

Supplementary Materials

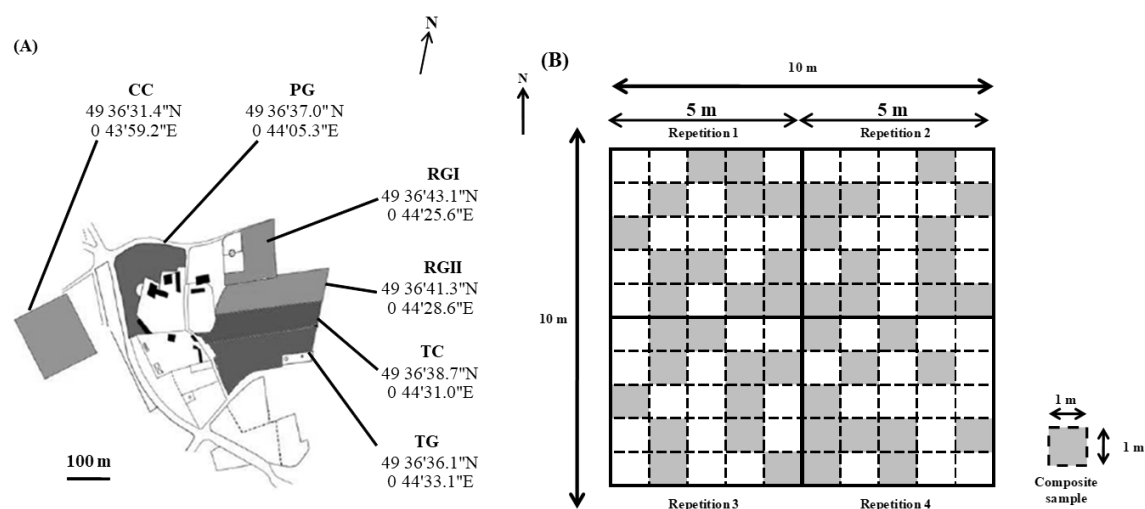


Figure S1. Plots positions in the area of the study (A) and sampling protocol (B).

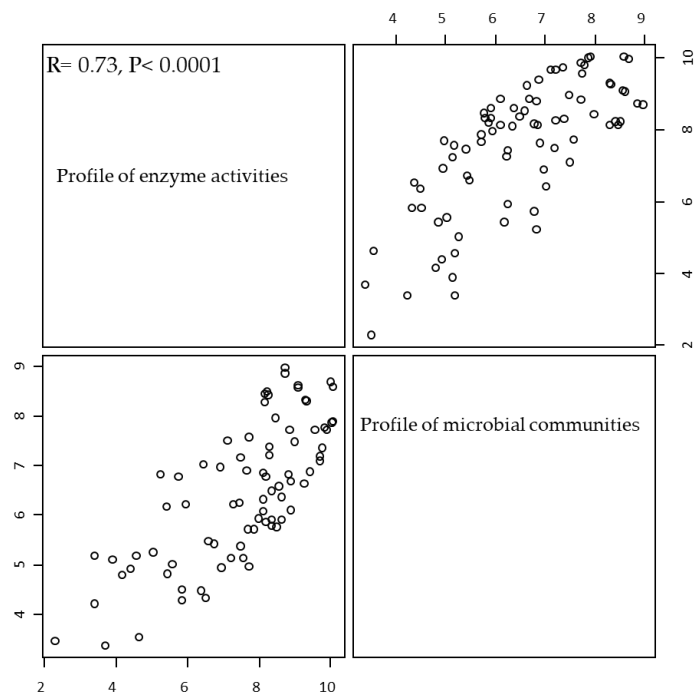


Figure S2. Correlation between microbial abundance and enzyme activities profiles

