

<sup>1</sup> Supplementary Figures & Tables: A commercial seaweed  
<sup>2</sup> extract structured microbial communities associated with  
<sup>3</sup> tomato and pepper roots and significantly increased crop  
<sup>4</sup> yield

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Tomato [cv: Totem Hybrid#A371, William Dam Seeds Ltd]							
		P+		P-			
bloc 1	P+F-	P-F-	P+F+	P-F+	P+F-	P-F-	P+F+
bloc 4	P+F+	P-F+	P+F-	P-F-	P+F+	P-F+	P+F-
bloc 2							
bloc 5							
bloc 3							
bloc 6							
bloc 7							
bloc 8							

Pepper [cv: Ace Hybrid#318, William Dam Seeds Ltd]							
		P-F-		P+F+			
bloc 1	P-F-	P+F+	P+F+	P+F-	P-F-	P+F+	P-F-
bloc 4	P+F-	P-F+	P+F+	P-F-	P+F+	P-F-	P+F-
bloc 2							
bloc 5							
bloc 3							
bloc 6							
bloc 7							
bloc 8							

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10 **Table S1:** Randomized split block design for the tomato and pepper experiments

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Table S2: Soil characteristics (in *ppm* unless specified otherwise)

Soil Characteristics	Average value
pH	6.01
Conductivity (mmhos/cm)	0.68
Nitrate (N)	62.40
Ammonium	0.09
Phosphorus	0.41
Potassium	29.30
Calcium	64.40
Magnesium	13.80
Chloride	28.50
Sulfate	19.30
Sodium	17.80
Zinc	0.12
Manganese	0.06
Cooper	0.81
Iron	0.90
Aluminium	1.66

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Table S3: Stella Maris® characteristics

Stella Maris® characteristics	Average value
Appearance	Viscous Brownish-Black Liquid
Odor	Marine Odor
Solubility in water (%)	100
pH	7.4 - 8.2
Carbohydrates	Alginic acid, Mannitol, Fucoidans
Organic matter content (%)	13.0 - 16.0
Total Nitrogen (N) (%)	0.1 - 0.6
Available phosphate (P2O5) (%)	< 0.2
Soluble potash (K2O) (%)	5.0 - 7.0
Sulphur (S) (%)	0.3 - 0.6
Magnesium (Mg) (%)	0.05 - 0.15
Calcium (Ca) (%)	0.05 - 0.15
Sodium (Na) (%)	0.7 - 1.2
Iron (Fe) (ppm)	30 - 90
Cooper (Cu) (ppm)	< 4
Manganese (Mn) (ppm)	3 - 11
Boron (B) (ppm)	20 - 40

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Table S4: Summary of sequencing statistics and bioinformatics identification of ASV

	fungi-soil	fungi-root	bacteria-soil	bacteria-root
No sequences (sum)	976,000	309,000	920,000	535,000
No sequences (mean)	50,847	32,208	47,907	56,365
No seq. filtered (mean)	32,626	12,714	29,662	37,642
No seq. filt. merged (mean)	29,300	12,094	14,060	30,706
No seq. filt. merg. no chimeras (mean)	25,476	9,849	13,521	30,408
No samples	192	96	192	96
No samples trimmed	189	81	192	95
No ASV (sum)	6,112	845	9,352	2,023
No ASV trimmed (sum)	413	106	807	262
No ASV trimmed per sample (mean)	125	29	194	45

21      *No sequences (sum)*: Total number of paired-end sequencing reads per biotope. *No sequences*  
 22    (*mean*): Average number of paired-end sequencing reads per sample. *No seq. filtered (mean)*: Total  
 23    number of filtered paired-end sequencing reads per sample. *No seq. filt. merged (mean)*: Number  
 24    of filtered paired-end sequencing reads merged per sample. *No seq. filt. merg. no chimeras (mean)*:  
 25    Average Number of filtered paired-end sequencing reads merged, removing chimeras per sample.  
 26    *No samples*: Number of samples. *No samples trimmed*: Number of samples, filtering out low  
 27    quality samples. *No ASV (sum)*: Total number of ASV. *No ASV trimmed (sum)*: Total number of ASV,  
 28    filtering out low abundance ASV and chloroplast or mitochondrial ASV for bacterial samples. *No*  
 29    *ASV trimmed per sample (mean)*: Average number of filtered ASV per sample.

