



Table S1. Post hoc-adonis (PERMANOVA) for soil bacterial community structure for RCST.

	Pair-wise comparison	R ²	p-value	FDR adjusted p -value
Umbeluzi	10YF vs PH	0.071361	0.001	0.006
	10YF vs 1YF	0.096168	0.001	0.006
	PH vs 1YF	0.083499	0.002	0.012
	PH vs 5mR	0.101005	0.001	0.006
Chokwe	PH vs 5YF	0.071956	0.024	0.072
	PH vs 5mR	0.091288	0.002	0.006

Table S2. Differentially abundant phylotypes in Umbeluzi.

Genus	p values	FDR	PH	1YF	5mR	10YF	LDA score
Bacillus	0.000	0.001	29257.00	90743.00	45740.00	604370.00	5.46
Pseudomonas	0.000	0.002	299120.00	125400.00	192690.00	24729.00	5.14
Sphingomonas	0.003	0.007	173500.00	436930.00	307390.00	193290.00	5.12
uncultured_Rubrobacteria_bacterium	0.001	0.004	593.73	23431.00	2572.80	258560.00	5.11
Nocardioides	0.000	0.001	11290.00	185800.00	10117.00	257680.00	5.09
Rubrobacter	0.004	0.010	1116.10	22168.00	0.00	230130.00	5.06
uncultured_soil_bacterium	0.000	0.001	236050.00	181130.00	316010.00	118860.00	4.99
MND1	0.000	0.001	210110.00	87014.00	220460.00	33929.00	4.97
Solirubrobacter	0.000	0.001	2723.10	62489.00	4169.10	171320.00	4.93
Gaiella	0.000	0.001	14292.00	76795.00	30916.00	180680.00	4.92
uncultured_prokaryote	0.000	0.000	123890.00	37051.00	157910.00	1968.70	4.89
Blastococcus	0.000	0.001	0.00	89743.00	0.00	154710.00	4.89
Geodermatophilus	0.000	0.001	0.00	89078.00	0.00	155430.00	4.89
Flavisolibacter	0.002	0.007	44666.00	183290.00	64568.00	44264.00	4.84
Sideroxydans	0.000	0.001	134310.00	9249.80	122300.00	0.00	4.83
uncultured_Gemmatimonadetes_bacterium	0.000	0.001	129900.00	44537.00	134690.00	24953.00	4.74
Geobacter	0.001	0.003	80000.00	109140.00	29196.00	390.09	4.74
uncultured_Syntrophaceae_bacterium	0.000	0.001	41396.00	2173.30	86865.00	0.00	4.64
uncultured_bacterium_DA008	0.000	0.001	84927.00	47470.00	72227.00	0.00	4.63
Nitrospira	0.000	0.000	61167.00	25283.00	86687.00	4081.80	4.62
uncultured_Holophaga_sp_	0.000	0.002	45718.00	45827.00	87315.00	4258.80	4.62
Acidibacter	0.004	0.010	48355.00	105900.00	23505.00	23299.00	4.62
Mycobacterium	0.000	0.001	0.00	34600.00	803.60	81732.00	4.61
Lysobacter	0.000	0.002	57434.00	34663.00	82091.00	780.18	4.61
Dongia	0.003	0.008	26271.00	107450.00	25112.00	70812.00	4.61
uncultured_gamma_proteobacterium	0.000	0.002	81284.00	52047.00	71101.00	1716.70	4.60
uncultured_microorganism	0.000	0.001	73562.00	78327.00	79817.00	4238.40	4.58
Hydrogenophaga	0.000	0.000	73960.00	0.00	42548.00	0.00	4.57
Gemmatimonas	0.000	0.002	28056.00	77291.00	61621.00	3601.70	4.57
Arenimonas	0.001	0.003	59071.00	75901.00	27349.00	1613.00	4.57
anaerobic_bacterium_MO_CFX2	0.000	0.001	67484.00	2386.30	75517.00	7027.00	4.56
Ohtaekwangia	0.000	0.002	78450.00	44260.00	12034.00	6269.00	4.56
uncultured_archaeon	0.000	0.000	64337.00	7998.90	71131.00	238.44	4.55
Dechloromonas	0.001	0.003	69468.00	9852.10	15232.00	0.00	4.54
Flavobacterium	0.002	0.007	64510.00	47262.00	30021.00	584.86	4.50
Rhodopirellula	0.001	0.004	846.86	462.29	130.94	59129.00	4.47
Thiobacillus	0.000	0.001	57723.00	577.86	29328.00	0.00	4.46
Ellin6055	0.000	0.001	2742.80	56955.00	2624.80	0.00	4.45
Bradyrhizobium	0.000	0.002	28233.00	84507.00	35784.00	35233.00	4.45
Cellvibrio	0.003	0.007	29833.00	56177.00	22686.00	0.00	4.45
Azotobacter	0.002	0.006	31931.00	54656.00	0.00	0.00	4.44
Devosia	0.002	0.006	6271.40	60423.00	23266.00	23862.00	4.43
Stenotrophobacter	0.000	0.002	41907.00	52868.00	49455.00	0.00	4.42
uncultured_Chlorobi_bacterium	0.001	0.004	21609.00	5060.70	53828.00	1916.40	4.41
Aridibacter	0.000	0.002	43228.00	54960.00	25262.00	6152.20	4.39
SWB02	0.000	0.001	47575.00	17428.00	15342.00	0.00	4.38
Cephalotococcus	0.000	0.002	53188.00	24190.00	11425.00	6008.30	4.37
uncultured_subdivision_3_bacterium	0.000	0.002	40793.00	26152.00	47273.00	0.00	4.37

