediation strategies.

| | PFS | ASS | C |
|---|---|---|---|
| Nodes Num | 62 | 68 | 79 |
| Edges Num | 100 | 100 | 100 |
| Average Degree | 3.23 | 2.94 | 2.53 |
| Nodes Connectivity | 0 | 0 | 0 |
| Edges Connectivity | 0 | 0 | 0 |
| Average Path Length | 5.41 | 6.78 | 1.90 |
| Graph Diameter | 30.3 | 47.0 | 12 |
| Graph Density | 0.0529 | 0.0439 | 0.0325 |
| Clustering Coefficient | 0.392 | 0.378 | 0.0563 |
| Betweenness Centralization | 0.424 | 0.306 | 0.153 |
| Degree Centralization | 0.111 | 0.0606 | 0.365 |
| Modularity | 0.561 | 0.684 | 0.624 |

**Table S6.** Genus information for Figure 4.

| No. | Genus of figure 4(a) | Abundance | Phylum group | No. | Genus of figure 4(b) | Abundance | Phylum group |
|---|---|---|---|---|---|---|---|
| 1 | unclassified_Enterobacteriaceae | 0.007833 | Proteobacteria | 1 | Steroidobacter | 0.00602 | Proteobacteria |
| 2 | unclassified_Rokubacteriales | 0.002720 | Methylomirabilota | 2 | Flavitalea | 0.004803 | Bacteroidota |
| 3 | unclassified_Chitinophagaceae | 0.006611 | Bacteroidota | 3 | unclassified_TRA3_20 | 0.00283 | Proteobacteria |
| 4 | Taibaiella | 0.003049 | Bacteroidota | 4 | Anseongella | 0.011321 | Bacteroidota |
| 5 | unclassified_Chloroflexi | 0.007259 | Chloroflexi | 5 | Allorhizobium_Neorhizobium_Pararhizobium_Rhizobium | 0.003147 | Proteobacteria |
| 6 | unclassified_Microbacteriaceae | 0.003331 | Actinobacteriota | 6 | Truepera | 0.006722 | Deinococcota |
| 7 | MND1 | 0.010810 | Proteobacteria | 7 | unclassified_Steroidobacteraceae | 0.003745 | Proteobacteria |
| 8 | unclassified_Longimicrobiaceae | 0.016057 | Gemmatimonadota | 8 | unclassified_Longimicrobiaceae | 0.012891 | Gemmatimonadota |
| 9 | Haliangium | 0.004970 | Myxococcota | 9 | unclassified_Subgroup_7 | 0.008601 | Acidobacteriota |
| 10 | Streptomyces | 0.003188 | Actinobacteriota | 10 | unclassified_Xanthobacteraceae | 0.008759 | Proteobacteria |
| 11 | Sporocytophaga | 0.002572 | Bacteroidota | 11 | unclassified_B1_7BS | 0.003372 | Proteobacteria |
| 12 | unclassified_B1_7BS | 0.004235 | Proteobacteria | 12 | Haliangium | 0.004086 | Myxococcota |
