

บทความที่น่าสนใจประจำเดือนพฤษภาคม 2557

สาขาวิทยาศาสตร์และเทคโนโลยี

1	Title:	Bacterial community structure in fumigated soil
	Author:	Cristina A. Domínguez-Mendoza, Juan M. Bello-López, Yendi E. Navarro-Noya, Arit S. de León-Lorenzana, Laura Delgado-Balbuena, Selene Gómez-Acata, Victor M. Ruiz-Valdiviezo, Daniel A. Ramirez-Villanueva, Marco Luna-Guido, Luc Dendooven
	Journal:	Soil Biology and Biochemistry, Volume 73, June 2014, Pages 122–129
	Abstract:	<p>Soil microbial biomass has been determined since the mid 1970's by the chloroform fumigation incubation technique as proposed by Jenkinson and Powlson (1976). The microbial biomass C can be determined by subtracting the CO₂ emitted from an unfumigated soil (mineralization of soil organic matter) from that emitted from a chloroform fumigated inoculated soil (mineralization of soil organic matter and killed soil microorganisms) and dividing the difference by a proportionality factor (kC = 0.45). The question remained which microorganisms recolonized a fumigated soil. An arable soil was fumigated for one day with ethanol-free chloroform or left unfumigated and incubated aerobically after removal of the chloroform for 10 days. The bacterial population structures were determined in the fumigated and unfumigated soil after 0, 1, 5 and 10 days by means of 454 pyrosequencing of the 16S rRNA gene. Fumigating the arable soil reduced significantly the relative abundance of phylotypes belonging to different groups, but increased the relative abundance of only four genera belonging to two phyla (Actinobacteria and Firmicutes) and two orders (Actinomycetales and Bacillales). The relative abundance of phylotypes belonging to the Micromonospora (Micromonosporaceae) increased significantly from 0.2% in the unfumigated soil to 6.7% in the fumigated soil and that of Bacillus (Bacillaceae) from 3.6% to 40.8%, Cohnella (Paenibacillaceae) from undetectable amounts to 0.6% and Paenibacillus (Paenibacillaceae) from 0.3% to 4.2%. The relative percentage of phylotypes belonging to the Acidobacteria, Bacteroidetes, Chloroflexi, Gemmatimonadetes and Proteobacteria (α-β-, δ- and γ-Proteobacteria) were significantly lower in the fumigated than in the unfumigated soil and in most of them the relative abundance of different bacterial orders (i.e. Gp3, Gp4, Gp6, Sphingobacteriales, Gemmatimonadales, Rhodospirillales, Burkholderiales, Xanthomonadales) was reduced strongly ($P < 0.001$). It was found that the relative abundance of a wide range of bacteria was reduced shortly after fumigating an arable soil, but only a limited group of bacteria increased in a fumigated arable soil indicating a capacity to metabolize the killed soil microorganisms or recolonize a fumigated soil.</p>
	Database:	ScienceDirect

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Title:	A theoretical analysis of microbial eco-physiological and diffusion limitations to carbon cycling in drying soils
Author:	S. Manzoni, S.M. Schaeffer, G. Katul, A. Porporato, J.P. Schimel
Journal:	Soil Biology and Biochemistry, Volume 73, June 2014, Pages 69–83
Abstract:	Soil microbes face highly variable moisture conditions that force them to develop adaptations to tolerate or avoid drought. Drought conditions also limit the supply of vital substrates by inhibiting diffusion in dry conditions. How these biological and physical factors affect carbon (C) cycling in soils is addressed here by means of a novel process-based model. The model accounts for different microbial response strategies, including different modes of osmoregulation, drought avoidance through dormancy, and extra-cellular enzyme production. Diffusion limitations induced by low moisture levels for both extra-cellular enzymes and solutes are also described and coupled to the biological responses. Alternative microbial life-history strategies, each encoded in a set of model parameters, are considered and their effects on C cycling assessed both in the long term (steady state analysis) and in the short term (transient analysis during soil drying and rewetting). Drought resistance achieved by active osmoregulation requiring large C investment is not useful in soils where growth in dry conditions is limited by C supply. In contrast, dormancy followed by rapid reactivation upon rewetting seems to be a better strategy in such conditions. Synthesizing more enzymes may also be advantageous because it causes larger accumulation of depolymerized products during dry periods that can be used upon rewetting. Based on key model parameters, a spectrum of life-history strategies thus emerges, providing a possible classification of microbial responses to drought.
Database:	ScienceDirect