OLB12	0.000	0.000	45590.00	2405.00	130.94	0.00	4.36
uncultured_bacterium_126	0.002	0.007	20998.00	45836.00	43207.00	0.00	4.36
mle1_7	0.000	0.002	24528.00	15943.00	45748.00	1180.50	4.35
Phenylobacterium	0.000	0.002	18749.00	51673.00	39840.00	8113.50	4.34
Pirellula	0.001	0.003	14151.00	57860.00	25933.00	15775.00	4.34
uncultured_Desulfovibrio_sp_	0.000	0.001	40761.00	25729.00	3903.60	0.00	4.31
Luteolibacter	0.000	0.001	24759.00	4724.80	38314.00	1488.90	4.27
Flavitalea	0.000	0.002	5785.40	42565.00	7840.80	5473.00	4.27
uncultured_candidate_division_SPAM_bacterium	0.000	0.001	27118.00	0.00	36744.00	0.00	4.26
uncultured_planctomycete	0.000	0.002	28660.00	13549.00	34882.00	0.00	4.24
Janthinobacterium	0.001	0.003	34959.00	16517.00	24599.00	0.00	4.24
Desulfobulbus	0.001	0.005	34316.00	0.00	0.00	9891.80	4.23
Vogesella	0.004	0.010	9338.70	0.00	32532.00	0.00	4.21
Lacunisphaera	0.000	0.002	28238.00	18475.00	2028.60	0.00	4.15
Terrimonas	0.002	0.007	23481.00	17781.00	26783.00	0.00	4.13
Hyphomonas	0.001	0.003	26133.00	463.93	5942.40	0.00	4.12
Actinobacte-							
ria_bacterium_RBG_19FT_COMBO_70_19	0.002	0.006	10187.00	4762.30	26085.00	0.00	4.12
WCHB1_32	0.001	0.003	25884.00	1789.70	2678.70	0.00	4.11
Candida-							
tus_Saccharibacteria_bacterium_RAAC3_TM7_1	0.001	0.004	1869.80	24241.00	0.00	20378.00	4.08
Spirochaeta_2	0.000	0.001	14249.00	3273.50	21451.00	0.00	4.03
uncultured_Bacteroidetes_bacterium	0.000	0.001	21576.00	6948.80	880.39	0.00	4.03
uncultured_Acidobacteria_bacterium	0.001	0.004	18270.00	15872.00	21048.00	0.00	4.02
Sh765B_TzT_35	0.000	0.001	16999.00	231.96	20467.00	0.00	4.01
Reyranella	0.001	0.003	2376.20	21503.00	3283.90	884.10	4.01
Geothermobacter	0.000	0.002	19389.00	0.00	4060.10	0.00	3.99
uncultured_Pelobacter_sp_	0.000	0.001	18800.00	2188.60	14453.00	0.00	3.97
Erythrobacter	0.000	0.002	0.00	0.00	17420.00	6848.10	3.94
ADurb_Bin063_1	0.000	0.002	15447.00	0.00	12022.00	0.00	3.89
Polycyclovorans	0.001	0.003	5731.90	2774.90	14882.00	429.17	3.86
uncultured_Rhodospirillales_bacterium	0.001	0.003	13519.00	4090.80	3406.60	0.00	3.83
uncultured_Myxococcales_bacterium	0.003	0.007	13631.00	1879.60	12365.00	0.00	3.83
Syntrophobacter	0.002	0.005	8423.70	2441.00	13072.00	0.00	3.82
Prostheco bacter	0.000	0.002	12957.00	1078.10	9413.00	0.00	3.81
unidentified_eubacterium_clone_BSV40	0.000	0.002	10405.00	1641.00	1312.30	0.00	3.72
uncultured_sludge_bacterium_H5	0.001	0.004	8663.70	0.00	9992.70	0.00	3.70
Lentimicrobium	0.000	0.002	9180.70	144.88	857.59	0.00	3.66
OLB13	0.001	0.004	8330.70	4431.70	3060.40	0.00	3.62
Armatimonadetes_bacterium_55_13	0.003	0.007	3452.20	0.00	3439.70	0.00	3.24
Haliangium	0.004	0.011	127360.00	91158.00	85897.00	40983.00	4.64
Ramlibacter	0.005	0.011	44837.00	35538.00	75254.00	4681.10	4.55
Skermanella	0.005	0.012	5947.70	78460.00	7307.40	5341.10	4.56
Rheinheimera	0.005	0.012	65355.00	12820.00	48345.00	0.00	4.51
Neo_b11	0.005	0.012	2934.40	11983.00	392.83	0.00	3.78
Bdellovibrio	0.005	0.013	10116.00	9497.50	3031.20	3167.00	3.55
Diplosphaera	0.006	0.014	14661.00	4136.20	785.67	0.00	3.87
Syntrophorhabdus	0.006	0.015	8424.40	1155.70	5557.30	0.00	3.62
uncultured	0.006	0.015	1416100	864560.0	1299600	1285600	5.44
Ignavibacterium	0.007	0.015	14976.00	1250.00	16279.00	8764.50	3.88
Anaeromyxobacter	0.007	0.015	75361.00	34560.00	53392.00	24255.00	4.41
Agromyces	0.007	0.016	19805.00	19363.00	23130.00	0.00	4.06
Cyanothece_PCC_7424	0.007	0.016	15893.00	601.25	7571.80	0.00	3.90
bacterium_WX65	0.007	0.016	5808.10	2991.10	42812.00	0.00	4.33
Hirschia	0.007	0.016	18510.00	8277.40	10937.00	0.00	3.97
uncultured_Acidobacterium_sp_	0.007	0.016	16972.00	7032.80	16532.00	0.00	3.93
uncultured_Gaiella_sp_	0.008	0.016	0.00	28634.00	1440.40	24424.00	4.16
Desulfatiglans	0.008	0.018	13820.00	122.83	6517.20	2026.70	3.84
Pelagibius	0.009	0.019	6722.20	4545.40	0.00	245780.00	5.09
Streptomyces	0.010	0.020	13507.00	116570.00	17703.00	164000.00	4.88
Chthonomonas	0.010	0.021	914.77	7169.80	1304.80	0.00	3.55
Chryseolinea	0.010	0.021	120.09	38273.00	526.15	9688.00	4.28
Ellin6067	0.011	0.022	134210.00	105040.00	74120.00	37226.00	4.69
Pedomicrobium	0.011	0.022	10874.00	3322.90	27446.00	5326.30	4.08