| 13 | Pseudolabrys | 0.004998 | Proteobacteria | 13 | unclassified_SC_I_84 | 0.008555 | Proteobacteria |
| 14 | unclassified_Steroidobacteraceae | 0.003948 | Proteobacteria | 14 | Devosia | 0.010291 | Proteobacteria |
| 15 | Comamonas | 0.007793 | Proteobacteria | 15 | Achromobacter | 0.006171 | Proteobacteria |
| 16 | unclassified_Thermomonosporaceae | 0.004185 | Actinobacteriota | 16 | P3OB_42 | 0.004592 | Myxococcota |
| 17 | Enterobacter | 0.003199 | Proteobacteria | 17 | Fluviicola | 0.004324 | Bacteroidota |
| 18 | unclassified_Sphingobacteriaceae | 0.002488 | Bacteroidota | 18 | Leucobacter | 0.003379 | Actinobacteriota |
| 19 | unclassified_Subgroup_17 | 0.003603 | Acidobacteriota | 19 | Nitrospira | 0.017999 | Nitrospirota |
| 20 | P3OB_42 | 0.005931 | Myxococcota | 20 | Dongia | 0.006157 | Proteobacteria |
| 21 | unclassified_Azospirillales | 0.004600 | Proteobacteria | 21 | Mycobacterium | 0.00481 | Actinobacteriota |
| 22 | TM7a | 0.004652 | Patescibacteria | 22 | unclassified_Cyanobacteriales | 0.002972 | Cyanobacteria |
| 23 | Ramlibacter | 0.010240 | Proteobacteria | 23 | unclassified_Azospirillales | 0.004232 | Proteobacteria |
| 24 | unclassified_Fodinicurvataceae | 0.004871 | Proteobacteria | 24 | unclassified_Chloroflexi | 0.006102 | Chloroflexi |
| 25 | Arenimonas | 0.003696 | Proteobacteria | 25 | Arenimonas | 0.003811 | Proteobacteria |
| 26 | Bacillus | 0.003087 | Firmicutes | 26 | Longimicrobium | 0.002852 | Gemmatimonadota |
| 27 | Actinomadura | 0.009126 | Actinobacteriota | 27 | Bryobacter | 0.008256 | Acidobacteriota |
| 28 | Massilia | 0.008152 | Proteobacteria | 28 | Proteus | 0.007587 | Proteobacteria |
| 29 | YC_ZSS_LKJ147 | 0.003580 | Gemmatimonadota | 29 | Streptomyces | 0.003187 | Actinobacteriota |
| 30 | Edaphobaculum | 0.006431 | Bacteroidota | 30 | Phenylobacterium | 0.004676 | Proteobacteria |
| 31 | unclassified_TRA3_20 | 0.003550 | Proteobacteria | 31 | Novosphingobium | 0.005598 | Proteobacteria |
| 32 | Candidatus_Udaeobacter | 0.003838 | Verrucomicrobiota | 32 | Alcaligenes | 0.00527 | Proteobacteria |

