INTEGRATION OF MICROORGANISMS INTO THE FLOWS OF GRASSLAND AND FOREST ECOSYSTEMS

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Abstract
Terrestrial ecosystems are dominated by higher plants as major biomass producers. Microorganisms present in the soil complete the energy and carbon circuits, mediating information and substance fluxes in plant-soil system. Bacteria and Actinomycetes act as successional groups, populations having dimensions directly proportional with the pressure of ecological factors. Heterotrophy and autotrophy succeed each other, due to the amount of substances present in ecosystem, the way it is arranged influencing aero-anaerobiosis processes. Geographic gradients work in complex with management to select a flora adapted to the specific conditions of each ecosystem.

Keywords: grasslands, soil, bacteria, biogeochemical circuits

INTRODUCTION

In terrestrial ecosystems, primary biomass producers are superior plants, releasing energy and carbon in the soil through roots and dead vegetal biomass (Jorgensen and Fath, 2014; i Guillén and Camarasa, 2000). Primary decomposers in these ecosystems are bacteria and fungi, at the base of the trophic chain as food for protozoa and nematodes (Maboreke *et al.*, 2018).

The key position of microorganisms in the food chain, the reduced size and the high surface / volume ratio make them have a high affinity for low concentrations of substrates present in ecosystem (Cotner and Biddanda, 2002; Schulz *et al.*, 2013). Because of this, they are particularly sensitive and respond quickly to the occurrence of environmental pressors or contaminants, even at low concentrations (Classen *et al.*, 2015; Grenni *et al.*, 2018; Zhang *et al.*, 2016).

Grasslands and forests are ecosystems spread across all types of eco-regions, with a high dynamics of the processes for matter transformation (Chapin, 2003; Hillel and Hatfield, 2005). Plant diversity in the vegetation cover is completed by an infinite variety of microorganisms, with a role in mediating information and material flows between plants and soil (Lange *et al.*, 2014).

Microorganisms possess the unique feature of being invisible to the eye, with dimensions of 0.2 - 200 μm. The global distribution of these microscopic organisms is at the level of each ecosystem due to the evolutionary adaptation to any living environment (Hibbing *et al*., 2010; Ponomarova and Patil, 2015). The most complex and abundant microbial group is that of bacteria with a high metabolic capacity and use of a high variety of substrates.

Adaptation of the rhizospheric potential of plants to microbial functional groups has led to a selection of organisms directed towards the equilibrium and temporal stability of grasslands (Jacoby *et al*., 2017; Paul, 2014).

INTEGRATION OF MICROORGANISMS IN SOIL PROCESSES

For evaluating a whole ecosystem, the stresses due to eutrophication, drought, acidification or the impact of human management are considered. The direct effect of environmental changes include the reduction of biodiversity, and the modification of vital functions related to the use and conversion of nutrients, which requires the selection of high sensitivity indicators (Amedie, 2013; Bellard *et al*., 2012).

Forest ecosystems are dominated by tall species, which translates into a lower amount of light at ground level. The lack of light and the high amount of leaves the trees have left on the surface of the soil is more difficult to decompose by the microbial community over a much longer period of time (Sayer, 2006). In terms of microbial diversity, forests are dominated by fungi, these microorganisms being more effective in degrading wood biomass and especially lignin. In direct contact with the roots of the plants there are ectomycorrhizal fungi, capable of symbiosis and extension of the root system of the trees (Johnson and Gehring, 2008; Smith and Read, 1997). These fungi have the role of absorbing nutrients and transferring them to the trees, receiving instead products synthesized from photosynthesis processes.

The presence of microorganisms in the functional processes of terrestrial ecosystems offers the perspective of a phenomenon of orientation plant diversity toward values related to the transfer processes (Taylor *et al*., 2014). At the same time, plant diversity is an activator of microbial diversity by enhancing the diversity of nutritional resources as a result of the export of root exudates into the soil and of plant decomposition resources.

For the fungal component, capable of symbiotic partnerships with plant rhizosphere, diversity is directly correlated with the number of species present in the ecosystem (Hassani *et al*., 2018; Steinauer *et al*., 2016).