uncultured_Caldilineaceae_bacterium	0.011	0.023	18273.00	21463.00	12515.00	620.39	4.02
Microlunatus	0.012	0.024	0.00	11574.00	0.00	25422.00	4.10
Steroidobacter	0.012	0.024	10826.00	37701.00	1702.30	26138.00	4.26
Candidatus_Udaeobacter	0.013	0.025	833.49	56114.00	9795.40	166090.00	4.92
uncultured_Nitrospirae_bacterium	0.015	0.028	10161.00	127.61	7589.20	0.00	3.71
uncultured_Pedospaera_sp_	0.015	0.030	25335.00	15127.00	1445.70	5955.70	4.08
uncultured_bacterium	0.016	0.031	537560.00	478230.00	725870.00	640300.00	5.09
Algoriphagus	0.016	0.031	24916.00	18632.00	13934.00	0.00	4.10
Sporocytophaga	0.018	0.033	4782.50	4355.50	0.00	780.18	3.38
Sorangium	0.018	0.033	4546.30	9252.40	9014.10	0.00	3.67
uncultured_Desulfuromonadaceae_bacterium	0.018	0.033	2583.80	2871.80	9243.80	2342.30	3.54
uncultured_Actinomycetales_bacterium	0.018	0.033	4776.20	0.00	4050.40	82025.00	4.61
Azoarcus	0.018	0.033	21545.00	6025.00	31776.00	17120.00	4.11
Chthoniobacter	0.019	0.035	4275.60	33102.00	12056.00	1630.90	4.20
Pontibacter	0.021	0.037	11108.00	16221.00	33395.00	780.18	4.21
Conexibacter	0.021	0.037	1211.30	9205.80	0.00	50031.00	4.40
OM27_clade	0.022	0.038	12621.00	8098.70	2109.40	2314.80	3.72
Pajaroellobacter	0.023	0.041	19617.00	23470.00	8374.00	2896.90	4.01
Niastella	0.024	0.042	593.73	12467.00	8538.70	850.45	3.77
uncultured_delta_proteobacterium	0.025	0.044	19092.00	7067.20	19826.00	868.54	3.98
uncultured_Acidobacteriaceae_bacterium	0.026	0.044	3733.30	26031.00	392.83	0.00	4.11
Pseudolabrys	0.026	0.044	3264.10	38774.00	8519.70	1560.40	4.27
Adhaeribacter	0.028	0.046	9870.20	31585.00	21139.00	0.00	4.20

