

Supplementary Materials

Table S1. Primer set selected for the quantification of the main groups of microorganisms evaluated in this study.

Target Gene	Primer set name	Sequence (5' to 3')	Length (bp)	Reference
Bacteria 16S	341 F	CCTACGGGAGGCAGCAG	174	López Gutierrez et al. 2004 [39]
	515 R	ATTCCGCGGCTGGCA		
Fungal ITS4-5	ITS5F	GGAAGTAAAAGTCGTAACAAGG	651	Schoch et al. 2012 [41]
	ITS4R	TCCTCCGTCTATTGATATGC		
Glomeromycetes (SSU rRNA)	AML1	ATCAACTTTCGATGGTAGGATAG A	800	Lee et al 2008 [38]
	AML2	GAACCCAAACACTTTGGTTTCC		
Archaea 16S	Arc771 F	ACGGTGAGGGATGAAAGCT	220	Ochsenreiter et al. 2003 [40]
	Arc 957 R	CGGCGTTGACTCCAATTG		

Table S2. Selected properties at the end of the cover crops in the rotations with (a) maize and with (b) wheat.

(a) Rotation with maize

Cover Crop	Previous CaC	CC Biomass (kg ha ⁻¹)		Soil Coverage (%)		AMF Colonization (%)		Mycelium Length (cm g ⁻¹)	
CON	Maize	0	±0*	0.0	±0.0*	0.0	±0.0*	4.02	±1.72 a
VET	Maize	926	±440 ab	73.0	±8.7 a	35.5	±14.0 d	6.43	±1.44 b
MEL	Maize	617	±83 a	70.0	±8.6 a	26.8	±10.9 bc	5.89	±0.55 ab
BAR	Maize	1321	±265 c	72.0	±11.2 a	20.1	±9.2 ab	12.47	±0.37 c
B+V	Maize	835	±311 a	69.2	±5.2 a	16.6	±4.9 a	4.31	±0.58 a
B+M	Maize	1273	±602 bc	68.4	±8.2 a	32.6	±5.2 cd	4.65	±1.70 a

(b) Rotation with wheat

Cover Crop	Previous CaC	CC Biomass (kg.ha ⁻¹)		Soil Coverage (%)		AMF Colonization (%)		Mycelium Length (cm g ⁻¹)	
CON	Wheat	0	±0.0*	0.0	±0.0*	0.0	±0.0	7.12	±1.82 b
VET	Wheat	963	±310 b	78.8	±6.1 b	24.9	±12.8 a	4.61	±1.77 a
MEL	Wheat	442	±284 a	71.6	±11.2 ab	37.3	±12.7 b	8.34	±1.11 b
BAR	Wheat	1132	±388 b	76.8	±6.5 b	22.0	±12.3 a	8.50	±1.37 b
B+V	Wheat	1104	±288 b	64.2	±5.6 a	21.9	±12.0 a	4.76	±0.72 a
B+M	Wheat	902	±351 b	74.4	±7.5 b	35.7	±10.4 b	3.56	±0.84 a

*; This treatment did not has cover crop and its cover crop biomass, soil coverage and arbuscular mycorrhizal colonization were "0". ±; standard deviation of each mean (without take into account the block factor). Different letters after the means indicate significant differences with $p < 0.05$ according to LSD and after applying the generalized linear model and taking into account the block factor; CON: control without CC; VET: vetch; MEL: melilotus; BAR: barley; B+V: barley with vetch and B+M: barley with melilotus.

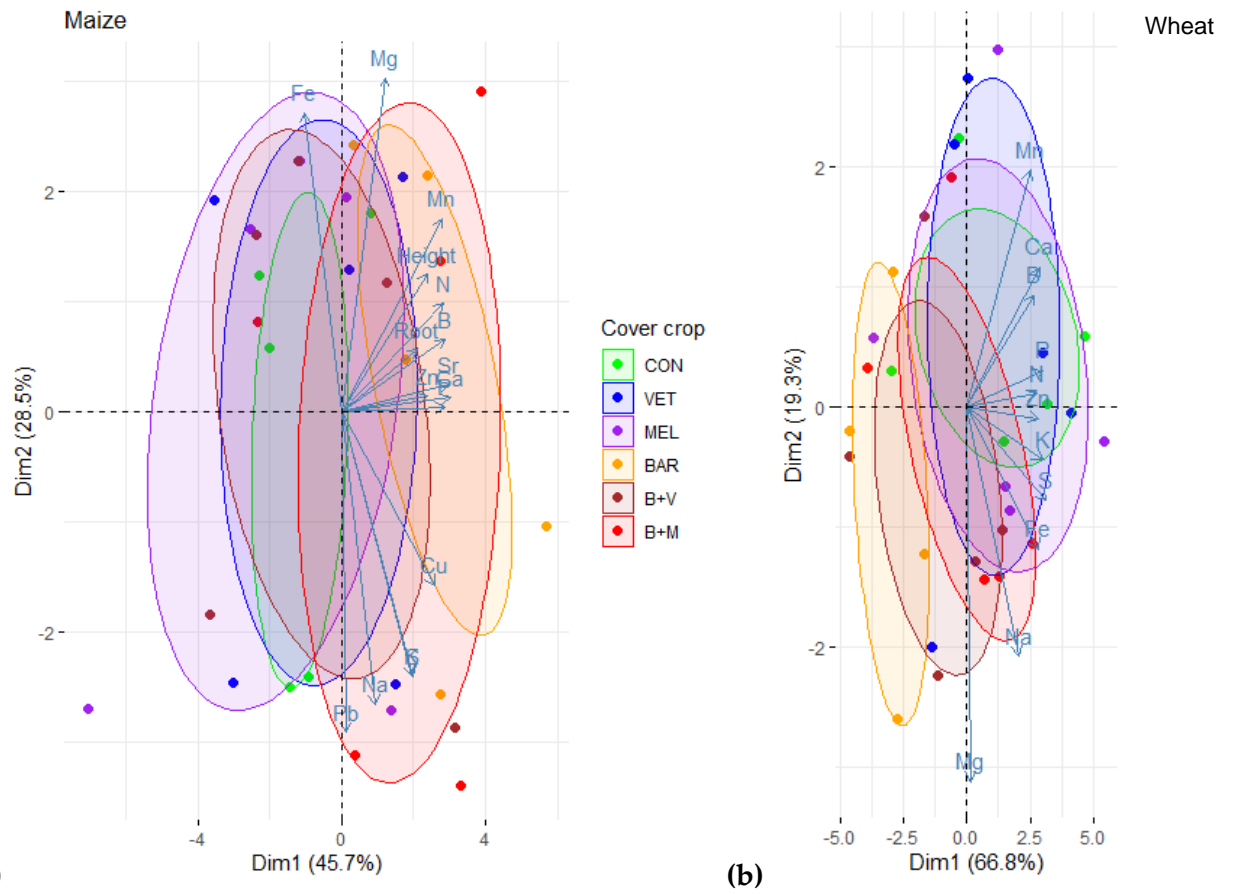


Figure S1. Principal component analysis biplot of macro and micro nutrients and confidence ellipses of each treatment in (a) maize shoots and (b) in wheat shoots.