Interaction with microorganisms is one of the crucial components of a plant's presence in an ecosystem. From a plant perspective, dominant species tend to apply a high selection pressure to microorganisms, stimulating the emergence of a microflora with high functionality for their own requirements (Bardgett *et al*., 2005;Bever *et al*., 2012; Nolan *et al*., 2015).

From the perspective of microbial community, the pressure applied in the rhizosphere is balanced between species and stimulates the conservation of plants diversity. The properties of the dominant species, in conditions of reduction of the floristic diversity, act in complex with its own microbial component and create negative changes in the functioning of the meadows; the synergistic interactions between the microbial component and the high diversity of plants are located at the opposite end, leading to an incentive for biomass production and efficient use of resources (Allan *et al*., 2011; Hedlund *et al*., 2003; Uddin and Robinson, 2017; Wohlgemuth *et al.,* 2016). Increasing the level of CO_2 in the atmosphere produces strong changes in the microbial specificity of the meadows, altering the operation of related processes in the soil. Microbial diazotrophic communities in areas with higher amounts of CO_2 react by attracting and stimulating the activity of non-symbiotic N_2 fixation, which leads to a change in the natural ratio between the two types of functional groups (Santi *et al*., 2013; Tu *et al*., 2016).

In assessing a grassland or forest ecosystem microorganisms can play a role of bioindicators due to their high genetic diversity, with large differences in microbial populations that architect a community (Cheng *et al*, 2013; Karimi *et al.,* 2017). Another feature is their high abundance in relation to the small dimension, which is a solution of the geometric ladder problem and the direct results reporting at the level of the harvested samples.

CHARACTERISTICS OF THE SOIL MICROFLORA

Soil microorganisms are involved as key factors in transforming matter and making it available for plants. Microbial diversity is high both at group level - bacteria, actinomycetes, fungi, algae - and at the level of processes they carry (Balestrini *et al*., 2015; Gougoulias *et al*., 2014; Kennedy and Gewin, 1997).

Soil bacteria are considered to be the most abundant microorganisms in this area with high diversity, with specific oxygen and substrate requirements: they can be autotrophic or heterotrophic, aerobic, anaerobic or optionally anaerobic (Koorem *et al*., 2014; Lartey, 2006; Meliani *et al*., 2012; Ward, 2011). Within this microbial group a segment of filamentous microorganisms known as actinomycetes has been developed. Both bacteria and actinomycetes are known for their importance in the nutrient circuit and the decomposition of organic contaminants. In addition, they are found in interaction with plants as rhizospheric microorganisms around their roots (Das *et al*., 2007; Dixon and Tilston, 2010; Maheshwari, 2010; de Jesus Sousa and Olivares, 2016). Some of the existing soil populations are pathogenic for plants (*Agrobacterium tumefaciens*) and humans (*Clostridium perfringens* or *Bacillus anthracis*).

At the surface of agar culture media, bacteria form viscous colonies, ranging from colorless colonies to bright colors with orange, yellow or pink tones. On the opposite side, actinomycetes have a filamentous growth which visually differentiates them from bacteria, with white, colony, hard and low pressure-resistant that break easily. *Actinomycetes* are more resistant to water stress, with an ecological advantage over bacteria, especially in arid areas, on dry and alkaline soils.

Cultivating bacteria on culture media are present in the range of 10^7 - 10^8 / g of soil, while all bacterial populations reach 10^{10} individuals / g soil and their diversity / g soil can reach values of over 10,000 species.

These microorganisms are present in soil with generally lower values than bacteria with at least one or two orders of magnitude. Bacterial and dominant actinomycete genres are *Arthrobater*, *Streptomyces*, *Pseudomonas* and *Bacillus*.

Medium cultivation of bacteria from the associated microflora samples (Lv *et al.*, 2014; Reitner and Thiel, 2011; Wei *et al.*, 2017; Yun *et al.*, 2016) is dominated by phylums *Bacteroidetes, Proteobacteria* and *Actinobacteria*. Instead, a monospecific culture analysis shows a dominance of phylums *Actinobacteria, Proteobacteria* (especially *Alphaproteobacteria* and *Deltaproteobacteria,* with a lower level of G*ammaproteobacteria*), respectively *Acidobacteria* and *Bacteroidetes*.