Table S3. Differentially abundant phylotypes in Chokwe.

Genus	p values	FDR	5mR	PH	5YF	LDA score
MND1	0.001	0.025	94559.00	402810.00	298320.00	5.19
RB41	0.002	0.031	286940.00	110630.00	75872.00	5.02
Sphingomonas	0.004	0.043	263830.00	74562.00	107610.00	4.98
Micromonospora	0.004	0.043	121350.00	0.00	17909.00	4.78
Nocardioides	0.003	0.034	154900.00	46861.00	37211.00	4.77
Agromyces	0.001	0.025	106000.00	8690.30	48316.00	4.69
Subgroup_10	0.001	0.026	111620.00	20358.00	32858.00	4.66
Rubrobacter	0.008	0.048	122400.00	34934.00	40505.00	4.64
Desulfuromonas	0.007	0.048	0.00	13666.00	82764.00	4.62
Lysobacter	0.001	0.025	81104.00	2990.10	28170.00	4.59
Sideroxydans	0.006	0.046	2229.90	57490.00	80564.00	4.59
Haliangium	0.008	0.049	86477.00	161620.00	133200.00	4.57
uncultured_Chloroflexi_bacterium	0.007	0.048	123500.00	62719.00	52389.00	4.55
SWB02	0.006	0.046	20414.00	48845.00	82824.00	4.49
Acidibacter	0.007	0.048	26390.00	70564.00	85143.00	4.47
uncultured_deep_sea_bacterium	0.002	0.028	23121.00	58676.00	5722.60	4.42
Adhaeribacter	0.006	0.046	52263.00	220.74	12438.00	4.42
Nitrospira	0.001	0.025	24859.00	58201.00	13577.00	4.35
Dechloromonas	0.001	0.025	0.00	43859.00	0.00	4.34
Pelagibius	0.001	0.025	0.00	0.00	40009.00	4.30
Diplosphaera	0.001	0.025	0.00	1199.10	38600.00	4.29
Aridibacter	0.002	0.028	49722.00	31230.00	10675.00	4.29
Candidatus_Koribacter	0.004	0.043	701.61	37533.00	24498.00	4.27
Kribbella	0.008	0.049	48073.00	11249.00	13676.00	4.27
Vogesella	0.001	0.025	0.00	35400.00	0.00	4.25
Brevundimonas	0.005	0.046	29330.00	0.00	7988.20	4.17
mle1_7	0.008	0.049	50121.00	31197.00	20638.00	4.17
uncultured_Chloroflexus_sp_	0.001	0.025	32596.00	5018.60	3991.20	4.16
Hirschia	0.006	0.046	4163.10	12316.00	30672.00	4.12
Lacunisphaera	0.004	0.043	0.00	14501.00	24156.00	4.08
Gemmata	0.001	0.028	28097.00	5601.30	9189.20	4.05
Kouleothrix	0.002	0.030	21192.00	1379.10	0.00	4.03