| No. | Genus of figure 4(a) | Abundance | Phylum group | No. | Genus of figure 4(b) | Abundance | Phylum group |
|---|---|---|---|---|---|---|---|
| 33 | Novosphingobium | 0.005697 | Proteobacteria | 33 | unclassified_Rhodospirillaceae | 0.003549 | Proteobacteria |
| 34 | Fluviicola | 0.004105 | Bacteroidota | 34 | Pseudolabrys | 0.005889 | Proteobacteria |
| 35 | Longimicrobium | 0.002883 | Gemmatimonadota | 35 | Thermomonas | 0.010168 | Proteobacteria |
| 36 | Luteitalea | 0.002487 | Acidobacteriota | 36 | YC_ZSS_LKJ147 | 0.002852 | Gemmatimonadota |
| 37 | unclassified_Vicinamibacteraceae | 0.035301 | Acidobacteriota | 37 | unclassified_Blastocatellaceae | 0.004696 | Acidobacteriota |
| 38 | Ellin6067 | 0.007151 | Proteobacteria | 38 | Bacillus | 0.003728 | Firmicutes |
| 39 | Pedobacter | 0.003523 | Bacteroidota | 39 | DMER64 | 0.006911 | Bacteroidota |
| 40 | Mycobacterium | 0.005729 | Actinobacteriota | 40 | Edaphobaculum | 0.004123 | Bacteroidota |
| 41 | unclassified_Blastocatellaceae | 0.004805 | Acidobacteriota | 41 | unclassified_Sphingomonadaceae | 0.014552 | Proteobacteria |
| 42 | Paracoccus | 0.003614 | Proteobacteria | 42 | Sphingomonas | 0.073493 | Proteobacteria |
| 43 | Steroidobacter | 0.005694 | Proteobacteria | 43 | Luteimonas | 0.053666 | Proteobacteria |
| 44 | unclassified_Xanthobacteraceae | 0.009514 | Proteobacteria | 44 | unclassified_Enterobacteriaceae | 0.00433 | Proteobacteria |
| 45 | Devosia | 0.011257 | Proteobacteria | 45 | unclassified_Rhizobiaceae | 0.011203 | Proteobacteria |
| 46 | unclassified_Comamonadaceae | 0.015659 | Proteobacteria | 46 | RB41 | 0.037705 | Acidobacteriota |
| 47 | Ilumatobacter | 0.002831 | Actinobacteriota | 47 | unclassified_Microscillaceae | 0.010682 | Bacteroidota |
| 48 | Flavisolibacter | 0.009170 | Bacteroidota | 48 | Ellin6067 | 0.00664 | Proteobacteria |
| 49 | Nitrospira | 0.020324 | Nitrospirota | 49 | unclassified_Bacteria | 0.020872 | unclassified_Bacteria |
| 50 | Thermomonas | 0.016048 | Proteobacteria | 50 | Rickettsia | 0.008571 | Proteobacteria |
| 51 | Luteimonas | 0.051423 | Proteobacteria | 51 | Flavisolibacter | 0.008043 | Bacteroidota |
| 52 | RB41 | 0.041722 | Acidobacteriota | 52 | Klebsiella | 0.019966 | Proteobacteria |
| 53 | Pseudomonas | 0.025978 | Proteobacteria | 53 | unclassified_Vicinamibacterales | 0.037832 | Acidobacteriota |
| 54 | Lysobacter | 0.016520 | Proteobacteria | 54 | unclassified_Vicinamibacteraceae | 0.02967 | Acidobacteriota |
| 55 | unclassified_Microscillaceae | 0.012780 | Bacteroidota | 55 | uncultured_Firmicutes_bacterium | 0.006943 | Methylomirabilota |
| 56 | unclassified_SC_I_84 | 0.008901 | Proteobacteria | 56 | Ramlibacter | 0.009691 | Proteobacteria |
| 57 | Flavitalea | 0.005108 | Bacteroidota | 57 | MND1 | 0.009822 | Proteobacteria |
| 58 | Phenylobacterium | 0.004620 | Proteobacteria | 58 | unclassified_Chitinophagaceae | 0.006857 | Bacteroidota |
| 59 | Gemmatimonas | 0.011454 | Gemmatimonadota | 59 | Chryseolinea | 0.005211 | Bacteroidota |
| 60 | Bryobacter | 0.008896 | Acidobacteriota | 60 | Pseudomonas | 0.025369 | Proteobacteria |
| 61 | Chryseolinea | 0.007342 | Bacteroidota | 61 | unclassified_Gemmatimonadaceae | 0.025196 | Gemmatimonadota |
| 62 | uncultured_Firmicutes_bacterium | 0.007832 | Methylomirabilota | 62 | Lysobacter | 0.015365 | Proteobacteria |
| 63 | Anseongella | 0.013471 | Bacteroidota | | | | |
| 64 | Truepera | 0.007133 | Deinococcota | **No.** | **Genus of figure 4(a)** | **Abundance** | **Phylum group** |
| 65 | Dongia | 0.006441 | Proteobacteria | 67 | unclassified_Gemmatimonadaceae | 0.026899 | Gemmatimonadota |
| 66 | unclassified_Vicinamibacterales | 0.041590 | Acidobacteriota | 68 | Sphingomonas | 0.067671 | Proteobacteria |