These aspects indicate a different capacity for competition across the microbial community of each species and a higher potential for cultivation of actinomycetes on environments in monospecific cultures.

REACTION OF MICROFLORA TO PRESSORS

Grazing acts to increase the abundance of microorganisms associated with nitrification processes as an immediate response to the manure, but is reduced as a group in the community immediately after the end of this type of activity (Le Roux *et al.*, 2008; Griffiths and Philippot, 2013). Microbial diversity decreases with increasing altitude, especially belowground fungi, but increases as a specificity in high altitude ecosystems (França *et al.*, 2016; Siles and Margesin, 2017). Increasing the altitude gradient stimulates the installation of autotrophic microorganisms as the dominant group in the soil microflora, a phenomenon correlated positively with the capture of a higher amount of CO_2, visible in alpine grasslands. The lower amount of plant biomass and the origin of a small variety of species act more strongly to reduce the abundance of microorganisms than to reduce diversity, which means that the latitudinal and longitudinal gradients have a lower effect than the altitude on the composition of microbial community in soil.

The installation of certain microbial taxa as dominant in the grasslands is correlated with the local climate and soil pH, while the richness of species is correlated with the annual precipitation level, which imprint to this parameter filter character for microbial architecture (Zuo *et al.*, 2012; Yan *et al.*, 2015; Yashiro *et al.*, 2016; When *et al.*, 2017). Under dominant conditions of a small number of plant species, mycorrhizal microflora can reduce its diversity, but without affecting the symbiotic potential and stimulating plant growth.

Current soil fertility is a much more restrictive parameter for mycorrhizal fungi than for bacteria in the rhizosphere, and the reduction in diversity acts to lower the quality of substrate available to saprophytic fungi and reduces their diversity (Asmelash *et al.*, 201; Denison and Kiers, 2011; Gahan and Schmalenberger, 2014; Philippot *et al.*, 2013; Rillig and Mummey, 2006). An excess of nutrients in soil leads to a change in the community towards tolerant populations of this phenomenon, concealing the ephemeral distribution of microorganisms in relation to the stress factor but enhancing the complexity of the community. A modification of the C and N ratio, especially in grassland ecosystems converted to arable land, propagates in the level of transformation and accumulation of amino acids, reducing the effective functionality of the microbial population complex (Panpatte *et al.*, 2017).

For meadows, the duration of maintenance of a management system imprints a selective dynamics of microbial groups - in stable systems, microbial biomass has higher values, while short-term changes reduce this parameter. Fungal biomass decreases after a period of 10 years in favor of total bacterial biomass (Blagodatskaya and Kuzyakov, 2013; Truu *et al.,* 2009).

A related increase in vesicular-arbuscular fungi and gram negative bacteria biomass indicates an increase in the nutrient circuit in the medium and a stability of microbial mediated processes (Abbasi *et al.*, 2015; Berruti *et al.*, 2016).

At the microbial community level, low abundance taxa are much more distant than the abundant ones, indicating their subsequent occurrence in the ecosystem.

CONCLUSIONS

Taxa present in grassland and forest ecosystems are directly dependent on nutrients and applied management. Geo-positioning amplifies the pressors present in ecosystem, stimulating the emergence of successive biological processes. The complexity of microbial communities is closely related to the carbon / nitrogen ratio and the availability of organic matter.

REFERENCES

1. Abbasi H., Akhta A., Sharf R. (2015) Vesicular Arbuscular mycorrhizal (VAM) fungi: a tool for sustainable agriculture. Am J Plant Nutr Fertil Technol, 5, 40-49.ity composition in constructed wetlands. Science of the total environment, 407(13): 3958-3971.
2. Allan E., Weisser W., Weigelt A., Roscher C., Fischer M., Hillebrand H. (2011) More diverse plant communities have higher functioning over time due to turnover in complementary dominant species. Proceedings of the National Academy of Sciences, 108(41): 17034-17039.
3. Amedie F.A. (2013) Impacts of Climate Change on Plant Growth, Ecosystem Services, Biodiversity, and Potential Adaptation Measure (Doctoral dissertation, MS thesis in Atmospheric Science, University of Gothenburg, Sweden)
4. Asmelash F., Bekele T., Birhane E. (2016) The potential role of arbuscular mycorrhizal fungi in the restoration of degraded lands. Frontiers in microbiology, 7: 1095.

