**Supplementary materials**

**Organic matter accelerated microbial iron reduction and available phosphorus release in reflooded paddy soils**

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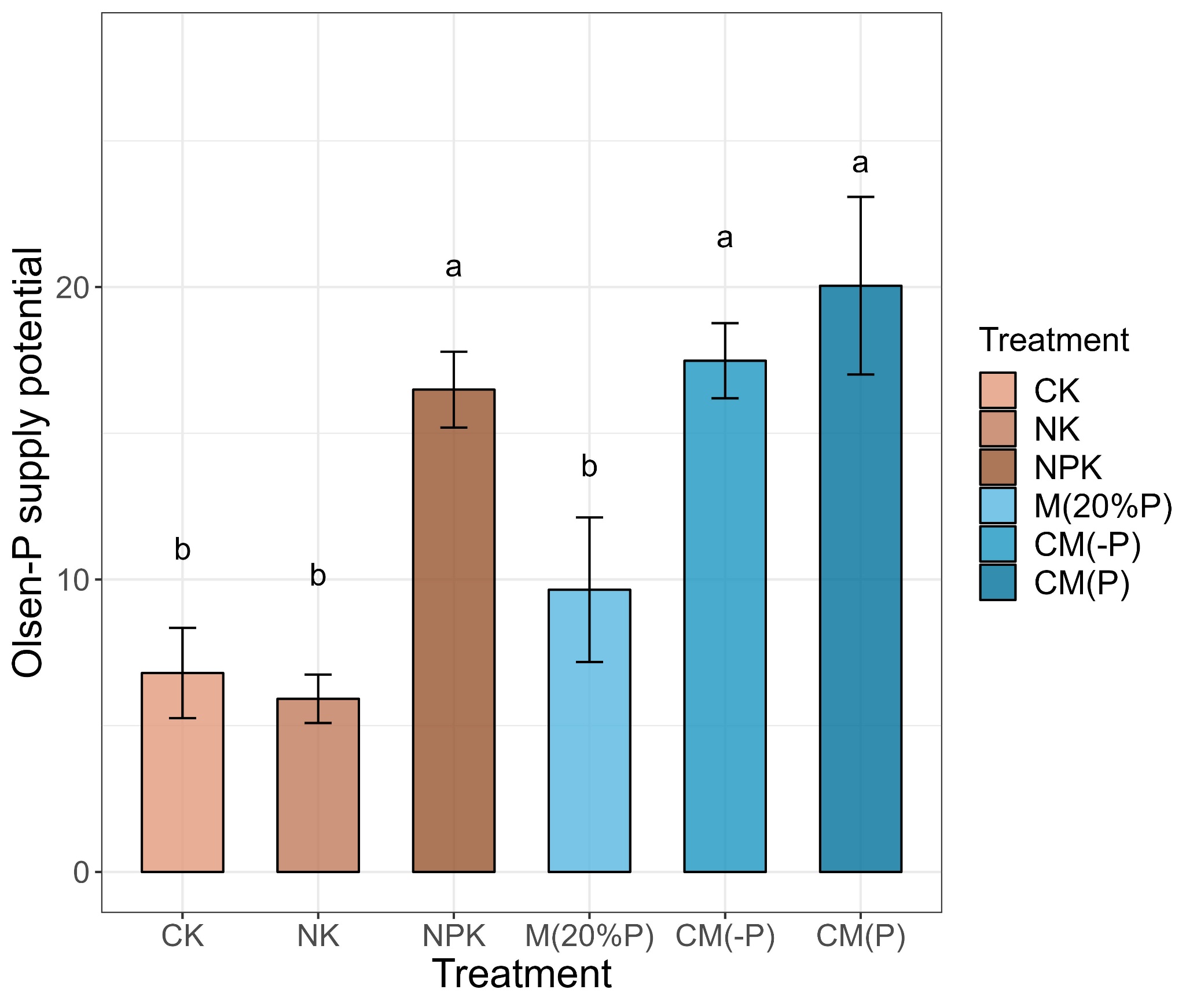
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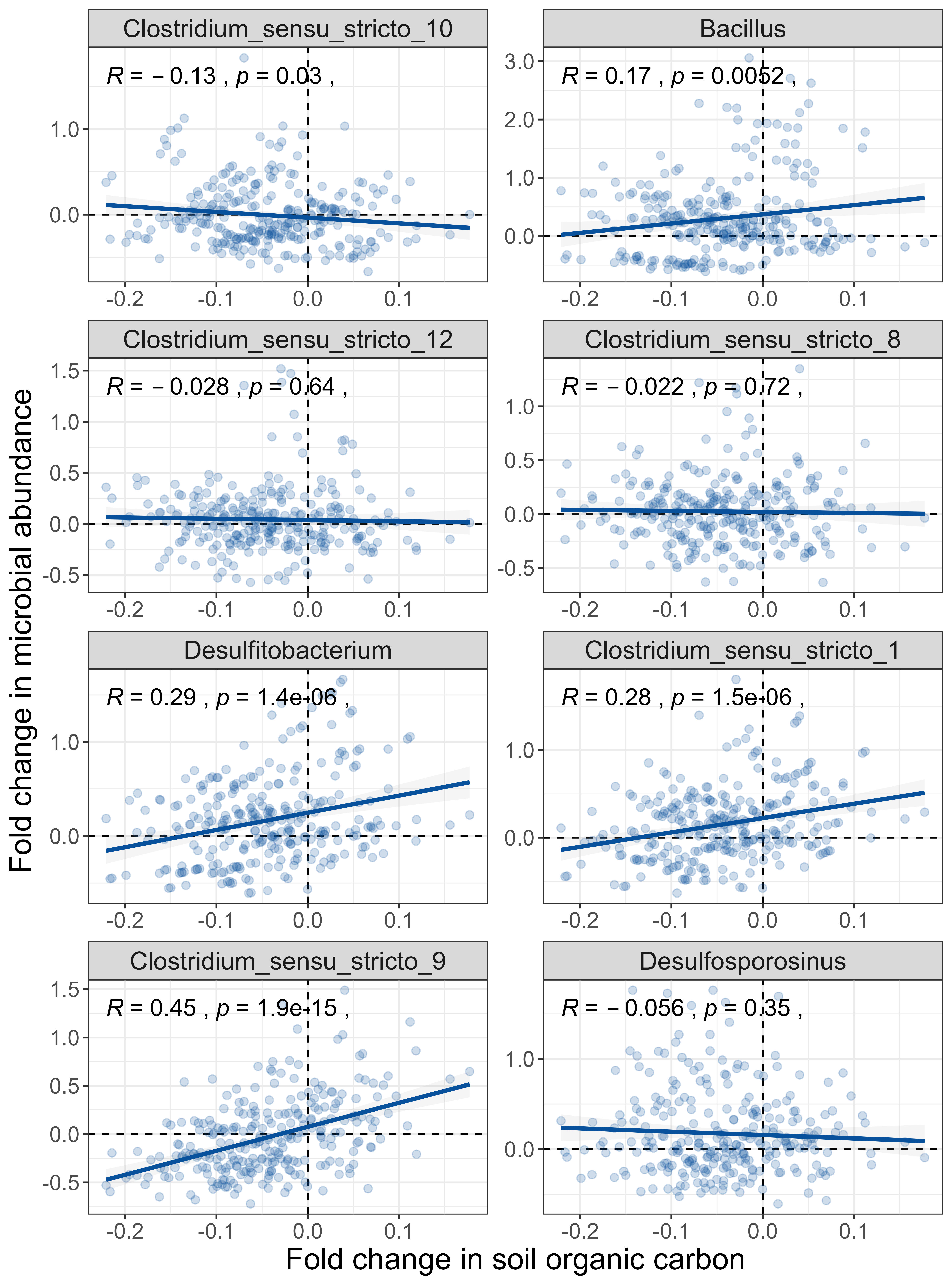
# The authors contributed to the manuscript equally.

