

Supplementary Figures



Figure S1: Representative shoot and root lengths of seedlings at 15 DAI in cm; randomly selected representative seedlings from both of the treatments and untreated controls showing the lengths in cm scale. D represents the seedlings treated with BTL-M2; Control is the untreated control seedlings and PF represents the seedlings treated with BRRh-4.

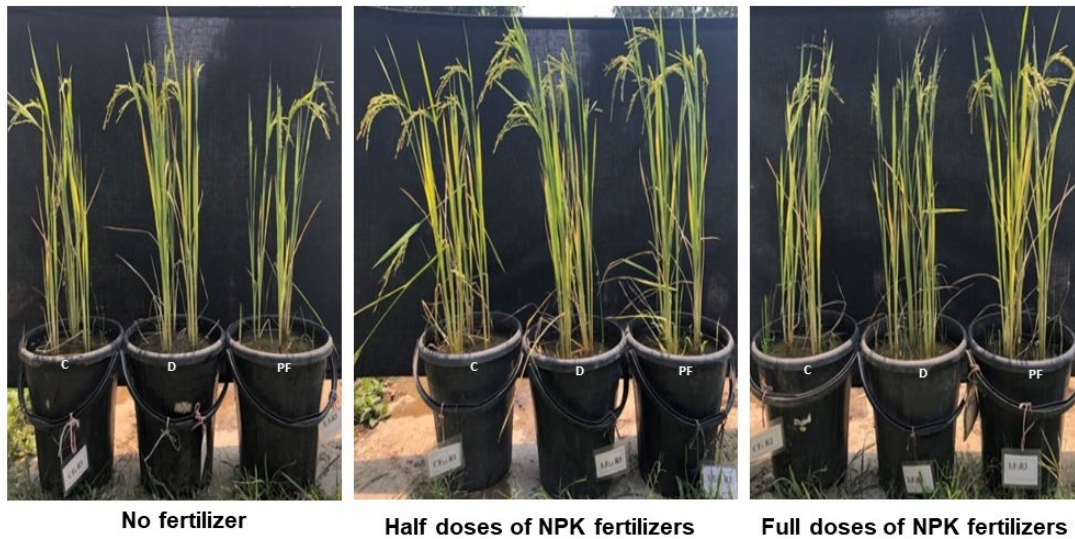


Figure S2: Effect of BTL-M2 (D) and BRRh-4 (PF) on growth of rice under varying doses of recommended nitrogenous (N), phosphatic (P) and potassium (K) fertilizers. Here, C represents non-treated controls. Zero dose or no chemical fertilizers used. Half dose: 50% of recommended N, P, and K fertilizers used. Full dose: 100% of recommended N, P, and K fertilizers used.