5. Balestrini R., Lumini E., Borriello R., Bianciotto V. (2015) Plant-soil biota interactions. Soil Microbiology, Ecology and Biochemistry, p. 311-338.
6. Bardgett R., Hopkins D., Usher M. (Eds.) (2005) Biological diversity and function in soils. Cambridge University Press.
7. Bellard C., Bertelsmeier C., Leadley P., Thuiller W., Courchamp F. (2012) Impacts of climate change on the future of biodiversity. Ecology letters, 15(4): 365-377.
8. Berruti A., Lumini E., Balestrini R., Bianciotto V. (2016) Arbuscular mycorrhizal fungi as natural biofertilizers: let's benefit from past successes. Frontiers in microbiology, 6: 1559.
9. Bever J.D., Platt T.G., Morton E.R. (2012) Microbial population and community dynamics on plant roots and their feedbacks on plant communities. Annual review of microbiology, 66: 265-283.
10. Blagodatskaya E., Kuzyakov Y. (2013) Active microorganisms in soil: critical review of estimation criteria and approaches. Soil Biology and Biochemistry, 67: 192-211.
11. Chapin III F.S. (2003) Effects of plant traits on ecosystem and regional processes: a conceptual framework for predicting the consequences of global change. Annals of Botany, 91(4): 455-463.
12. Cheng F., Peng X., Zhao P., Yuan J., Zhong C., Cheng Y., Zhang S. (2013) Soil microbial biomass, basal respiration and enzyme activity of main forest types in the Qinling Mountains. PLoS One, 8(6): e67353.
13. Classen A.T., Sundqvist M.K., Henning J.A., Newman G.S., Moore, J.A., Cregger M.A., Patterson C.M. (2015) Direct and indirect effects of climate change on soil microbial and soil microbial-plant interactions: What lies ahead?. Ecosphere, 6(8): 1-21.
14. Cotner J.B., Biddanda B.A. (2002) Small players, large role: microbial influence on biogeochemical processes in pelagic aquatic ecosystems. Ecosystems, 5(2): 105-121.
15. Das M., Royer T.V., Leff L.G. (2007) Diversity of fungi, bacteria, and actinomycetes on leaves decomposing in a stream. Applied and environmental microbiology, 73(3): 756-767.
16. de Jesus Sousa J.A., Olivares F.L. (2016) Plant growth promotion by streptomycetes: ecophysiology, mechanisms and applications. Chemical and Biological Technologies in Agriculture, 3(1): 24.
17. Denison R.F., Kiers E.T. (2011) Life histories of symbiotic rhizobia and mycorrhizal fungi. Current Biology, 21(18): R775-R785.

18. Dixon G.R., Tilston E.L. (Eds.) (2010) Soil microbiology and sustainable crop production. Springer Science & Business Media.
19. França L., Sannino C., Turchetti B., Buzzini P., Margesin R. (2016) Seasonal and altitudinal changes of culturable bacterial and yeast diversity in Alpine forest soils. Extremophiles, 20(6): 855-873.
20. Gahan J., Schmalenberger A. (2014) The role of bacteria and mycorrhiza in plant sulfur supply. Frontiers in plant science, 5: 723.
21. Gougoulias C., Clark J.M., Shaw L.J. (2014) The role of soil microbes in the global carbon cycle: tracking the below-ground microbial processing of plant-derived carbon for manipulating carbon dynamics in agricultural systems. Journal of the Science of Food and Agriculture, 94(12): 2362-2371.
22. Grenni P., Ancona V., Caracciolo A.B. (2018) Ecological effects of antibiotics on natural ecosystems: A review. Microchemical Journal, 136: 25-39.
23. Griffiths B.S., Philippot L. (2013) Insights into the resistance and resilience of the soil microbial community. FEMS microbiology reviews, 37(2): 112-129.
24. Hassani M.A., Durán P., Hacquard S. (2018) Microbial interactions within the plant holobiont. Microbiome, 6(1): 58.
25. Hedlund K., Santa Regina I., Van der Putten W.H., Lepš J., Diaz T., Korthals G.W., ... Rodríguez Barrueco C. (2003) Plant species diversity, plant biomass and responses of the soil community on abandoned land across Europe: idiosyncracy or above-belowground time lags. Oikos, 103(1): 45-58.
26. Hibbing M.E., Fuqua C., Parsek M.R., Peterson S.B. (2010) Bacterial competition: surviving and thriving in the microbial jungle. Nature Reviews Microbiology, 8(1): 15.
27. Hillel D., Hatfield J.L. (Eds.) (2005) Encyclopedia of Soils in the Environment (Vol. 3) Amsterdam: Elsevier.
28. i Guillén R.F., Camarasa J. M. (Eds.) (2000) Encyclopedia of the biosphere: Deciduous forests (Vol. 7) Gale/Cengage Learning.
29. Jacoby R., Peukert M., Succurro A., Koprivova A., Kopriva S. (2017) The role of soil microorganisms in plant mineral nutrition—current knowledge and future directions. Frontiers in Plant Science, 8: 1617.
30. Johnson N.C., Gehring C.A. (2007) Mycorrhizas: symbiotic mediators of rhizosphere and ecosystem processes. In The Rhizosphere, p. 73-100.
31. Jorgensen S.E., Fath B. (2014) Encyclopedia of ecology. Newnes.