The supplementary information includes the Figures S1-4 and Tables 1-5.

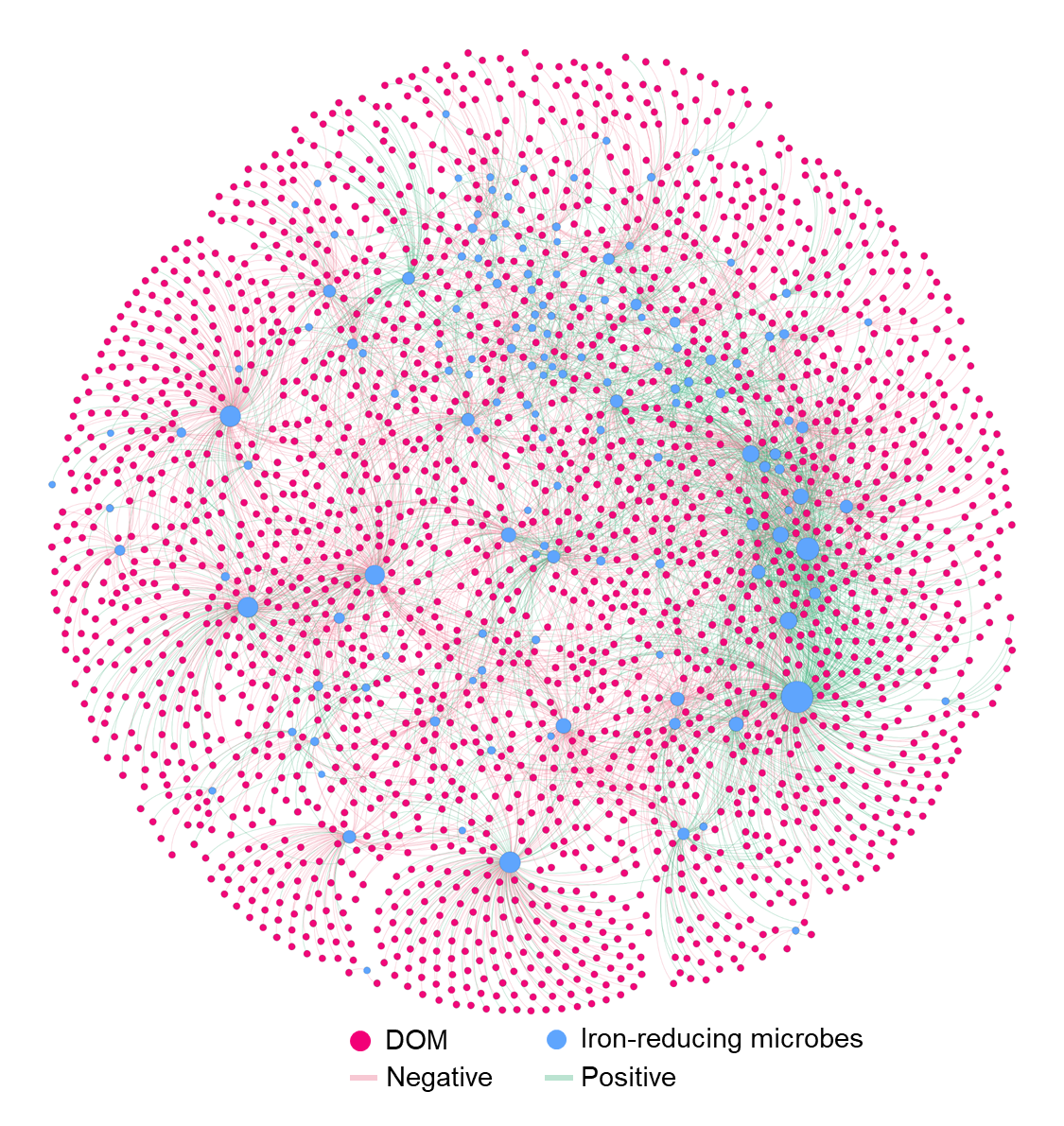
**Supplementary Figures**



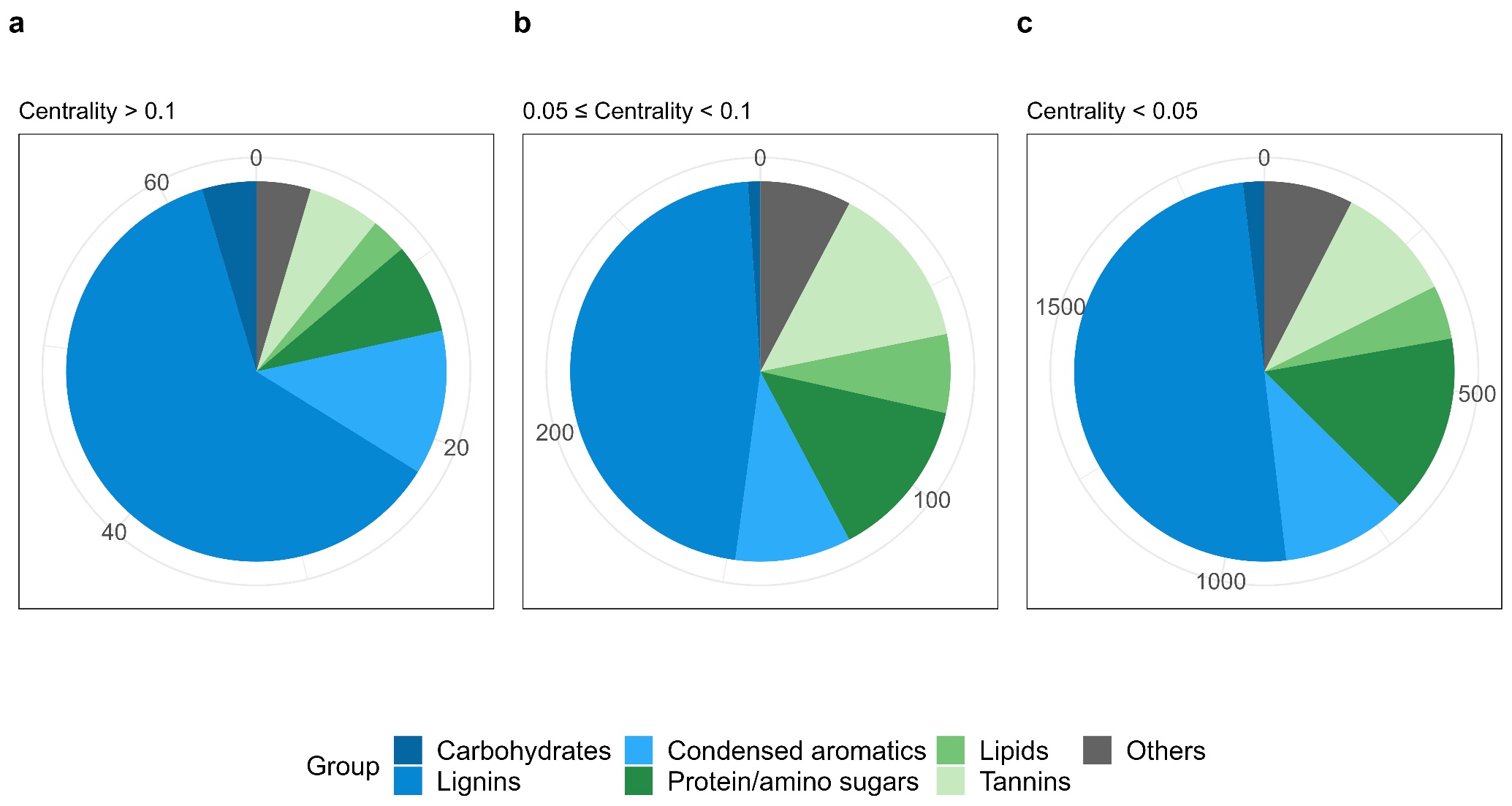
**Figure S1.** P activation potential supplying to plants under anaerobic flooding conditions, calculated as the difference between the Olsen-P content at day 0 and day 25 (ΔOlsen-P, mg kg-1). Error bar represents the standard deviation. Letters above bars indicate significant difference between treatments testing with ANOVA with Tukey’s test (*p* < 0.05).