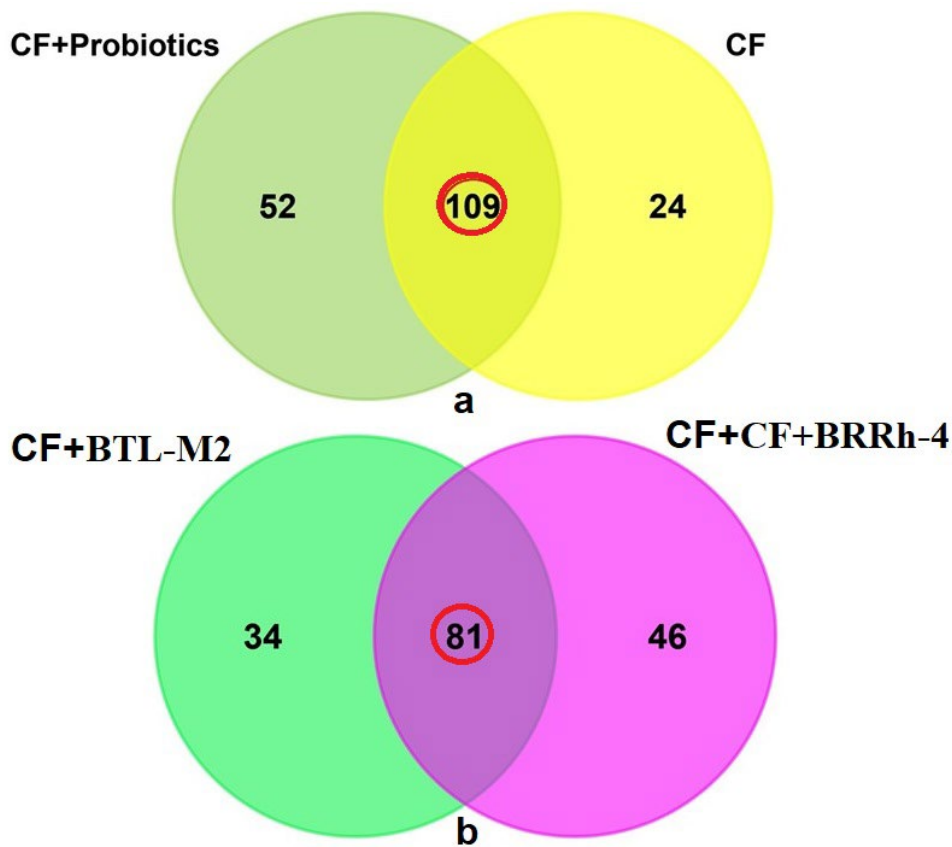


Figure S3: Microbiome diversity between chemical fertilizer (CF), and CF and probiotics bacteria treated metagenomes. (a) Venn diagram representing the unique and shared bacterial genera detected in these metagenomes. A total of 185 bacterial genera were detected in both metagenomes, and of them 109 genera were found to be common in the given conditions. (b) Microbiome diversity between CF + BTL-M2 and CF + BRRh-4 treated metagenomes. Venn diagram representing the unique and shared bacterial genera detected in CF + BTL-M2 and CF + BRRh-4 treated samples. A total of 161 bacterial genera were detected in both metagenomes where 81 genera were found to be shared between the two conditions.

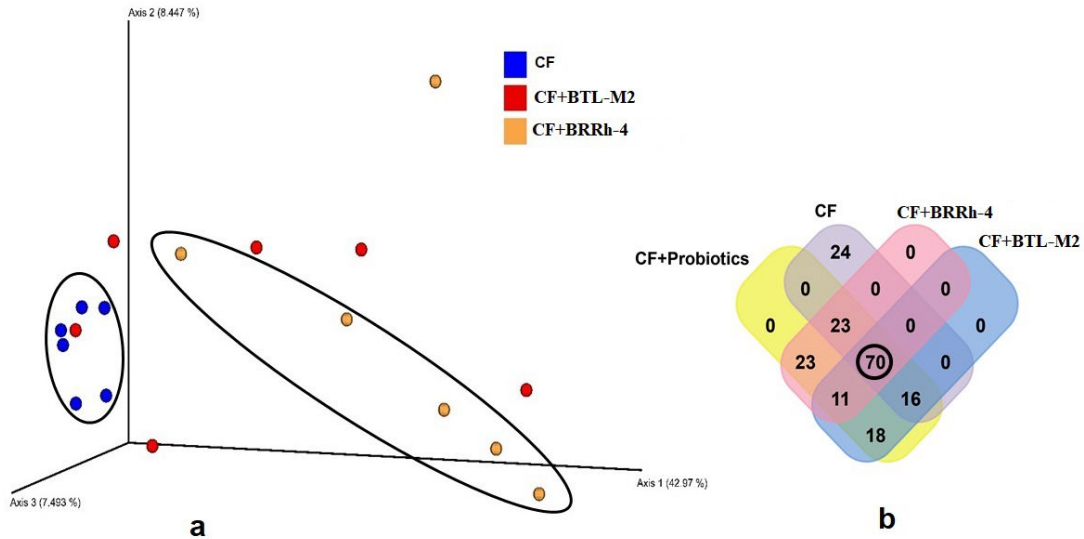


Figure S4: Taxonomic composition of microbiome in chemical fertilizer (CF), and CF + probiotics treatment (at genus level). (a) The PCA plot (beta diversity) based on Bray-Curtis metrics showed that most of the CF samples (blue colored) clustered closely (encircled in black) while the samples of CF + probiotics treated samples were distributed diversely (red and yellow colored) showing significant (Kruskal-Wallis test, $p = 0.002$) microbial disparity between the sample groups. However, among the probiotics treated samples more diversity differences were found in CF + BTL-M2 treated (red colored) sample group compared to CF + BRRh-4 treated (yellow colored) sample group (encircled in black). (b) Venn diagram comparison of bacterial genera in CF, CF + BTL-M2 and CF + BRRh-4 treated samples. Microbiome sharing between the conditions are indicated by black circles. More information on taxonomic composition and diversity can be found in Data S1.