32. Karimi B., Maron P.A., Boure N.C.P., Bernard N., Gilbert D., Ranjard L. (2017) Microbial diversity and ecological networks as indicators of environmental quality. Environmental Chemistry Letters, 15(2): 265-281.
33. Kennedy A.C., Gewin V.L. (1997) Soil microbial diversity: present and future considerations. Soil Science, 162(9): 607-617.
34. Koorem K., Gazol A., Öpik M., Moora M., Saks Ü., Uibopuu A., Zobel M. (2014) Soil nutrient content influences the abundance of soil microbes but not plant biomass at the small-scale. PLoS One, 9(3): e91998.
35. Lange M., Habekost M., Eisenhauer N., Roscher C., Bessler H., Engels C., Gleixner G. (2014) Biotic and abiotic properties mediating plant diversity effects on soil microbial communities in an experimental grassland. PloS one, 9(5): e96182.
36. Lartey R.T. (2006) Dynamics of soil flora and fauna in biological control of soil inhabiting plant pathogens. Plant Pathol. J, 5: 125-142.
37. Le Roux X., Poly F., Currey P., Commeaux C., Hai B., Nicol G. W., ... Klumpp K. (2008) Effects of aboveground grazing on coupling among nitrifier activity, abundance and community structure. The ISME journal, 2(2): 221.
38. Lv X., Yu J., Fu Y., Ma B., Qu F., Ning K., Wu H. (2014) A meta-analysis of the bacterial and archaeal diversity observed in wetland soils. The Scientific World Journal.
39. Maboreke H.R., Bartel V., Seiml-Buchinger R., Ruess L. (2018) Micro-Food Web Structure Shapes Rhizosphere Microbial Communities and Growth in Oak. Diversity, 10(1): 15.
40. Maheshwari D.K. (Ed.) (2010) Plant growth and health promoting bacteria (Vol. 18) Springer Science & Business Media.
41. Meliani A., Bensoltane A., Mederbel K. (2012) Microbial diversity and abundance in soil: related to plant and soil type. American Journal of Plant Nutrition and Fertilization Technology, 2(1): 10-18.
42. Nolan N.E., Kulmatiski A., Beard K.H., Norton J.M. (2015) Activated carbon decreases invasive plant growth by mediating plant–microbe interactions. AoB Plants, 7.
43. Panpatte D.G., Jhala Y.K., Vyas R.V., Shelat H.N. (Eds.)(2017) Microorganisms for Green Revolution.
44. Paul E.A. (2014) Soil microbiology, ecology and biochemistry. Academic press.

