

1 ***Plants, People, Planet Supporting Information***

2 Article title: Effect of organic farming on root microbiota, seed production and pathogen
3 resistance in winter wheat fields.

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8 The following Supporting Information is available for this article:

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10 **Fig. S1** Rarefaction curves of all bacterial and fungal endospheric samples.

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12 **Table S1** Correlations between environmental variables on sampled fields (Pearson's
13 coefficient)

14

15 **Table S2** Characteristics of the correlation networks for bacterial and fungal assemblages
16 sampled in mid-March and in late May.

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18 **Table S3** Results of the linear models analyzing the effect of environmental parameters on
19 microbial richness and evenness.

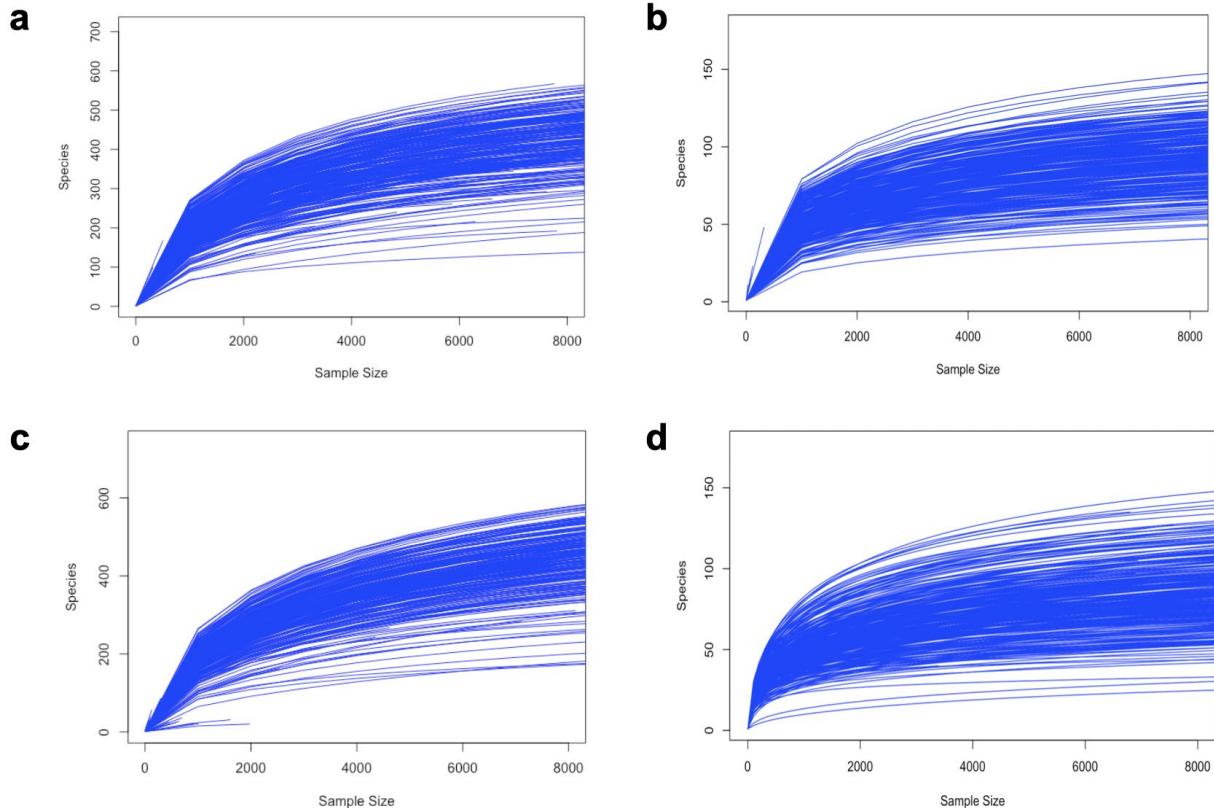
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21 **Table S4** Results of the CCA analysis, proportion of the inertia explained by the environmental
22 parameters, statistical results of the ANOVA type II analyses.