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Title:	Quantifying the impact of microbes on soil structural development and behaviour in wet soils
Author:	J.R. Helliwell, A.J. Miller, W.R. Whalley, S.J. Mooney, C.J. Sturrock
Journal:	Soil Biology and Biochemistry, Volume 74, July 2014, Pages 138–147
Abstract:	There is evidence that microbial populations play an important role in altering soil pore geometry, but a full understanding of how this affects subsequent soil behaviour and function is still unclear. In particular the role of microorganisms in soil structural evolution and its consequence for pore morphological development is lacking. Using a combination of bio-chemical measurements and X-ray Computed Tomography (CT) imaging, a temporal comparison of microscale soil structural development in contrasting soil environments was made. The aim was to quantify the effect of microbial activity in the absence of other features likely to cause soil deformation (e.g. earthworms, roots etc.) on soil structural development in wet soils, defined by changes in the soil porous architecture i.e. pore connectivity, pore shape and pore volume during a 24 week period.

	Three contrasting soil textures were examined and changes compared between field soil, sterilised soil and a glucose enhanced soil treatment. Our results indicate that soil biota can significantly alter their microhabitat by changing soil pore geometry and connectivity, primarily through localised gaseous release. This demonstrates the ability of microorganisms to modify soil structure, and may help reveal the scope by which the microbial-rich rhizosphere can locally influence water and nutrient delivery to plant roots.
Database:	ScienceDirect

4	Title:	Determination of enzymatic activities using a miniaturized system as a rapid method to assess soil quality
	Author:	R. Boluda, L. Roca-Pérez, M. Iranzo, C. Gil and S. Mormeneo
	Journal:	European Journal of Soil Science, Volume 65, Issue 2, pages 286–294, March 2014
	Summary:	Soil quality determination requires the analysis of a number of soil attributes using different approaches. In recent years, one of the most promising approaches has been the determination of enzymatic activities. Generally, only a few enzymes have been analysed and related to other soil properties such as total carbon, nitrogen content or microbial biomass carbon. The aim of this work was to investigate the possible use of the API ZYM strip, a semi-quantitative miniaturized system that determines 19 enzymatic activities, to study soil quality. To this end, we tested the system in different soil types, including albic Arenosols, mollic Leptosols, rendzic Leptosols, haplic Leptosols and calcareic Regosols. Fresh samples were sieved through a 2-mm sieve in the field and soil extracts were prepared by mixing 2–20 g (depending on the soil horizon characteristics) from each sample with 2–20 ml of sterile water. Next, 65- μ l aliquots of the supernatant extract were placed into each API ZYM microtube and were incubated at 37°C for 16 hours. Our results show important qualitative and quantitative differences among the different soil types studied, with soil characteristics and biological properties correlating with biochemical information. The results provide useful information not only to determine soil quality, but also to assess changes in the soil environment. As a whole, our results suggest that the use of the API ZYM system could prove most useful in soil environmental studies. Finally, some suggestions are presented, including modifications to the system that could improve its application in this field.
	Database:	Wiley Online Library

5	Title:	Modelling the impacts of maize decomposition on glyphosate dynamics in mulch
	Author:	Aslam, S., Benoit, P., Chabauty, F., Bergheaud, V., Geng, C., Vieublé-Gonod, L. and Garnier, P.
	Journal:	European Journal of Soil Science, Volume 65, Issue 2, pages 231–247, March 2014

Summary:	The retention of crop residues as mulch on the soil surface in conservation agriculture systems greatly influences the fate of pesticides, as most of the applied pesticide is intercepted by mulch before moving to the soil. This work was conducted in order to model the effect of maize decomposition on glyphosate degradation in mulch and soil. Labelled ¹⁴ C-glyphosate degradation was monitored for 49 days in three treatments with the same soils but with maize residues at different stages of decomposition (0, 20 and 49 days). Fresh residues of maize (0 days) exhibited an evolution of their biochemical fractions to a greater extent than decomposed residues. Glyphosate mineralization was faster in the 0-day treatment in mulch residues and in the soil layer below the mulch. However, a greater formation of non-extractable residues (NERs) was observed in mulch residues and soils in the 20- and 49-day treatments than in the 0-day treatment. Modelling maize mulch decomposition with the COP-soil model indicated that microbial activity was different in the three treatments and depended on the initial composition of maize residues. Glyphosate mineralization in mulch and soil can be simulated with an assumption of co-metabolism by coupling the modules of pesticide degradation and mulch carbon decomposition. Glyphosate and its metabolites, including soluble and adsorbed fractions, were simulated with the same adsorption coefficients for all treatments. The simulation of NER formation, however, suggested that more than one microbial population may be involved in the degradation process and could be added in the future development of the model.
Database:	Wiley Online Library