Supplementary Tables

Table S1: Taxonomic distribution of microbiome at phylum level in root and rhizosphere soil metagenomes.

Phyla	Root	Rhizosphere soils
Bacteroidetes	42.910	67.254
Firmicutes	29.031	17.320
Proteobacteria	13.513	14.188
Planctomycetes	5.779	0.002
Thermi	4.151	0.004
Actinobacteria	2.015	1.125
Verrucomicrobia	1.076	0.093
Chloroflexi	0.875	0.00
Spirochaetes	0.184	0.00
Euryarchaeota	0.236	0.014
Nitrospirae	0.092	0.00
Cyanobacteria	0.140	0.00

Table S2: Taxonomic distribution of microbiome in root and rhizosphere soil metagenomes at order level.

Orders	Root	Rhizosphere soils
<i>Bacteroidales</i>	39.604	67.254
<i>Bacillales</i>	19.187	1.539
<i>Clostridiales</i>	9.437	15.473
<i>Planctomycetales</i>	5.213	0.002
<i>Deinococcales</i>	4.151	0.004
<i>Flavobacteriales</i>	3.157	0.000
<i>Sphingomonadales</i>	2.709	0.000
<i>Vibrionales</i>	2.563	6.272
<i>Rhizobiales</i>	2.513	0.077
<i>Burkholderiales</i>	1.798	1.369
<i>Actinomycetales</i>	1.682	1.125
<i>Rhodospirillales</i>	1.345	3.525
<i>Aeromonadales</i>	0.493	0.875
<i>Enterobacteriales</i>	0.762	0.558
<i>Pseudomonadales</i>	0.342	0.675
<i>Pasteurellales</i>	0.000	0.492
<i>Chthoniobacterales</i>	0.840	0.002
<i>Erysipelotrichales</i>	0.392	0.179
<i>Alteromonadales</i>	0.055	0.287
<i>Gemmatales</i>	0.485	0.000
<i>Anaerolineales</i>	0.438	0.000
<i>Caldilineales</i>	0.363	0.000
<i>Bifidobacteriales</i>	0.332	0.000
<i>Xanthomonadales</i>	0.239	0.031
Other orders	1.902	0.261

Table S3: Taxonomic distribution of top 30 bacterial genera in root and rhizosphere soil metagenomes.

Genera	Root (R)	Rhizosphere soil (S)
<i>Prevotella</i>	24.961	52.022
Unclassified	25.122	3.016
<i>Bacteroides</i>	2.607	12.383
<i>Faecalibacterium</i>	3.901	9.494
<i>Bacillus</i>	11.030	1.205
<i>Vibrio</i>	1.775	5.945
<i>Roseomonas</i>	0.814	3.391
<i>Planctomyces</i>	4.050	0.013
<i>Deinococcus</i>	2.961	0.021
<i>Ruminococcus</i>	0.384	1.762
<i>Chryseobacterium</i>	2.301	0.000
<i>Exiguobacterium</i>	1.909	0.000
<i>Dialister</i>	0.000	1.161
<i>Novosphingobium</i>	1.563	0.000
<i>Sutterella</i>	0.219	0.981
<i>Butyrivibrio</i>	0.000	1.066
<i>Brevibacterium</i>	0.338	0.801
<i>Oscillospira</i>	0.373	0.723
<i>Succinivibrio</i>	0.184	0.836
<i>Megasphaera</i>	0.142	0.665
<i>Ancylobacter</i>	0.908	0.074
<i>Candidatus</i>	0.750	0.002
<i>Staphylococcus</i>	0.500	0.126
<i>Haemophilus</i>	0.000	0.475
<i>Corynebacterium</i>	0.570	0.033
<i>Parabacteroides</i>	0.370	0.172
<i>Massilia</i>	0.596	0.000
<i>Nocardioides</i>	0.591	0.000
<i>Enhydrobacter</i>	0.208	0.282
Other genera	10.868	3.352