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25 **Fig. S1 Rarefaction curves of all bacterial and fungal endospheric samples.** Curves show
26 the total assigned sequence-clusters detected relative to sample size in sequence number for
27 Bacteria in mid-March (a) and in late May (c) and Fungi in mid-March (b) and in late May (d).
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31 **Table S1 Correlations between environmental variables on sampled fields (Pearson's coefficient)** – Abbreviations: TFI – Treatment frequency
 32 indice; C/N – Carbon to nitrogen ratio; OM: Organic matter; P205 - Phosphorus
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 34

	Mechanical weeding	Tillage	Nitrogen input	TFI fungicide	TFI herbicide	TFI tot	pH	Soil nitrogen	C/N	OM	P2O5	Clay	Fine silt	Coarse silt	Sowing density	Cultivar number	Plant richness (field)
Mechanical weeding																	
Tillage	0.28																
Nitrogen input	-0.44	-0.56															
TFI fungicide	-0.52	-0.55	0.74														
TFI herbicide	-0.54	-0.54	0.82	0.74													
TFI tot	-0.56	-0.61	0.81	0.91	0.89												
pH	0.17	0.05	0.13	-0.06	-0.07	-0.13											
Soil nitrogen	0.05	-0.14	-0.003	-0.23	-0.07	-0.15	-0.11										
C/N	-0.07	0.12	0.11	-0.05	0.07	0.05	-0.04	-0.02									
OM	-0.02	-0.09	0.03	-0.24	-0.06	-0.14	-0.11	0.92	0.35								
P2O5	-0.07	-0.15	0.30	0.36	0.22	0.26	0.40	-0.26	-0.23	-0.33							
Clay	-0.05	-0.29	0.15	-0.07	0.12	0.07	-0.07	0.69	-0.28	0.53	-0.23						
Fine silt	0.16	-0.14	0.24	0.01	0.09	0.05	-0.11	0.37	0.08	0.38	-0.31	0.33					
Coarse silt	-0.05	0.29	-0.07	-0.01	0.004	-0.01	0.24	-0.68	0.17	-0.55	0.31	-0.56	-0.20				
Sowing density	0.35	0.21	-0.25	-0.47	-0.41	-0.47	0.33	0.05	0.01	0.05	-0.27	0.12	0.18	-0.06			
Cultivar number	0.46	0.36	-0.69	-0.66	-0.70	-0.74	0.10	0.29	-0.10	0.24	-0.20	-0.04	-0.16	-0.12	0.13		
Plant richness (field)	0.63	0.38	-0.64	-0.79	-0.76	-0.81	0.10	0.27	0.11	0.31	-0.31	0.006	0.15	-0.02	0.44	0.74	
Plant richness (margin)	0.23	0.32	-0.31	-0.43	-0.39	-0.51	0.18	0.33	0.05	0.34	-0.12	0.01	0.08	0.004	0.21	0.64	0.47

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Table S2 Characteristics of the correlation networks for bacterial and fungal assemblages sampled in mid-March and in late May. “OF” stands for organic field, “CF” for conventional field.

	Bacteria				Fungi			
	March		May		March		May	
	CF	OF	CF	OF	CF	OF	CF	OF
<i>Network properties</i>								
#Nodes	417	508	519	474	94	109	94	78
#Edges	944	2305	1935	957	130	135	156	79
#Clusters	23	26	20	22	20	26	19	23
Modularity	0.85	0.55	0.71	0.87	0.88	0.88	0.86	0.88
Connectance	0.011	0.018	0.014	0.009	0.030	0.023	0.036	0.026

Table S3 Results of the linear models analyzing the effect of environmental parameters on microbial richness and evenness. Only significant tests were presented. Parameter estimates, statistical results of the ANOVA type II analyses (Chi-sq test and p-value: (t): p < 0.1; * p < 0.05; ** p < 0.01; *** p < 0.001) for the independent variables, and model parameters. A1mgt and A2mgt: Coordinates along axis 1 and 2 of PCA based on the management parameters; A1sol and A2sol: Coordinates along axis 1 and 2 of PCA based on the soil parameters; A1flo and A2flo: Coordinates along axis 1 and 2 of PCA based on the plant diversity parameters. All the variables were calculated at the field scale (N=34 for bacteria in March, N=29 for bacteria in May; N=35 for fungi).