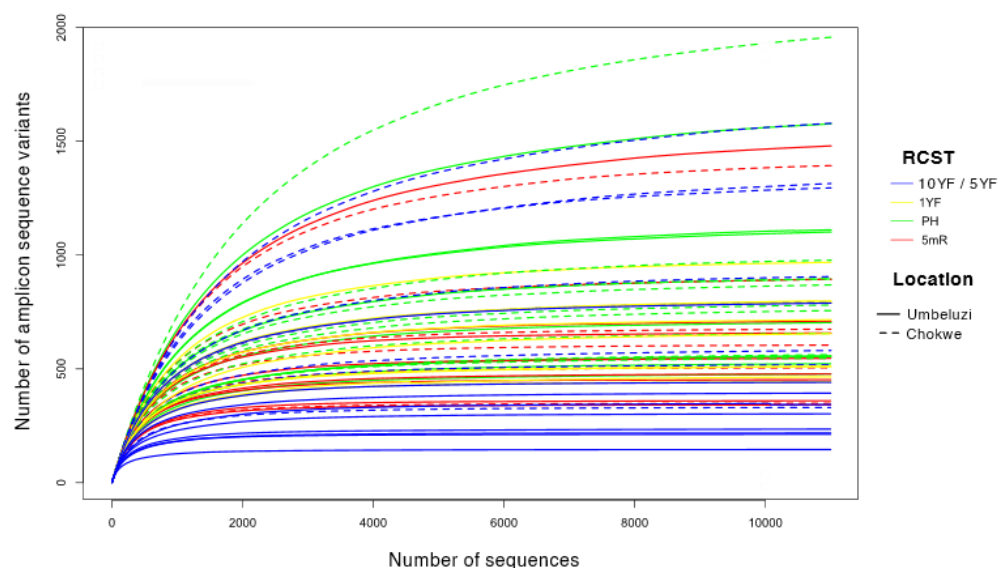
Table S4. Goodness of fit of environmental variable with significant influence on bacterial communities in Chokwe.

Properties	Umbeluzi				Chokwe			
	RDA1	RDA2	R ²	Pr. (>r)	RDA1	RDA2	R ²	Pr. (>r)
pH (H ₂ O)	−0.919	−0.393	0.136	0.115	0.458	0.889	0.824	0.001***
EC (mS/cm)	−0.978	−0.206	0.249	0.017 *	0.495	0.869	0.864	0.001***
Moisture (g H ₂ O kg ^{−1})	0.269	−0.963	0.004	0.943	−0.292	−0.956	0.566	0.001***
SOC (g kg ^{−1})	−0.282	−0.959	0.072	0.311	−0.976	0.214	0.589	0.001***
NH ₄ ⁺ -N (mg N kg ^{−1})	0.458	−0.889	0.178	0.001***	−0.999	0.034	0.436	0.005
NO ₃ [−] -N (mg N kg ^{−1})	0.542	−0.841	0.215	0.003 **	0.502	0.865	0.830	0.001***
Total N (g kg ^{−1} dry soil)	−0.957	0.290	0.057	0.426	−0.750	0.662	0.294	0.032*
P-Olsen (mg kg ^{−1})	0.872	−0.488	0.011	0.846	−0.996	−0.088	0.470	0.004**
Egner Rhien K (mg kg ^{−1})	−0.987	0.155	0.084	0.289	0.915	0.403	0.061	0.543

* Significant at 0.05 probability level; ** Significant at 0.01 probability level; ***Significant at 0.001 probability level. EC, Electrical conductivity; OM, Organic matter; SOC, Soil organic carbon.