Table S5: Variance explained by the terms in the PERMANOVA models.

	fungi-soil	fungi-root	bacteria-soil	bacteria-root
amendment	0.02***	0.08***	0.04***	0.19***
planted	0.21***	NA	0.13***	NA
species	0.02***	0.26***	0.02***	0.20***
amendment:planted	0.01**	NA	0.02***	NA
amendment:species	0.01*	0.04*	0.03***	0.05***
planted:species	0.01	NA	0.01**	NA
amendment:planted:species	0.01	NA	0.01*	NA

30       $r^2$  (percentage of variance explained by the term in the model); \* $p\text{-value}<0.05$ , \*\* $<0.005$ , \*\*\* $<0.0005$

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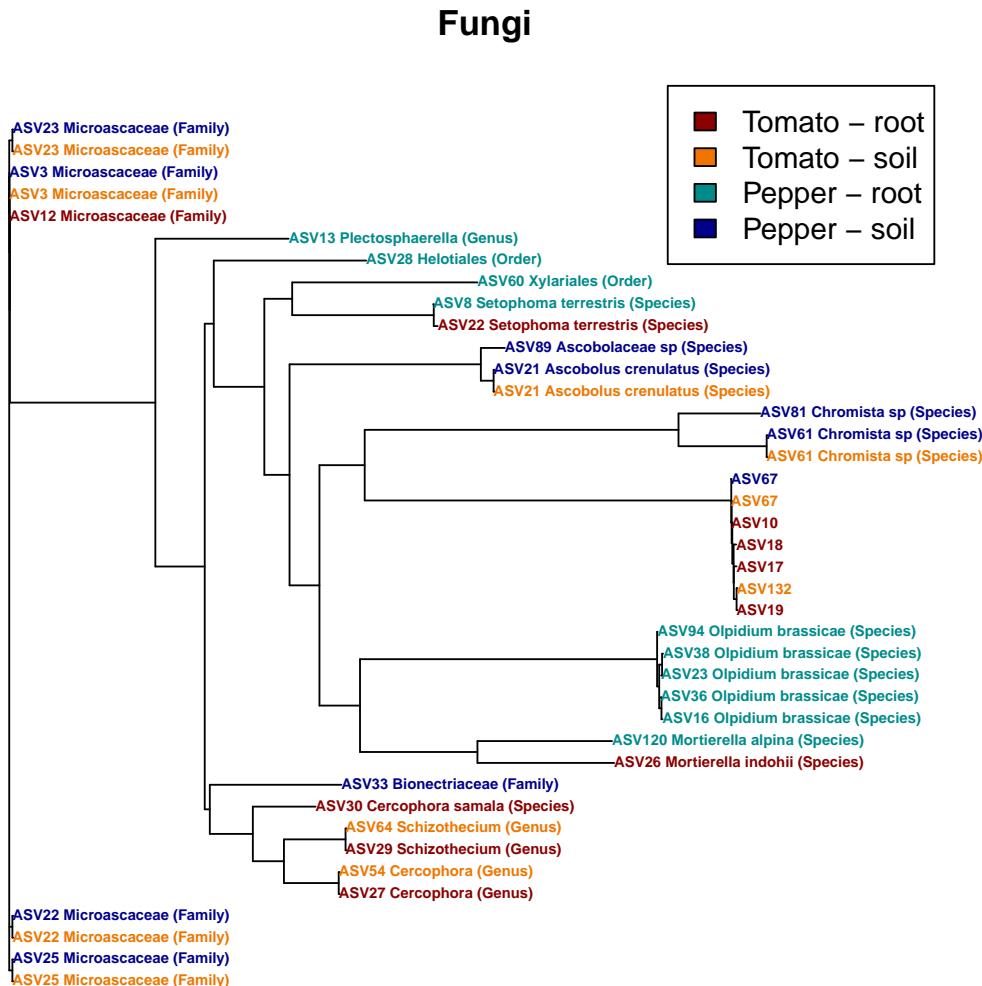
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34 **Figure S1: Plant productivity.** Photos were taken at the end of the experimental treatment. In  
35 each photo, amended plants are on the left. **A:** pepper shoots, **B:** pepper roots, **C:** pepper fruits  
36 and **D:** tomato fruits.