6	Title:	Aggregation kinetics of natural soil nanoparticles in different electrolytes
	Author:	Zhu, X., Chen, H., Li, W., He, Y., Brookes, P. C. and Xu, J.
	Journal:	European Journal of Soil Science, Volume 65, Issue 2, pages 206–217, March 2014
	Summary:	In the space of just a few years, nanotechnology has become a topical subject not only in academia, but also in the daily lives of people. In order to investigate the properties of natural nanoparticles (NNPs) and to obtain a better understanding of their environmental behaviour and impacts from a new perspective, transmission electron microscope (TEM), zeta potential analysis and time-resolved dynamic light scattering (DLS) analysis were used to examine the main properties and aggregation kinetics of NNPs extracted from Chinese soils added to various concentrations of the electrolytes NaCl, CaCl ₂ and LaCl ₃ . The NNPs that were less than 100 nm remained stable for 100 days. The classic Derjaguin-Landau-Verwey-Overbeek (DLVO) model partially revealed the aggregation behaviour of NNPs, in which ionic strength, composition and size may play important roles. The influence of hematite and natural organic matter (NOM) was demonstrated by aggregation kinetics and critical coagulation concentrations (CCC). The size of NNPs could also change the maximum total potential energy of interactions in the systems (VT(h)). These factors make the aggregation of

	NNPs in electrolytes different from that of soil colloids and influence the environmental behaviour of NNPs.
Database:	Wiley Online Library

7	Title:	Natural variation in the regulation of leaf senescence and relation to N and root traits in wheat
	Author:	K. B. Hebbar, J. Rane, S. Ramana, N. R. Panwar, S. Ajay, A. Subba Rao, P. V. V. Prasad
	Journal:	Plant and Soil, May 2014, Volume 378, Issue 1-2, pp 99-112
	Abstract:	<p>Objectives</p> <p>To identify parameters that can be used for the analysis of natural variation in leaf senescence of wheat; and to understand the association between the onset and progression of leaf senescence with N uptake and root traits.</p> <p>Methods</p> <p>Chlorophyll content and the proportion of yellow leaves were used as senescence indicators and their relation with other morphological and physiological traits were measured in contrasting early senescing (ES) and late senescing (LS) wheat lines.</p> <p>Results</p> <p>There were significant genotype effects on the onset and progress of senescence. The ES lines in which leaf senescence commenced early had significantly lower root biomass and N uptake than LS lines. The strong negative association between the extent of leaf senescence with root biomass and N uptake indicated that the poor root growth induced N limitation caused the early senescence of ES lines.</p> <p>Conclusions</p> <p>The leaf senescence development in ES lines was precocious and constitutive as the trait expressed even under optimal growth conditions suggesting they could be useful in understanding the genetic regulation of senescence under different abiotic stress situations. Accelerated leaf senescence in wheat could be a mechanism to compensate for limitations in the root system that tend to restrict nutrient uptake.</p>
	Database:	SpringerLink

8	Title:	Carbon mineralization in soil of roots from twenty crop species, as affected by their chemical composition and botanical family
	Author:	Marciel Redin, René Guénon, Sylvie Recous, Raquel Schmatz, Luana Liberalesso de Freitas, Celso Aita, Sandro José Giacomini
	Journal:	Plant and Soil, May 2014, Volume 378, Issue 1-2, pp 205-214