**Figure S2.** The Pearson’s correlation between (pairwise) fold changes in soil organic carbon content and the relative abundance of major iron-reducing microbes.



**Figure S3.** Network analysis of associations between DOM and iron-reducing microbes. Only significant correlations (the absolute value of R > 0.6 and *p* < 0.01) between DOM and iron-reducing microbes or among iron-reducing microbes were included in this network. Blue and red dots represent iron-reducing microbe and DOM, respectively. Green and pink links represent positive and negative correlations, respectively.



**Figure S4.** The count of DOM’s classifications with different centrality within the network.

**Supplementary Tables**

**Table S1** Fertilization treatment and nutrient input in the field experiment (kg ha-1)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Crop | Treatment | Chemical (kg ha-1) | | |  | Organic (kg ha-1) | | |
| N | P2O5 | K2O |  | N | P2O5 | K2O |
| Early-season rice | CK | 0 | 0 | 0 |  | 0 | 0 | 0 |
| NK | 165 | 0 | 150 |  | 0 | 0 | 0 |
| NPK | 165 | 90 | 150 |  | 0 | 0 | 0 |
| M(20%P) | 0 | 0 | 0 |  | 11 | 18 | 5 |
| CM(P) | 154 | 72 | 145 |  | 11 | 18 | 5 |
| CM(-P) | 154 | 58 | 145 |  | 11 | 18 | 5 |
| Late-season rice | CK | 0 | 0 | 0 |  | 0 | 0 | 0 |
| NK | 195 | 0 | 150 |  | 0 | 0 | 0 |
| NPK | 195 | 90 | 150 |  | 0 | 0 | 0 |
| M(20%P) | 0 | 0 | 0 |  | 9 | 18 | 5 |
| CM(P) | 187 | 72 | 145 |  | 9 | 18 | 5 |
| CM(-P) | 187 | 58 | 145 |  | 9 | 18 | 5 |

**Table S2** Physicochemical properties of the paddy soil, rice yield, and aboveground P uptake under 5-year different fertilization regimes.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Treatment | CK | NK | NPK | M(20%P) | CM(-P) | CM(P) | *p* value |
| pH | 5.30b | 5.17c | 5.18c | 5.28b | 5.44a | 5.49a | \*\*\* |
| SOC (g kg-1) | 28.15ab | 27.72b | 29.63ab | 27.33b | 30.67a | 30.96a | \*\* |
| Feox (g kg-1) | 2.23b | 2.19b | 1.96c | 2.50a | 2.30b | 2.30b | \*\*\* |
| Alox (g kg-1) | 0.84ab | 0.82ab | 0.87a | 0.77b | 0.87a | 0.80ab | \* |
| Pox (mg kg-1) | 49.52b | 12.14c | 165.41a | 60.72b | 158.25a | 147.92a | \*\*\* |
| TP (mg kg-1) | 436.38cd | 401.00d | 582.09a | 446.07c | 535.45b | 533.10b | \*\*\* |
| DPS (%) | 2.25c | 0.56d | 7.93a | 2.67c | 6.96b | 6.74b | \*\*\* |
| NH4+(mg kg-1) | 66.80b | 102.81a | 101.78a | 73.47b | 97.48a | 104.15a | \*\*\* |
| NO3-(mg kg-1) | 67.54b | 117.74a | 120.84a | 61.33b | 111.32a | 107.92a | \*\*\* |
| Rice yield (Mg ha-1) | 4.76d | 6.13c | 7.00b | 4.97d | 7.30ab | 7.57a | \*\*\* |
| Aboveground P uptake (kg ha-1) | 13.55d | 24.72c | 31.83b | 14.94d | 32.71ab | 35.03a | \*\*\* |

Different letter in the same row means significant differences at *p* < 0.05 tested with ANOVA Tukey’s HSD. SOC, soil organic matter; Feox, Alox, and Pox, ammonium oxalate extracted Fe, Al, and P, respectively; TP, total P; DPS, degree of P saturation.