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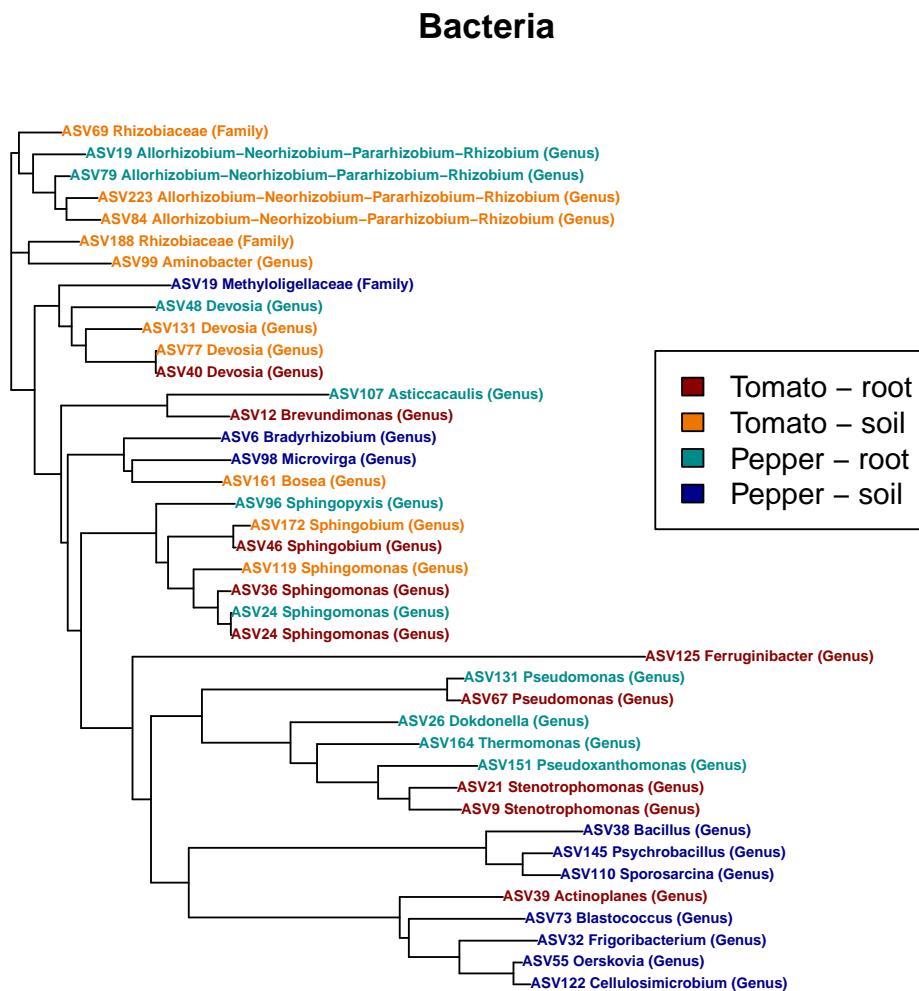


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41 **Figure S2: Neighbor-Joining trees of candidates ASV (fungi) most positively associated with**  
 42 **productivity measures as identified in Figure 5. The most accurate taxonomy assigned accord-**  
 43 **ing to the RDP bayesian classifier (form Phylum to species) was added as tip labels.**

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47 **Figure S3: Neighbor-Joining trees of candidates ASV (bacteria) most positively associated with**  
 48 **productivity measures as identified in Figure 6. The most accurate taxonomy assigned accord-**  
 49 **ing to the RDP bayesian classifier (form Phylum to species) was added as tip labels.**

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