Table S5. Topological properties for the ecological networks in Figure 6.

Parameter	Umbeluzi		Chokwe	
	Cultivated	Fallow	Cultivated	Fallow
Nodes	209	112	190	239
Edges*	156	101	458	472
Average degree	1.49	1.804	4.821	3.950
Average path length	1.77	1.279	4.457	1.688
Diameter	7	3	13	5
Density	0.007	0.016	0.026	0.017
Modularity	0.848	0.874	0.747	0.928
Connected components	115	63	68	76
Average clustering coefficient	0.477	0.852	0.557	0.823
Test statistics for power law distribution (p)	0.35	1.00	0.41	0.66

**Figure S1.** Rarefaction curve of Amplicon sequence variants sampled to a depth of 11 000 sequences per sample. 10YF, ten years fallow; 5YF, five years fallow; 1YF, one year fallow; PH, Postharvest; 5mR, five months off-season recovery period. “10YF /5YF” denotes

fallow fields in Umbeluzi or Chokwe, respectively.

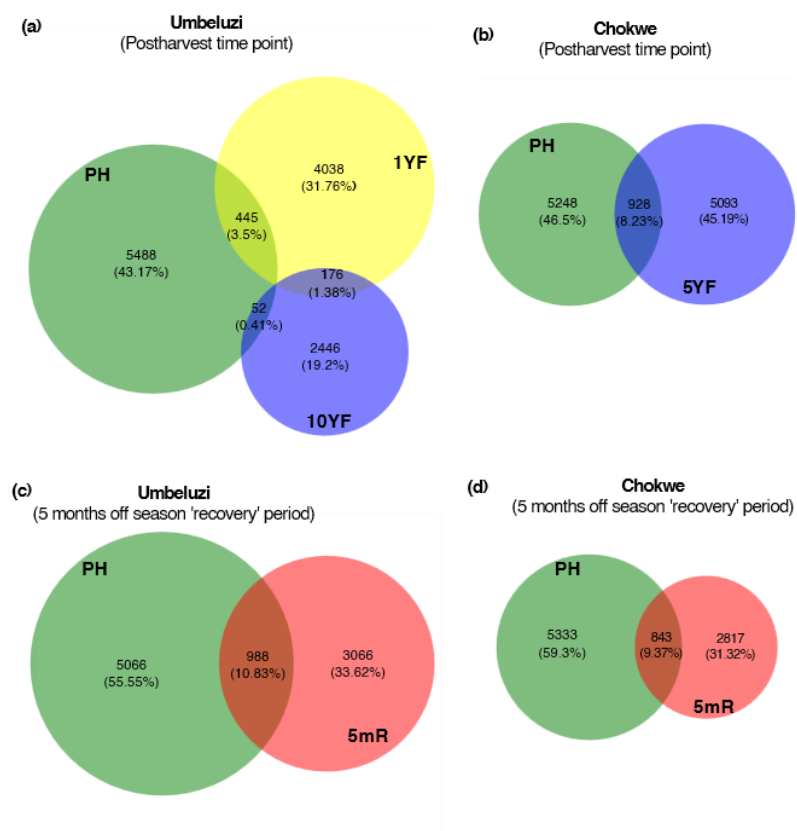


Figure S2. Shared and unique ASVs of RCST in Umbeluzi and Chokwe. Venn diagram was computed using the DeepVenn online tool (<http://www.deepvenn.com/>). 10YF, ten years fallow; 5YF, five years fallow; 1YF, one year fallow; PH, Postharvest; 5mR, five months off-season recovery period. "10YF /5YF" denotes fallow fields in Umbeluzi or Chokwe, respectively.