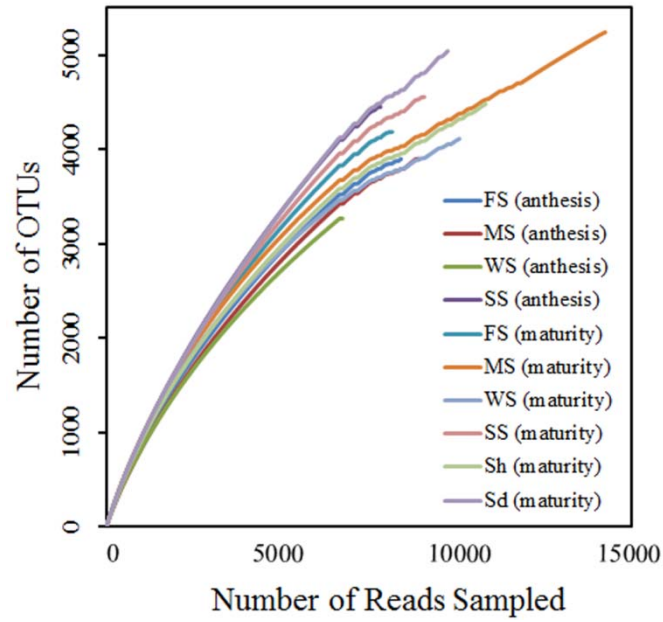


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Supplementary materials

2 **Appendix A.** Rarefaction analysis of the different samples. Rarefaction curves of OTUs clustered at
3 97% sequence identity across different environmental samples.



4

5 **Appendix B.** Differences of microbial community among cropping systems as examined by the
6 dissimilarity test of ADONIS.

7

Cropping systems	ADONIS	
	R^2	P value
MM-SS ^a	0.39	<0.01^b
SS-WW ^a	0.49	<0.01
MM-WW	0.52	<0.01

8 ^a Abbreviations: MM, maize-maize; SS, sunflower-sunflower; WW, wheat-wheat.

9 ^b Boldface values indicate significant differences ($P<0.01$)

10 **Appendix C.** Estimated OTU richness, diversity indices and estimated sample coverage for 16S
 11 rDNA libraries of sunflower soil samples

Library	NS	OTUs ^a	Estimated OTU richness			Shannon ^b	SC ^c
			ACE	Chao 1			
Anthesis	SS	9154	4493	19667 (18928;20444)	11857 (11121;12674)	7.88(7.85;7.91)	0.66
	FS	9394	3894	12468 (11987;12976)	8565 (8060;9133)	7.62(7.59;7.65)	0.74
	WS	8001	3260	10265 (9828; 10731)	6752 (6350; 7207)	7.36(7.33; 7.39)	0.75
	MS	9821	3896	12221 (11745; 12726)	8086 (7642; 8583)	7.39(7.36; 7.43)	0.75
Maturity	SS	9909	4551	15796 (15223; 16399)	10614 (10005; 11291)	7.91(7.88; 7.94)	0.70
	FS	9210	4180	12788 (12312; 13291)	8828 (8346; 9366)	7.86(7.84; 7.89)	0.72
	WS	10881	4105	9460 (9139; 9802)	7497 (7128; 7912)	7.82(7.79; 7.84)	0.80
	MS	15275	5225	11249 (10920; 11596)	8961 (8594; 9367)	8.00(7.98; 8.02)	0.82
	Sd	10596	5038	27436 (26514; 28399)	14946 (13976; 16022)	7.96(7.94; 7.99)	0.66
	Sh	11569	4471	12695 (12259; 13155)	8642 (8219; 9113)	7.81(7.79; 7.84)	0.77
Total		103810					

12 Abbreviations: ESC, estimated sample coverage; NS, number of sequences for each library;
 13 OTU, operational taxonomic unit; MM, maize-maize; SS, sunflower-sunflower; WW, wheat-wheat;
 14 WS, wheat-sunflower; MS, maize-sunflower; FS, fallow-sunflower; Sh, health sunflower; Sd,
 15 disease sunflower.