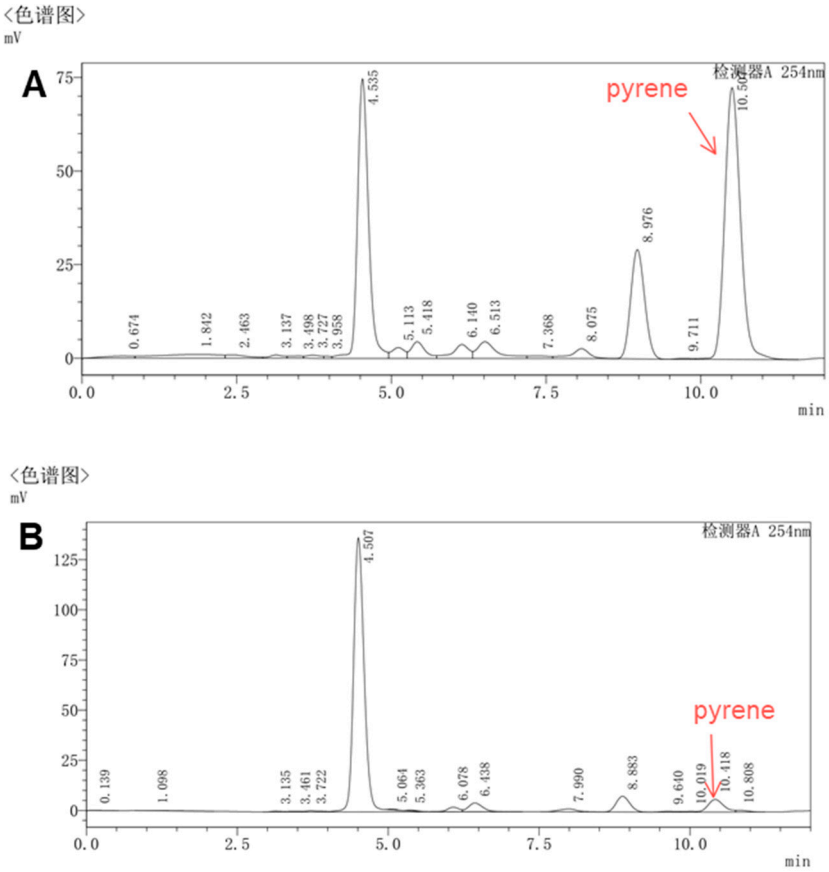



**Fig. S1**. Chromatogram of CETN19 at (**a**) 0 and (**b**) 30 treatment days.

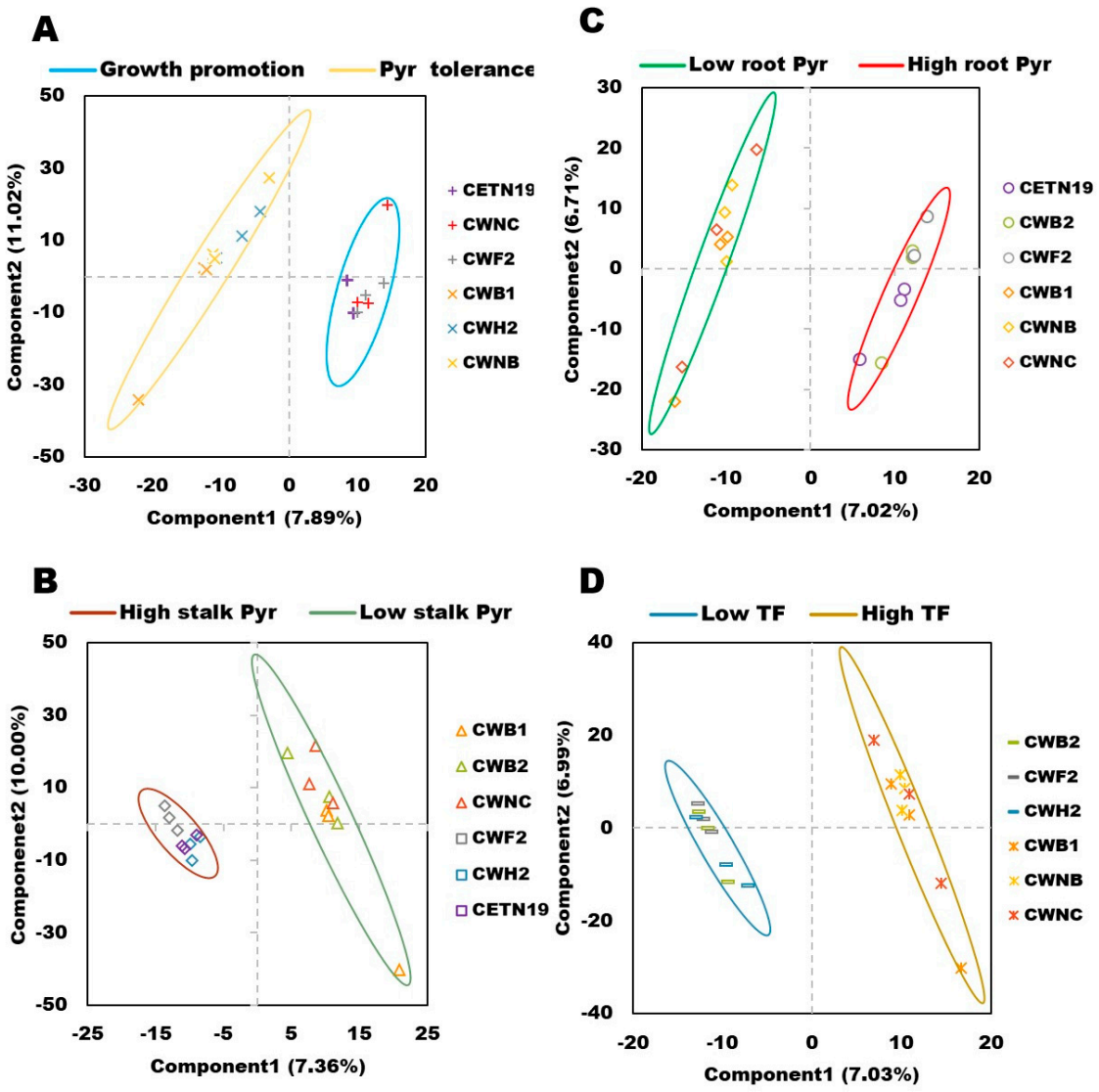



**Fig. S2.** Correlations of different treatments based on (**a**) growth promotion, (**b**) pyrene accumulation in corn