Abstract:	<p>Background and aims</p> <p>Our objective was to relate chemical composition of roots of a wide range of annual crops to root decomposition, so as to assess roots potential contribution to soil carbon (C).</p> <p>Methods</p> <p>Roots from 20 different crops and 4 botanical families, collected under field conditions were incubated in soil for 120 days at 25 °C. The initial chemical composition of roots was determined. The C mineralization was assessed by the continuous measurement of CO₂ release and using single exponential model. PCA analysis was used to explore qualitative pattern in root quality and decomposition.</p> <p>Results</p> <p>PCA analysis showed that chemical characteristics (traits) differentiated plant families. The mineralization of root C varied greatly in terms of kinetics and in the total amount of C mineralized (36 % to 59 % of added C). Mineralization constant (k value) was negatively correlated with hemicelluloses and positively with N content. Poaceae roots that combined high hemicelluloses, low cellulose and low total N, showed low degradation rate and cumulative C mineralization.</p> <p>Conclusions</p> <p>The chemical composition of roots, as for the above-ground parts of plants, can correctly predict their rate of decomposition in soils. The taxonomic affiliation enhances the understanding of the chemical determinants of quality of roots.</p>
Database:	SpringerLink

9	Title:	Kinetics of short-term carbon mineralization in roots of biofuel crops in soils
	Author:	F. A. Rivas, M. A. Tabatabai, D. C. Olk, M. L. Thompson
	Journal:	Biology and Fertility of Soils, April 2014, Volume 50, Issue 3, pp 527-535
	Abstract:	<p>Various crops have been used for energy production while striving to maintain C storage derived from roots in soils. To better understand and document the rates of root decomposition in biofuel cropping systems, we compared the evolution of CO₂ from roots incubated with samples of two Iowa Mollisols (Clarion and Nicollet). Root samples were collected from experimental plots for four cropping systems: a multispecies reconstructed prairie, grown with and without N fertilization, and continuous corn, grown with and without a ryegrass cover crop. Major structural components of the root samples (lignin, cellulose, and hemicellulose) as well as chemical composition (total C and N) were assessed. The root materials were incubated for 30 days at room temperature (22 °C) by using an incubation apparatus with continuous airflow. The decomposition rates and half-lives of rapidly and slowly decomposable C fractions were calculated by fitting a two-component first-order kinetic model to the data. Mineralizable C ranged from 7 to 13 % of the added C. When the data for the two</p>

	<p>soils were combined, the CO₂-C evolved was positively correlated with both the C/N ratio ($r = 0.88^{**}$, $p < 0.01$) and the lignin/N ratio ($r = 0.89^{**}$, $p < 0.01$) of the roots. For the Clarion soil, first-order decomposition rate constants for the rapid fraction ranged from 0.07 to 0.69 day⁻¹, whereas for the Nicollet soil they ranged from 0.09 to 0.66 day⁻¹. For both soils, the half-lives of the rapidly decomposable fraction ranged from 1 to 10 days, and half-lives of 204 to 770 days were observed for the slowly decomposable fractions. Among the cropping systems studied, the rapidly decomposable fraction of roots derived from the unfertilized prairie treatment was the largest. Those root residues also had the highest hemicellulose index and higher concentrations of arabinose, galactose, glucose, and xylose sugars than did roots of the other crops. Other decomposition parameters, such as the decomposition rates and half-lives obtained from the two-component model, were not correlated with the root composition parameters studied. Our results suggest that lignin did not inhibit the early rate of root C mineralization in mixed perennial crops. That information could be useful in refining models of root C dynamics in daily time steps or at the scale of a single growing season.</p>
Database:	SpringerLink

10	Title:	Interactions between proteins and humic substances affect protein identification by mass spectrometry
	Author:	Mariarita Arenella, Laura Giagnoni, Grazia Masciandaro, Brunello Ceccanti, Paolo Nannipieri, Giancarlo Renella
	Journal:	Biology and Fertility of Soils, April 2014, Volume 50, Issue 3, pp 447-454
	Abstract:	<p>Soil proteomics is facing problems such as low yields of protein extraction from soil and low protein identification rates as compared to theoretical estimates of soil proteome. This work aimed to evaluate the effect of soil-borne humic substances (HS) on the identification of model proteins with different properties, such as myoglobin (Mb), α-glucosidase (αG), and β-glucosidase (βG), by using electrophoretic and ESI- and MALDI-mass spectrometry (MS) methodologies. Results showed that the contact between proteins and HS did not alter protein electrophoretic mobility but led to protein modifications that affected protein identification by MS. The decrease in protein identification parameters was more evident for Mb than for αG and βG, probably due to its lower molecular weight and less complex molecular structure. Analysis of MS data indicated that hydrophobic interactions could be responsible for the observed effects of contact between proteins and HS.</p>
	Database:	SpringerLink