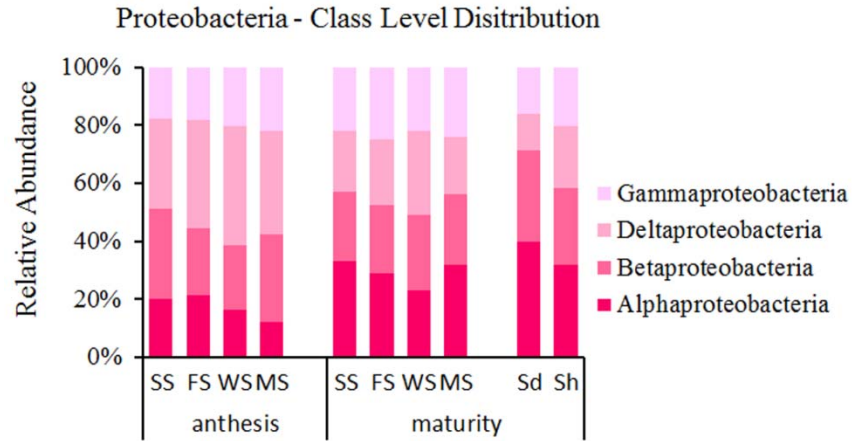
16 ^aCalculated with Furthest neighbor at the 3% distance level.

17 ^bShannon diversity index calculated using Furthest neighbor (3% distance).

18 ^cESC: $C_x = (1 - N_x/n)$, where N_x is the number of unique sequences and n is the total number of
 19 sequences.

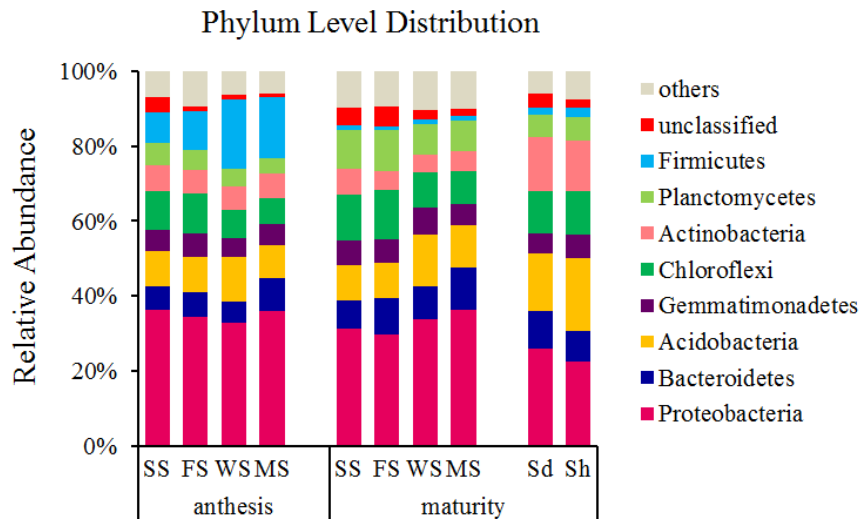
20 Values in brackets are 95% confidence intervals as calculated by Furthest neighbor.

21 **Appendix D.** Relative read abundance of Proteobacteria within the different communities.
 22 Sequences that could not be classified into any known group were assigned as ‘Unclassified’
 23 bacteria.



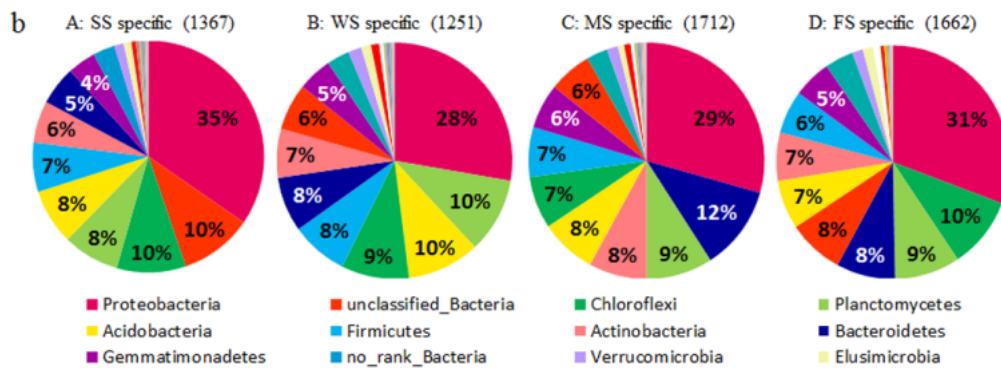
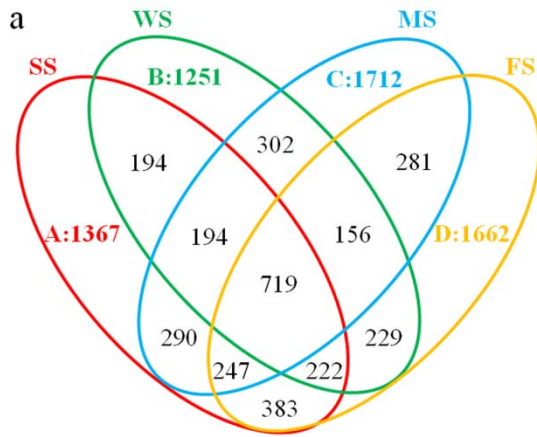
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27 **Appendix E.** Relative read abundance of different bacterial phyla within the different communities.
 28 Sequences that could not be classified into any known group were assigned as ‘Unclassified’
 29 bacteria.