stalks, (**c**) pyrene accumulation in corn roots, and (**d**) pyrene translocation factor.

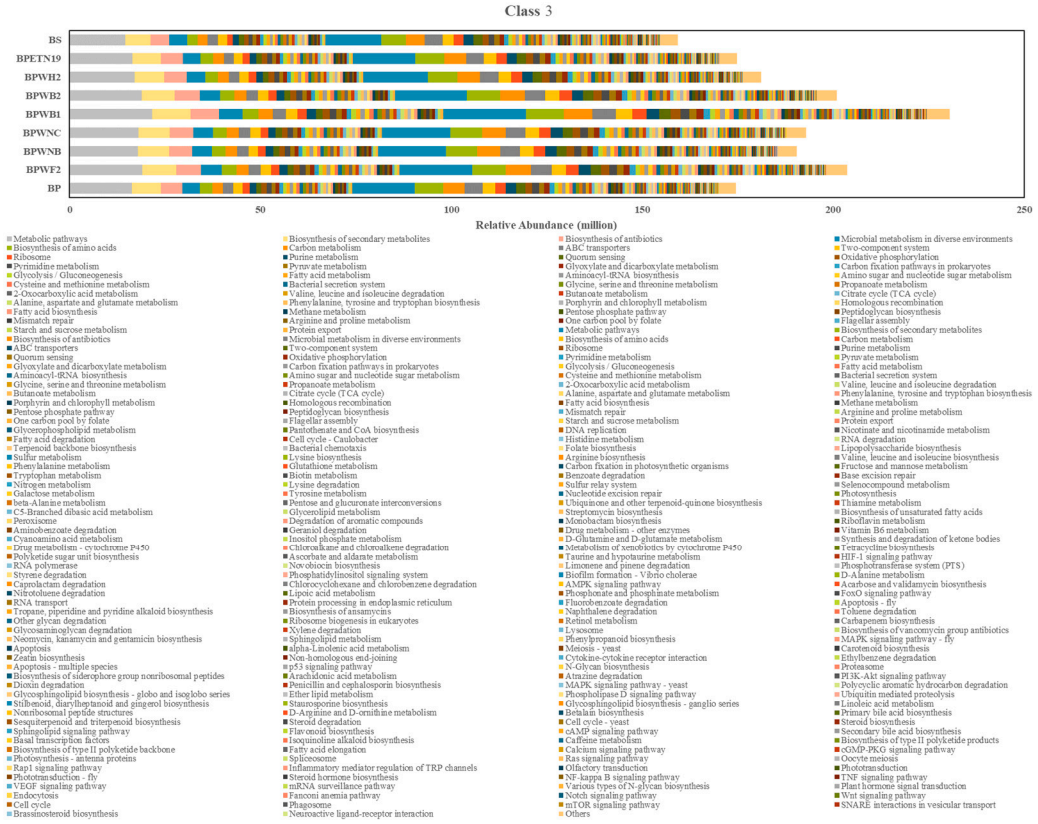



**Fig. S3.** KEGG third-level pathway of bacterial communities in pyrene-polluted soils across different treatments combined with corn, based on 16S rRNA gene prediction.