	Dependent variables	Independent variables						Model parameters	P value	R ²
		A1mgt	A2mgt	A1sol	A2sol	A1flo	A2flo			
Bacteria										
Bacteroidetes	Richness (March)	-3.10 (F=1.95ns.)		-2.72 (F=4.61*)	4.30 (F=4.69*)	-1.30 (F=0.28ns)			0.03	0.21
Firmicutes	Richness (March)	-0.46 (F=0.52ns)	-2.93 (F=5.70*)	0.46 (F=2.05ns)					0.04	0.17
Firmicutes	Evenness (March)			0.006 (F=1.13ns)	0.023 (F=6.45*)	-0.018 (F=6.53*)			0.01	0.24
Alphaproteobacteria	Evenness (March)	0.007 (F=4.95*)	0.007 (F=3.17; 0.09)		0.008 (F=5.08*)	0.003 (F=0.89ns)			0.003	0.33
Deltaproteobacteria	Evenness (March)	-0.002 (F=0.03ns)		0.01 (F=2.93ns)	0.04 (F=9.72**)	-0.02 (F=1.27ns)	0.02 (F=2.46ns)		0.02	0.26
Gammaproteobacteria	Evenness (March)	-0.004 (F=0.16ns)		0.02 (F=8.69**)		-0.01 (F=1.28ns)			0.04	0.17
Actinobacteria	Richness (May)	-3.10 (F=9.72**)	-3.96 (F=4.15ns)						0.004	0.30
Firmicutes	Richness (May)	-2.90 (F=12.76**)		-1.29 (F=2.53ns)	-1.91 (F=2.74ns)		-2.27 (F=2.52ns)		0.002	0.40
Alphaproteobacteria	Richness (May)	-6.99 (F=4.19ns)	-13.74 (F=4.31*)	-7.19 (F=4.43*)					0.009	0.29
Deltaproteobacteria	Richness	-2.74	-2.34	-1.02		°			0.0001	0.51

	(May)	(F=21.34***)	(F=5.45*)	(F=2.98ns)				
Gammaproteobacteria	Richness	-7.46	-4.47	-1.59	-2.22	-3.71	0.03	0.27
	(May)	(F=5.53*)	(F=1.30ns)	(F=0.59ns)	(F=0.64ns)	(F=1.14ns)		
Acidobacteria	Evenness	-0.014	-0.04		0.03		0.02	0.047
	(May)	(F=2.62ns)	(F=6.44*)		(F=4.98*)		(F=2.37ns)	0.22
Alphaproteobacteria	Evenness				0.01		-0.006	0.006
	(May)				(F=8.85**)		(F=2.45ns)	0.28
Fungi								
Glomeromycotina	Richness				-1.15	1.08	1.13	0.0005
	(March)				(F=7.13*)	(F=10.34**)	(F=4.42*)	0.37
Zygomycota	Richness			1.03	-1.56		1.35	0.006
	(March)			(F=4.62*)	(F=7.75*)		(F=4.62ns)	0.26
Ascomycota	Evenness				0.02			0.04
	(March)				(F=6.98*)			0.14
Basidiomycota	Evenness					-0.05		0.03
	(March)					(F=7.53*)		0.14
Chytridiomycota	Evenness	0.05					0.06	0.02
	(March)	(F=6.89*)					(F=2.84ns)	0.17
Zygomycota	Evenness	0.02	0.02		-0.05	0.035		0.02
	(March)	(F=1.16ns)	(F=0.77ns)		(F=9.27**)	(F=3.19ns)		0.22
Chytridiomycota	Richness	0.009	-0.795		1.09	0.64		0.025
	(May)	(F=0.0005ns)	(F=2.23ns)		(F=8.71**)	(F=2.11ns)		0.21
Ascomycota	Evenness	-0.011			0.02			0.0003
	(May)	(F=7.30*)			(F=16.06***)			0.36