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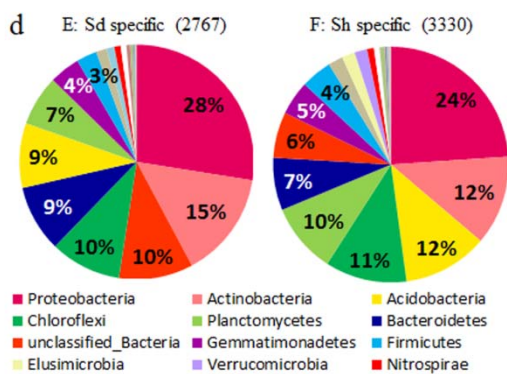
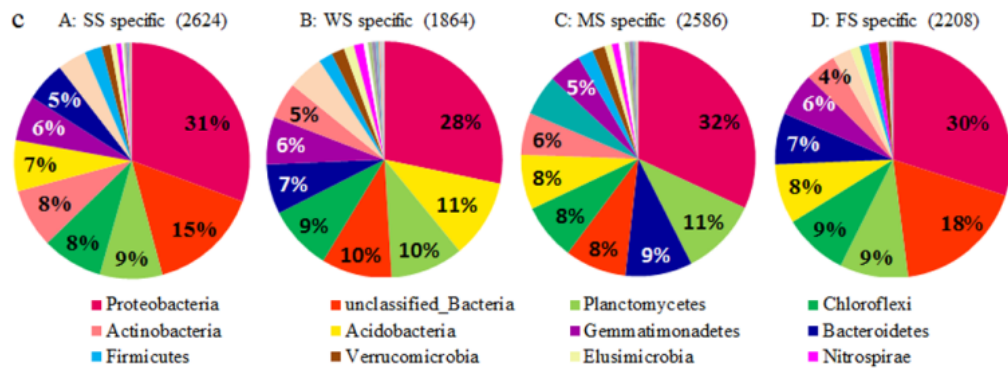
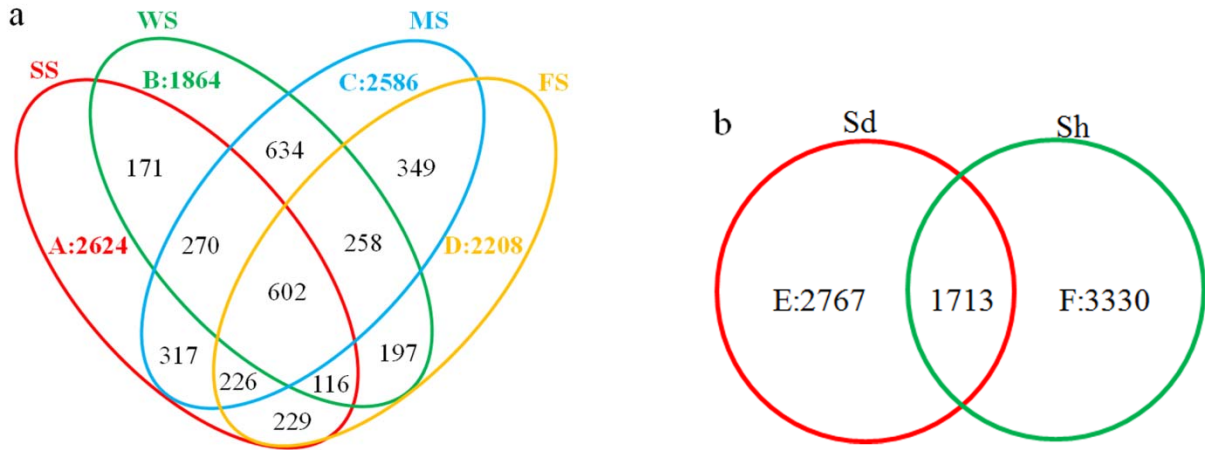
31 **Appendix F.** Specific OTUs analysis of the different libraries at anthesis: a for Venn diagram
 32 showing the shared and unique OTUs (3% distance level), b for the special species existing in each
 33 cropping system.



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36 **Appendix G.** Specific OTUs analysis of the different libraries at maturity: a for Venn diagram
 37 showing the unique and shared OTUs (3% distance level), b for special species existing in SS, FS,
 38 WS and MS and c for special species existing in Sd and Sh.



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