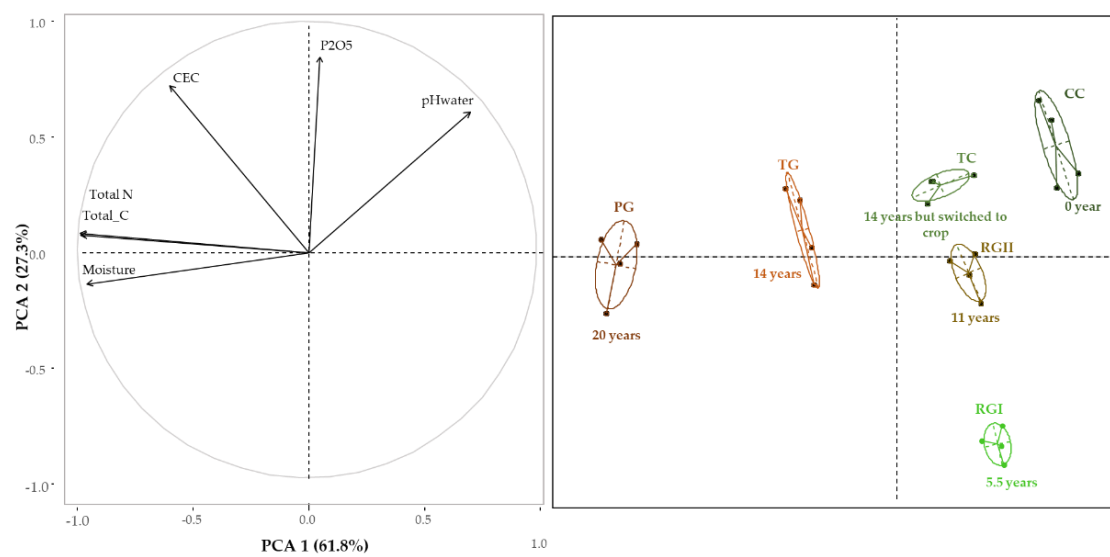


Figure S3. Principal component analysis and correlation circle of plots physicochemical

Table S1. Physicochemical characteristics explaining the variation of the abundance of microbial communities and enzyme activities by multiple regression analysis

	Total C	Total N	pH _{water}	CEC	P ₂ O ₅	Full model ¹	
	<i>P</i> <i>value</i>	<i>P</i> <i>value</i>	<i>P</i> <i>value</i>	<i>P</i> <i>value</i>	<i>P value</i>	(R) %	<i>P value</i>
Microbial communities							
Total dsDNA (µg g ⁻¹)	<0.01	ns	ns	ns	ns	68	<0.0001
Total microbial PLFA (nmol g ⁻¹)	ns	ns	ns	ns	ns	87	<0.0001
Microbial biomass carbon (mg C Kg ⁻¹)	ns	ns	ns	ns	ns	97	<0.0001
Bacterial dsDNA (µg g ⁻¹)	ns	ns	ns	ns	ns	58	<0.001
Total bacterial PLFA (nmol g ⁻¹)	ns	ns	ns	ns	ns	87	<0.001
Fungal dsDNA (µg g ⁻¹)	<0.01	<0.001	<0.01	<0.01	<0.01	55	<0.0001
Total fungal PLFA (nmol g ⁻¹)	<0.01	ns	ns	ns	ns	82	<0.0001
Total ergosterol (µg g ⁻¹)	ns	ns	<0.01	ns	ns	71	<0.0001
Free ergosterol (µg g ⁻¹)	<0.01	ns	ns	ns	ns	72	<0.0001
Global enzymes							<0.0001
DEH	ns	ns	ns	ns	ns	71	<0.0001
FDA	<0.01	<0.01	ns	ns	<0.01	68	<0.0001
C cycle enzymes							<0.0001
GAL	<0.05	ns	<0.01	ns	ns	94	<0.0001
GLU	ns	ns	<0.01	<0.05	<0.05	76	<0.0001
CEL	ns	ns	<0.001	ns	ns	88	<0.0001
LAC	ns	ns	ns	ns	ns	64	<0.0001
LIP	<0.05	ns	ns	ns	<0.01	91	<0.0001
XYL	ns	ns	ns	ns	ns	91	<0.0001
N cycle enzymes							<0.0001
ARYLN	ns	ns	<0.05	ns	ns	78	<0.0001
NAG	ns	ns	<0.01	ns	ns	91	<0.0001
URE	ns	ns	<0.05	ns	ns	96	<0.0001
S cycle enzyme							<0.0001
ARYLS	<0.01	<0.05	<0.0001	ns	ns	98	<0.0001
P cycle enzymes							<0.0001
ACP	<0.001	ns	ns	ns	ns	93	<0.0001
AKP	<0.05	<0.05	ns	ns	ns	35	>0.05

¹Full model include all physicochemical characteristics (total C, total N, pH_{water}, CEC, P₂O₅) as explicative variables; ns : indicates not significant