45. Philippot L., Raaijmakers J.M., Lemanceau P., Van Der Putten W.H. (2013) Going back to the roots: the microbial ecology of the rhizosphere. Nature Reviews Microbiology, 11(11): 789.
46. Ponomarova O., Patil K.R. (2015) Metabolic interactions in microbial communities: untangling the Gordian knot. Current opinion in microbiology, 27: 37-44.
47. Reitner J., Thiel V. (Eds.) (2011) Encyclopedia of geobiology. Dordrecht: Springer.
48. Rillig M.C., Mummey D.L. (2006) Mycorrhizas and soil structure. New Phytologist, 171(1): 41-53.
49. Santi C., Bogusz D., Franche C. (2013) Biological nitrogen fixation in non-legume plants. Annals of botany, 111(5): 743-767.
50. Sayer E.J. (2006) Using experimental manipulation to assess the roles of leaf litter in the functioning of forest ecosystems. Biological reviews, 81(1): 1-31.
51. Schulz S., Brankatschk R., Dümig A., Kögel-Knabner I., Schloter M., Zeyer J. (2013) The role of microorganisms at different stages of ecosystem development for soil formation. Biogeosciences, 10(6): 3983-3996.
52. Siles J.A., Margesin R. (2017) Seasonal soil microbial responses are limited to changes in functionality at two Alpine forest sites differing in altitude and vegetation. Scientific Reports, 7(1): 2204.
53. Smith S.E., Read D.J. (1997) Structure and development of ectomycorrhizal roots. Mycorrrhizal symbiosis. Academic Press, London, 163-232.
54. Steinauer K., Chatzinotas A., Eisenhauer N. (2016) Root exudate cocktails: the link between plant diversity and soil microorganisms? Ecology and evolution, 6(20): 7387-7396.
55. Taylor T.N., Krings M., Taylor E.L. (2014) Fossil fungi. Academic Press.
56. Truu M., Juhanson J., Truu J. (2009) Microbial biomass, activity and commun
57. Tu Q., Zhou X., He Z., Xue K., Wu L., Reich P., Zhou J. (2016) The diversity and co-occurrence patterns of N 2-fixing communities in a CO 2-enriched grassland ecosystem. Microbial ecology, 71(3): 604-615.
58. Uddin M.N., Robinson R.W. (2017) Responses of plant species diversity and soil physical-chemical-microbial properties to Phragmites australis invasion along a density gradient. Scientific reports, 7(1): 11007.

59. Ward B.B. (2011) Nitrification: an introduction and overview of the state of the field. In Nitrification (pp. 3-8) American Society of Microbiology.
60. Wehn S., Taugourdeau S., Johansen L., Hovstad K.A. (2017) Effects of abandonment on plant diversity in semi-natural grasslands along soil and climate gradients. Journal of Vegetation Science.
61. Wei Z., Hu X., Li X., Zhang Y., Jiang L., Li J., Liao X. (2017) The rhizospheric microbial community structure and diversity of deciduous and evergreen forests in Taihu Lake area, China. PloS one, 12(4): e0174411.
62. Wohlgemuth D., Solan M., Godbold J. A. (2016) Specific arrangements of species dominance can be more influential than evenness in maintaining ecosystem process and function. Scientific reports, 6: 39325.
63. Yan H., Liang C., Li Z., Liu Z., Miao B., He C., Sheng L. (2015) Impact of precipitation patterns on biomass and species richness of annuals in a dry steppe. PloS one, 10(4): e0125300.
64. Yashiro E., Pinto-Figueroa E., Buri A., Spangenberg J.E., Adatte T., Niculita-Hirzel H., van der Meer J. R. (2016) Local environmental factors drive divergent grassland soil bacterial communities in the western Swiss Alps. Applied and environmental microbiology, 82(21): 6303-6316.
65. Yun Y., Wang H., Man B., Xiang X., Zhou J., Qiu X., Engel A. S. (2016) The Relationship between pH and Bacterial Communities in a Single Karst Ecosystem and Its Implication for Soil Acidification. Frontiers in microbiology, 7: 1955.
66. Zhang Q., Wu J., Yang F., Lei Y., Zhang Q., Cheng X. (2016) Alterations in soil microbial community composition and biomass following agricultural land use change. Scientific reports, 6: 36587.
67. Zuo X.A., Knops J.M.H., Zhao X.Y., Zhao H.L., Zhang T.H., Li Y.Q., Guo Y.R. (2012) Indirect drivers of plant diversity-productivity relationship in semiarid sandy grasslands. Biogeosciences, 9(4): 1277.