Table S4 Results of the canonical correspondence analyses testing the effect of environmental parameters on microbiota assemblages. Proportion of the inertia explained by the environmental parameters, statistical results of the analysis of variance (ANOVA type II) analyses (Chi-square test and p-value: (t): p < 0.1; * p < 0.05; ** p < 0.01; *** p < 0.001). A1mgt and A2mgt: Coordinates along axis 1 and 2 of PCA based on the management parameters; A1soil and A2soil: Coordinates along axis 1 and 2 of PCA based on the soil parameters; A1flo and A2flo: Coordinates along axis 1 and 2 of PCA based on the plant diversity parameters. All the variables were calculated at the field scale (N=34 for bacteria in March, N=29 for bacteria in May; N=35 for fungi).

	Constrained proportion	Environmental parameters						
		A1mgt	A2mgt	A1soil	A2soil	A1flo	A2flo	
Bacteria								
<i>March</i>								
Acidobacteria	34.8	1.21	1.67	34.18***	23.08***	0.54	1.53	
Actinobacteria	26.2	0.31	3.69	4.08*	2.25	0.03	3.69	
Bacteroidetes	22.9	4.01*	4.11*	7.68**	32.58***	0.17	3.10	
Firmicutes	31.9	0.01	2.40	15.96***	6.67**	2.74	1.12	
Alphaproteobacteria	26.9	2.21	2.58	8.76**	17.96***	0.05	3.11	
Deltaproteobacteria	26.0	1.39	2.28	1.34	25.92***	1.00	3.23	
Gammaproteobacteria	20.6	0.08	1.52	28.71***	9.61**	1.47	0.14	
<i>May</i>								
Acidobacteria	49.8	3.75	4.55*	0.10	5.22*	1.05	4.47*	
Actinobacteria	37.3	9.86**	1.43	0.01	1.23	0.48	0.66	
Bacteroidetes	26.2	0.48	1.71	0.45	6.40*	5.55*	0.002	
Firmicutes	25.4	0.27	0.41	3.51	0.83	0.61	0.01	
Alphaproteobacteria	30.6	0.27	0.06	2.75	26.83***	1.21	0.35	
Deltaproteobacteria	25.9	2.16	0.90	1.13	12.51**	2.33	0.07	
Gammaproteobacteria	27.6	3.67	3.97*	0.66	32.11***	0.14	6.72**	
Fungi								
<i>March</i>								
Ascomycota	16.3	0.74	3.74	0.34	2.85	2.68	3.53	
Basidiomycota	20.2	4.83*	14.25***	1.83	10.59**	0.001	6.53*	
Chytridiomycota	12.4	1.47	0.46	4.43*	7.32**	4.85*	0.04	
Glomeromycotina	13.1	2.58	0.26	0.87	1.94	0.71	0.001	
Zygomycota	18.5	1.49	0.33	0.41	4.17*	0.52	0.70	
<i>May</i>								
Ascomycota	18.3	6.36*	1.89	0.69	10.45**	0.005	0.06	
Basidiomycota	21.9	2.14	0.20	0.26	25.84***	0.13	0.88	
Chytridiomycota	29.6	10.56**	13.53***	0.05	1.32	1.32	9.99**	
Glomeromycotina	32.2	3.13	11.87***	0.03	3.59	3.86*	23.35***	
Zygomycota	22.6	7.59**	0.86	0.02	14.64***	2.56	3.51	