**Table S3** The parameters of logistics models for microbial Fe(III) reduction of soils under different fertilization regimes during the anaerobic incubation.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Treatment | Logistic model | | | |
| a (mg g-1) | Vmax  (mg g-1 d-1) | Tmax (d) | R2 |
| CK | 4.76a | 0.34b | 6.26b | 0.99 |
| NK | 4.77a | 0.29c | 6.82a | 0.98 |
| NPK | 4.53b | 0.35b | 4.62d | 0.96 |
| M(20%P) | 4.79a | 0.35b | 5.85c | 0.99 |
| CM(P) | 4.66ab | 0.45a | 4.15e | 0.97 |
| CM(-P) | 4.66ab | 0.45a | 4.20e | 0.96 |

a, the maximum iron reduction potential (Pmax); Vmax, maximum iron reduction rate; Tmax, time to achieve the Vmax; R2, fitting coefficient of the model.

**Table S4** The α-diversity of soil bacteria under different fertilization regimes.

|  |  |  |  |
| --- | --- | --- | --- |
| Treatment | Richness | Chao1 | Shannon |
| CK | 1957a | 2189.01a | 8.53a |
| NK | 1940a | 2165.04a | 8.48a |
| NPK | 1918a | 2190.38a | 7.28b |
| M(20%P) | 2067a | 2182.29a | 8.51a |
| CM(P) | 2057a | 2385.28a | 8.36a |
| CM(-P) | 1988a | 2229.54a | 8.39a |

**Table S5** The typical iron-reducing microbes classified in this study.

|  |  |  |
| --- | --- | --- |
| **No.** | **Genus** | **Family** |
| 1 | Acinetobacter | Moraxellaceae |
| 2 | Alicyclobacillus | Alicyclobacillaceae |
| 3 | Anaeromyxobacter | Anaeromyxobacteraceae |
| 4 | Bacillus | Bacillaceae |
| 5 | Brevibacillus | Brevibacillaceae |
| 6 | Candidatus\_Arthromitus | Clostridiaceae |
| 7 | Clostridium | Caloramatoraceae |
| 8 | Clostridium\_sensu\_stricto\_1 | Clostridiaceae |
| 9 | Clostridium\_sensu\_stricto\_2 | Clostridiaceae |
| 10 | Clostridium\_sensu\_stricto\_3 | Clostridiaceae |
| 11 | Clostridium\_sensu\_stricto\_5 | Clostridiaceae |
| 12 | Clostridium\_sensu\_stricto\_6 | Clostridiaceae |
| 13 | Clostridium\_sensu\_stricto\_7 | Clostridiaceae |
| 14 | Clostridium\_sensu\_stricto\_8 | Clostridiaceae |
| 15 | Clostridium\_sensu\_stricto\_9 | Clostridiaceae |
| 16 | Clostridium\_sensu\_stricto\_10 | Clostridiaceae |
| 17 | Clostridium\_sensu\_stricto\_11 | Clostridiaceae |
| 18 | Clostridium\_sensu\_stricto\_12 | Clostridiaceae |
| 19 | Clostridium\_sensu\_stricto\_13 | Clostridiaceae |
| 20 | Clostridium\_sensu\_stricto\_16 | Clostridiaceae |
| 21 | Clostridium\_sensu\_stricto\_19 | Clostridiaceae |
| 22 | Desulfitobacterium | Desulfitobacteriaceae |
| 23 | Desulfobacca | Desulfobaccaceae |
| 24 | Desulfobulbus | Desulfobulbaceae |
| 25 | Desulfosporosinus | Desulfitobacteriaceae |
| 26 | Desulfotomaculum | unidentified\_Desulfotomaculales |
| 27 | Desulfovirga | Syntrophobacteraceae |
| 28 | Novosphingobium | Sphingomonadaceae |
| 29 | Paenibacillus | Paenibacillaceae |
| 30 | Pseudomonas | Pseudomonadaceae |
| 31 | Sphingomonas | Sphingomonadaceae |
| 32 | Symbiobacterium | Symbiobacteraceae |
| 33 | Syntrophobacter | Syntrophobacteraceae |
| 34 | Syntrophorhabdus | Syntrophorhabdaceae |